

# Sequence Listing

- <110> Ashkenazi, Avi  
 Baker Kevin P.  
 Botstein, David  
 Desnoyers, Luc  
 Eaton, Dan  
 Ferrara, Napoleon  
 Filvaroff, Ellen  
 Fong, Sherman  
 Gao, Wei-Qiang  
 Gerber, Hanspeter  
 Gerritsen, Mary E.  
 Goddard, Audrey  
 Godowski, Paul J.  
 Grimaldi, J. Christopher  
 Gurney, Austin L.  
 Hillan, Kenneth J.  
 Kljavin, Ivar J.  
 Kuo, Sophia S.  
 Napier, Mary A.  
 Pan, James;  
 Paoni, Nicholas F.  
 Roy, Margaret Ann  
 Shelton, David L.  
 Stewart, Timothy A.  
 Tumas, Daniel  
 Williams, P. Mickey  
 Wood, William I.
- <120> Secreted and Transmembrane Polypeptides and Nucleic  
 Acids Encoding the Same
- <130> P2630P1C9
- <150> 09/918585  
 <151> 2001-07-30
- <150> 60/062250  
 <151> 1997-10-17
- <150> 60/064249  
 <151> 1997-11-03
- <150> 60/065311  
 <151> 1997-11-13
- <150> 60/066364  
 <151> 1997-11-21
- <150> 60/077450  
 <151> 1998-03-10
- <150> 60/077632  
 <151> 1998-03-11
- <150> 60/077641  
 <151> 1998-03-11

09978192 101501

<150> 60/077649  
<151> 1998-03-11

<150> 60/077791  
<151> 1998-03-12

<150> 60/078004  
<151> 1998-03-13

<150> 60/078886  
<151> 1998-03-20

<150> 60/078936  
<151> 1998-03-20

<150> 60/078910  
<151> 1998-03-20

<150> 60/078939  
<151> 1998-03-20

<150> 60/079294  
<151> 1998-03-25

<150> 60/079656  
<151> 1998-03-26

<150> 60/079664  
<151> 1998-03-27

<150> 60/079689  
<151> 1998-03-27

<150> 60/079663  
<151> 1998-03-27

<150> 60/079728  
<151> 1998-03-27

<150> 60/079786  
<151> 1998-03-27

<150> 60/079920  
<151> 1998-03-30

<150> 60/079923  
<151> 1998-03-30

<150> 60/080105  
<151> 1998-03-31

<150> 60/080107  
<151> 1998-03-31

<150> 60/080165  
<151> 1998-03-31

<150> 60/080194

05978192.101501

<151> 1998-03-31  
<150> 60/080327  
<151> 1998-04-01  
  
<150> 60/080328  
<151> 1998-04-01  
  
<150> 60/080333  
<151> 1998-04-01  
  
<150> 60/080334  
<151> 1998-04-01  
  
<150> 60/081070  
<151> 1998-04-08  
  
<150> 60/081049  
<151> 1998-04-08  
  
<150> 60/081071  
<151> 1998-04-08  
  
<150> 60/081195  
<151> 1998-04-08  
  
<150> 60/081203  
<151> 1998-04-09  
  
<150> 60/081229  
<151> 1998-04-09  
  
<150> 60/081955  
<151> 1998-04-15  
  
<150> 60/081817  
<151> 1998-04-15  
  
<150> 60/081819  
<151> 1998-04-15  
  
<150> 60/081952  
<151> 1998-04-15  
  
<150> 60/081838  
<151> 1998-04-15  
  
<150> 60/082568  
<151> 1998-04-21  
  
<150> 60/082569  
<151> 1998-04-21  
  
<150> 60/082704  
<151> 1998-04-22  
  
<150> 60/082804  
<151> 1998-04-22

<150> 60/082700  
<151> 1998-04-22

<150> 60/082797  
<151> 1998-04-22

<150> 60/082796  
<151> 1998-04-23

<150> 60/083336  
<151> 1998-04-27

<150> 60/083322  
<151> 1998-04-28

<150> 60/083392  
<151> 1998-04-29

<150> 60/083495  
<151> 1998-04-29

<150> 60/083496  
<151> 1998-04-29

<150> 60/083499  
<151> 1998-04-29

<150> 60/083545  
<151> 1998-04-29

<150> 60/083554  
<151> 1998-04-29

<150> 60/083558  
<151> 1998-04-29

<150> 60/083559  
<151> 1998-04-29

<150> 60/083500  
<151> 1998-04-29

<150> 60/083742  
<151> 1998-04-30

<150> 60/084366  
<151> 1998-05-05

<150> 60/084414  
<151> 1998-05-06

<150> 60/084441  
<151> 1998-05-06

<150> 60/084637  
<151> 1998-05-07

<150> 60/084639



<151> 1998-05-07  
 <150> 60/084640  
 <151> 1998-05-07  
 <150> 60/084598  
 <151> 1998-05-07  
 <150> 60/084600  
 <151> 1998-5-07  
 <150> 60/084627  
 <151> 1998-05-07  
 <150> 60/084643  
 <151> 1998-05-07  
 <150> 60/085339  
 <151> 1998-05-13  
 <150> 60/085338  
 <151> 1998-05-13  
 <150> 60/085323  
 <151> 1998-05-13  
 <150> 60/085582  
 <151> 1998-05-15  
 <150> 60/085700  
 <151> 1998-05-15  
 <150> 60/085689  
 <151> 1998-05-15  
 <150> 60/085579  
 <151> 1998-05-15  
 <150> 60/085580  
 <151> 1998-05-15  
 <150> 60/085573  
 <151> 1998-05-15  
 <150> 60/085704  
 <151> 1998-05-15  
 <150> 60/085697  
 <151> 1998-05-15  
 <150> 60/086023  
 <151> 1998-05-18  
 <150> 60/086430  
 <151> 1998-05-22  
 <150> 60/086392  
 <151> 1998-05-22

<150> 60/086486  
<151> 1998-05-22

<150> 60/086414  
<151> 1998-05-22

<150> 60/087208  
<151> 1998-05-28

<150> 60/087106  
<151> 1998-05-28

<150> 60/087098  
<151> 1998-05-28

<150> 60/091010  
<151> 1998-06-26

<150> 60/090863  
<151> 1998-06-26

<150> 60/091359  
<151> 1998-07-01

<150> 60/094651  
<151> 1998-07-30

<150> 60/100038  
<151> 1998-09-11

<150> 60/109304  
<151> 1998-11-20

<150> 60/113296  
<151> 1998-12-22

<150> 60/113621  
<151> 1998-12-23

<150> 60/123957  
<151> 1999-03-12

<150> 60/126773  
<151> 1999-03-29

<150> 60/130232  
<151> 1999-04-21

<150> 60/131022  
<151> 1999-04-26

<150> 60/131445  
<151> 1999-04-28

<150> 60/134287  
<151> 1999-05-14

<150> 60/139557

<151> 1999-06-16  
 <150> 60/141037  
 <151> 1999-06-23  
 <150> 60/142680  
 <151> 1999-07-07  
 <150> 60/145698  
 <151> 1999-07-26  
 <150> 60/146222  
 <151> 1999-07-28  
 <150> 60/162506  
 <151> 1999-10-29  
 <150> 09/040220  
 <151> 1998- 03-17  
 <150> 09/105413  
 <151> 1998-06-26  
 <150> 09/168978  
 <151> 1998-10-07  
 <150> 09/184216  
 <151> 1998-11-02  
 <150> 09/187368  
 <151> 1998-11-06  
 <150> 09/202054  
 <151> 1998-12-07  
 <150> 09/218517  
 <151> 1998-12-22  
 <150> 09/254465  
 <151> 1999-03-05  
 <150> 09/265686  
 <151> 1999-03-10  
 <150> 09/267213  
 <151> 1999-03-12  
 <150> 09/284291  
 <151> 1999-04-12  
 <150> 09/311832  
 <151> 1999-05-14  
 <150> 09/380137  
 <151> 1999-08-25  
 <150> 09/380138  
 <151> 1999-08-25

<150> 09/380142  
<151> 1999-08-25

<150> 09/709238  
<151> 2000-11-08

<150> 09/723749  
<151> 2000-11-27

<150> 09/747259  
<151> 2000-12-20

<150> 09/816744  
<151> 2001-03-22

<150> 09/816920  
<151> 2001-03-22

<150> 09/854280  
<151> 2001-05-10

<150> 09/854208  
<151> 2001-05-10

<150> 09/872035  
<151> 2001-06-01

<150> 09/874503  
<151> 2001-06-05

<150> 09/882636  
<151> 2001-06-14

<150> 09/886342  
<151> 2001- 06-19

<150> PCT/US98/21141  
<151> 1998-10-07

<150> PCT/US98/24855  
<151> 1998-11-20

<150> PCT/US99/00106  
<151> 1999-01-05

<150> PCT/US99/05028  
<151> 1999-03-08

<150> PCT/US99/05190  
<151> 1999-03-10

<150> PCT/US99/10733  
<151> 1999-05-14

<150> PCT/US99/12252  
<151> 1999-06-02

<150> PCT/US99/28313

<151> 1999-11-30

<150> PCT/US99/28551  
<151> 1999-12-02

<150> PCT/US99/28565  
<151> 1999-12-02

<150> PCT/US99/30095  
<151> 1999-12-16

<150> PCT/US99/31243  
<151> 1999-12-30

<150> PCT/US99/31274  
<151> 1999-12-30

<150> PCT/US00/00219  
<151> 2000-05-01

<150> PCT/US00/00277  
<151> 2000-01-06

<150> PCT/US00/00376  
<151> 2000-01-06

<150> PCT/US00/03565  
<151> 2000-02-11

<150> PCT/US00/04341  
<151> 2000-02-18

<150> PCT/US00/05841  
<151> 2000-03-02

<150> PCT/US00/07532  
<151> 2000-03-21

<150> PCT/US00/05004  
<151> 2000-02-24

<150> PCT/US00/06319  
<151> 2000-03-10

<150> PCT/US00/08439  
<151> 2000-03-30

<150> PCT/US00/13705  
<151> 2000-05-17

<150> PCT/US00/14042  
<151> 2000-05-22

<150> PCT/US00/14941  
<151> 2000-05-30

<150> PCT/US00/15264  
<151> 2000-06-02

<150> PCT/US00/20710  
<151> 2000-07-28

<150> PCT/US00/23328  
<151> 2000-08-24

<150> PCT/US00/32678  
<151> 2000-12-01

<150> PCT/US00/34956  
<151> 2000-12-20

<150> PCT/US01/06520  
<151> 2001-02-28

<150> PCT/US01/09552  
<151> 2001-03-22

<150> PCT/US01/17092  
<151> 2001-05-25

<150> PCT/US01/17800  
<151> 2001-06-01

<150> PCT/US01/19692  
<151> 2001-06-20

<150> PCT/US01/21066  
<151> 2001-06-29

<150> PCT/US01/21735  
<151> 2001-07-09

<160> 624

<210> 1  
<211> 1743  
<212> DNA  
<213> Homo sapiens

<400> 1  
ccaggtccaa ctgcacctcg gttctatcga ttgaattccc cggggaccc 50  
ctagagatcc ctgcacctcg acccacgcgt ccgccaagct ggccctgcac 100  
ggctgcaagg gagggctcctg tggacaggcc aggcagggtg gcctcaggag 150  
gtgcctccag gcggccagtg ggccctgagc cccagcaagg gctagggtcc 200  
atctccagtc ccaggacaca gcagcggcca ccatggccac gcctgggctc 250  
cagcagcatc agcagccccc aggaccgggg gaggcacagg tggccccac 300  
caccggagg agcagctcct gccctgtcc gggggatgac tgattctcct 350  
ccgccaggcc acccagagga gaaggccacc ccgcctggag gcacaggcca 400  
tgaggggctc tcaggaggtg ctgctgatgt ggcttctggt gttggcagt 450

ggcggcacag agcacgccta ccggcccggc cgtaggggtg tgtgctgtcc 500  
 cgggctcacg gggaccctgt ctccgagtcg ttcgtgcagc gtgtgtacca 550  
 gcccttcctc accacctgcg acggggcaccg ggctgcagc acctaccgaa 600  
 ccatttatag gaccgcctac cgccgcagcc ctgggctggc ccctgccagg 650  
 cctcgctacg cgtgctgccc cggctggaag aggaccagcg ggcttcctgg 700  
 ggctgtgga gcagcaatat gccagccgcc atgccggaac ggagggagct 750  
 gtgtccagcc tggccgctgc cgctgccctg caggatggcg gggtgacact 800  
 tgccagtcag atgtggatga atgcagtgt aggaggggagc gctgtcccca 850  
 gcgctgcac aacaccgccg gcagttactg gtgccagtgt tgggaggggc 900  
 acagcctgtc tgcagacggt aactctgtg tgcccaaggg agggccccc 950  
 aggggtggccc ccaaccgcagc aggagtggac agtgcaatga aggaagaagt 1000  
 gcagaggctg cagtccaggg tggacctgct ggaggagaag ctgcagctgg 1050  
 tgctggcccc actgcacagc ctggcctcgc aggactgga gcatgggctc 1100  
 ccggagccccg gcagcctcct ggtgcactcc ttccagcagc tcggccgcat 1150  
 cgactccctg agcagcaga tttccttcct ggaggagcag ctggggctcct 1200  
 gctcctgcaa gaaagactcg tgactgcca gcgcccagg ctggactgag 1250  
 cccctcacgc cgccctgcag ccccatgcc cctgcccaac atgctggggg 1300  
 tccagaagcc acctcggggt gactgagcgg aaggccaggc agggccttcc 1350  
 tccttttctc cctccccttc cctcgggagg gtccccagac cctggcatgg 1400  
 gatgggctgg gatTTTTTTT gtgaatccac ccctggctac cccaccctg 1450  
 gttaccccaa cggcatccca aggccagggt ggccctcagc tgaggggaagg 1500  
 tacgagttcc cctgctggag cctgggaccc atggcacagg ccaggcagcc 1550  
 cggaggctgg gtggggcctc agtgggggct gctgcctgac cccagcaca 1600  
 ataaaaatga aacgtgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
 aaaaaaaagg gcggccgcga ctctagagtc gacctgcaga agcttggccg 1700  
 ccatggccca acttgtttat tgcagcttat aatggttaca aat 1743

<210> 2  
 <211> 295  
 <212> PRT  
 <213> Homo sapiens  
 <400> 2

Met	Thr	Asp	Ser	Pro	Pro	Pro	Gly	His	Pro	Glu	Glu	Lys	Ala	Thr	
1				5					10					15	
Pro	Pro	Gly	Gly	Thr	Gly	His	Glu	Gly	Leu	Ser	Gly	Gly	Ala	Ala	
				20					25					30	
Asp	Val	Ala	Ser	Gly	Val	Gly	Ser	Gly	Arg	His	Arg	Ala	Arg	Leu	
				35					40					45	
Pro	Ala	Arg	Pro	Leu	Gly	Cys	Val	Leu	Ser	Arg	Ala	His	Gly	Asp	
				50					55					60	
Pro	Val	Ser	Glu	Ser	Phe	Val	Gln	Arg	Val	Tyr	Gln	Pro	Phe	Leu	
				65					70					75	
Thr	Thr	Cys	Asp	Gly	His	Arg	Ala	Cys	Ser	Thr	Tyr	Arg	Thr	Ile	
				80					85					90	
Tyr	Arg	Thr	Ala	Tyr	Arg	Arg	Ser	Pro	Gly	Leu	Ala	Pro	Ala	Arg	
				95					100					105	
Pro	Arg	Tyr	Ala	Cys	Cys	Pro	Gly	Trp	Lys	Arg	Thr	Ser	Gly	Leu	
				110					115					120	
Pro	Gly	Ala	Cys	Gly	Ala	Ala	Ile	Cys	Gln	Pro	Pro	Cys	Arg	Asn	
				125					130					135	
Gly	Gly	Ser	Cys	Val	Gln	Pro	Gly	Arg	Cys	Arg	Cys	Pro	Ala	Gly	
				140					145					150	
Trp	Arg	Gly	Asp	Thr	Cys	Gln	Ser	Asp	Val	Asp	Glu	Cys	Ser	Ala	
				155					160					165	
Arg	Arg	Gly	Gly	Cys	Pro	Gln	Arg	Cys	Ile	Asn	Thr	Ala	Gly	Ser	
				170					175					180	
Tyr	Trp	Cys	Gln	Cys	Trp	Glu	Gly	His	Ser	Leu	Ser	Ala	Asp	Gly	
				185					190					195	
Thr	Leu	Cys	Val	Pro	Lys	Gly	Gly	Pro	Pro	Arg	Val	Ala	Pro	Asn	
				200					205					210	
Pro	Thr	Gly	Val	Asp	Ser	Ala	Met	Lys	Glu	Glu	Val	Gln	Arg	Leu	
				215					220					225	
Gln	Ser	Arg	Val	Asp	Leu	Leu	Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	
				230					235					240	
Ala	Pro	Leu	His	Ser	Leu	Ala	Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	
				245					250					255	
Pro	Asp	Pro	Gly	Ser	Leu	Leu	Val	His	Ser	Phe	Gln	Gln	Leu	Gly	
				260					265					270	
Arg	Ile	Asp	Ser	Leu	Ser	Glu	Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	
				275					280					285	
Leu	Gly	Ser	Cys	Ser	Cys	Lys	Lys	Asp	Ser						



<210> 3  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 3  
 tggagcagca atatgccagc c 21

<210> 4  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 4  
 ttttcactc ctgtcgggtt gg 22

<210> 5  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 5  
 ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 6  
 <211> 2945  
 <212> DNA  
 <213> Homo sapiens

<400> 6  
 cgctcgcccc gtgcgcccct gcctccccgc agagtcccct cgcggcagca 50  
 gatgtgtgtg gggtcagccc acggcgggga ctatggtgaa attcccggcg 100  
 ctcacgcact actggcccct gatccggttc ttggtgcccc tgggcatcac 150  
 caacatagcc atcgacttgc gggagcaggc cttgaaccgg ggcattgctg 200  
 ctgtcaagga ggatgcagtc gagatgctgg ccagctacgg gctggcgtag 250  
 tccctcatga agttcttcac ggggcccatg agtgacttca aaaatgtggg 300  
 cctggtgttt gtgaacagca agagagacag gaccaaagcc gtccgtgtga 350  
 tgggtggtggc agggggccatc gctgccgtct ttcacacact gatagcttat 400  
 agtgatttag gatactacat tatcaataaa ctgcaccatg tggacgagtc 450

ggtggggagc aagacgagaa gggccttctt gtacctcgcc gcctttcctt 500  
 tcatggacgc aatggcatgg acccatgctg gcattctctt aaaacacaaa 550  
 tacagtttcc tgggtgggatg tgccatcaatc tcagatgtca tagctcaggt 600  
 tgtttttgta gccattttgc ttcacagtca cctggaatgc cgggagcccc 650  
 tgctcatccc gatcctctcc ttgtacatgg gcgcacttgt gcgctgcacc 700  
 accctgtgcc tgggctacta caagaacatt cacgacatca tccctgacag 750  
 aagtggcccc gagctggggg gagatgcaac aataagaaag atgctgagct 800  
 tctggtggcc tttggctcta attctggcca cacagagaat cagtcggcct 850  
 attgtcaacc tctttgtttc ccgggacctt ggtggcagtt ctgcagccac 900  
 agaggcagtg gcgattttga cagccacata ccctgtgggt cacatgccat 950  
 acggctgggtt gacggaaatc cgtgctgtgt atcctgcttt cgacaagaat 1000  
 aaccccgca acaaactggg gagcacgagc aacacagtca cggcagccca 1050  
 catcaagaag ttcaccttcg tctgcatggc tctgtcactc acgctctgtt 1100  
 tcgtgatgtt ttggacaccc aacgtgtctg agaaaatctt gatagacatc 1150  
 atcggagtgg actttgcctt tgcagaactc tgtgttggtc ctttgcggt 1200  
 cttctccttc ttcccagttc cagtcacagt gagggcgcat ctcaccgggt 1250  
 ggctgatgac actgaagaaa accttcgtcc ttgccccag ctctgtgctg 1300  
 cggatcatcg tcctcatcgc cagcctcgtg gtccatccct acctgggggt 1350  
 gcacgggtgcg accctgggag tgggctccct cctggcgggc tttgtgggag 1400  
 aatccacat ggctgcacat gctgcgtgct atgtctaccg gaagcagaaa 1450  
 aagaagatgg agaatgagtc ggccacggag ggggaagact ctgccatgac 1500  
 agacatgcct ccgacagagg aggtgacaga catcgtggaa atgagagagg 1550  
 agaatgaata aggcacggga cgccatgggc actgcaggga cggtcagtca 1600  
 ggatgacact tcggcatcat ctcttccctc tccatcgta tttgttccc 1650  
 tttttttgt tttgttttg taatgaaaga ggccttgatt taaaggtttc 1700  
 gtgtcaattc tctagcatac tgggtatgct cacactgacg gggggacct 1750  
 gtgaatggtc tttactgttg ctatgtaaaa aaaaacgaaa caactgactt 1800  
 catacccctg cctcacgaaa acccaaaaga cacagctgcc tcacggttga 1850  
 cgttgtgtcc tcctcccctg gacaatctcc tcttgaacc aaaggactgc 1900

agctgtgcc a tcgcgcctcg gtcaccctgc acagcaggcc acagactctc 1950  
ctgtccccct tcatcgctct taagaatcaa cagggttaaaa ctcggttcc 2000  
tttgatttgc ttcccagtca catggccgta caaagagatg gagccccggt 2050  
ggcctcttaa atttcccttc tgccacggag ttcgaaacca tctactccac 2100  
acatgcagga ggcgggtggc acgctgcagc ccggagtccc cggtcacact 2150  
gaggaacgga gacctgtgac cacagcaggc tgacagatgg acagaatctc 2200  
ccgtagaaaag gtttggtttg aaatgccccg ggggcagcaa actgacatgg 2250  
ttgaatgata gcatttcact ctgcgttctc ctagatctga gcaagctgtc 2300  
agttctcacc cccaccgtgt atatacatga gctaactttt ttaaattgtc 2350  
acaaaagcgc atctccagat tccagaccct gccgcatgac ttttctgaa 2400  
ggcttgcttt tccctcgctt ttctgaagg tcgcattaga gcgagtcaca 2450  
tgagcatcc taactttgca ttttagtttt tacagtgaac tgaagcttta 2500  
agtctcatcc agcattctaa tgccagggtg ctgtagggta acttttgaag 2550  
tagatatatt acctggttct gctatcctta gtcataactc tgcggtacag 2600  
gtaattgaga atgtactacg gtacttccct cccacaccat acgataaagc 2650  
aagacatttt ataacgatac cagagtcact atgtggtcct ccctgaaata 2700  
acgcattcga aatccatgca gtgcagtata tttttctaag ttttggaag 2750  
cagggttttt cctttaaaaa aattatagac acggttcact aaattgattt 2800  
agtcagaatt cctagactga aagaacctaa acaaaaaaat attttaaaga 2850  
tataaatata tgctgtatat gttatgtaat ttattttagg ctataataca 2900  
tttctatttt tcgcattttc aataaaatgt ctctaataca aaaaa 2945

<210> 7  
<211> 492  
<212> PRT  
<213> Homo sapiens

<400> 7  
Met Val Lys Phe Pro Ala Leu Thr His Tyr Trp Pro Leu Ile Arg  
1 5 10 15  
Phe Leu Val Pro Leu Gly Ile Thr Asn Ile Ala Ile Asp Phe Gly  
20 25 30  
Glu Gln Ala Leu Asn Arg Gly Ile Ala Ala Val Lys Glu Asp Ala  
35 40 45  
Val Glu Met Leu Ala Ser Tyr Gly Leu Ala Tyr Ser Leu Met Lys

50										55					60				
Phe	Phe	Thr	Gly	Pro	Met	Ser	Asp	Phe	Lys	Asn	Val	Gly	Leu	Val					
				65					70					75					
Phe	Val	Asn	Ser	Lys	Arg	Asp	Arg	Thr	Lys	Ala	Val	Leu	Cys	Met					
				80					85					90					
Val	Val	Ala	Gly	Ala	Ile	Ala	Ala	Val	Phe	His	Thr	Leu	Ile	Ala					
				95					100					105					
Tyr	Ser	Asp	Leu	Gly	Tyr	Tyr	Ile	Ile	Asn	Lys	Leu	His	His	Val					
				110					115					120					
Asp	Glu	Ser	Val	Gly	Ser	Lys	Thr	Arg	Arg	Ala	Phe	Leu	Tyr	Leu					
				125					130					135					
Ala	Ala	Phe	Pro	Phe	Met	Asp	Ala	Met	Ala	Trp	Thr	His	Ala	Gly					
				140					145					150					
Ile	Leu	Leu	Lys	His	Lys	Tyr	Ser	Phe	Leu	Val	Gly	Cys	Ala	Ser					
				155					160					165					
Ile	Ser	Asp	Val	Ile	Ala	Gln	Val	Val	Phe	Val	Ala	Ile	Leu	Leu					
				170					175					180					
His	Ser	His	Leu	Glu	Cys	Arg	Glu	Pro	Leu	Leu	Ile	Pro	Ile	Leu					
				185					190					195					
Ser	Leu	Tyr	Met	Gly	Ala	Leu	Val	Arg	Cys	Thr	Thr	Leu	Cys	Leu					
				200					205					210					
Gly	Tyr	Tyr	Lys	Asn	Ile	His	Asp	Ile	Ile	Pro	Asp	Arg	Ser	Gly					
				215					220					225					
Pro	Glu	Leu	Gly	Gly	Asp	Ala	Thr	Ile	Arg	Lys	Met	Leu	Ser	Phe					
				230					235					240					
Trp	Trp	Pro	Leu	Ala	Leu	Ile	Leu	Ala	Thr	Gln	Arg	Ile	Ser	Arg					
				245					250					255					
Pro	Ile	Val	Asn	Leu	Phe	Val	Ser	Arg	Asp	Leu	Gly	Gly	Ser	Ser					
				260					265					270					
Ala	Ala	Thr	Glu	Ala	Val	Ala	Ile	Leu	Thr	Ala	Thr	Tyr	Pro	Val					
				275					280					285					
Gly	His	Met	Pro	Tyr	Gly	Trp	Leu	Thr	Glu	Ile	Arg	Ala	Val	Tyr					
				290					295					300					
Pro	Ala	Phe	Asp	Lys	Asn	Asn	Pro	Ser	Asn	Lys	Leu	Val	Ser	Thr					
				305					310					315					
Ser	Asn	Thr	Val	Thr	Ala	Ala	His	Ile	Lys	Lys	Phe	Thr	Phe	Val					
				320					325					330					
Cys	Met	Ala	Leu	Ser	Leu	Thr	Leu	Cys	Phe	Val	Met	Phe	Trp	Thr					
				335					340					345					

Pro Asn Val Ser Glu Lys Ile Leu Ile Asp Ile Ile Gly Val Asp	350	355	360
Phe Ala Phe Ala Glu Leu Cys Val Val Pro Leu Arg Ile Phe Ser	365	370	375
Phe Phe Pro Val Pro Val Thr Val Arg Ala His Leu Thr Gly Trp	380	385	390
Leu Met Thr Leu Lys Lys Thr Phe Val Leu Ala Pro Ser Ser Val	395	400	405
Leu Arg Ile Ile Val Leu Ile Ala Ser Leu Val Val Leu Pro Tyr	410	415	420
Leu Gly Val His Gly Ala Thr Leu Gly Val Gly Ser Leu Leu Ala	425	430	435
Gly Phe Val Gly Glu Ser Thr Met Val Ala Ile Ala Ala Cys Tyr	440	445	450
Val Tyr Arg Lys Gln Lys Lys Lys Met Glu Asn Glu Ser Ala Thr	455	460	465
Glu Gly Glu Asp Ser Ala Met Thr Asp Met Pro Pro Thr Glu Glu	470	475	480
Val Thr Asp Ile Val Glu Met Arg Glu Glu Asn Glu	485	490	

<210> 8  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens  
 <220>  
 <221> unsure  
 <222> 33, 66, 96, 387  
 <223> unknown base

<400> 8  
 cctgacagaa gtgccccgga gctgggggag atncaacatt aagaagatgc 50  
 tgagcttctg gtgccttttg gctctaattc tggccacaca gagaancagt 100  
 cggcctattg tcaacctctt tgtttcccg gaccttggtg gcagttctgc 150  
 agccacagag gcagtggcga ttttgacagc cacataccct gtgggtcaca 200  
 tgccatacgg ctggttgacg gaaatccgtg ctgtgtatcc tgctttcgac 250  
 aagaataacc ccagcaacaa actggtgagc acgagcaaca cagtcacggc 300  
 ggccacatc aagaagttca ccttcgtctg catggctctg tcaactcacgc 350  
 tctgtttcgt gatgttttgg acaccaacg tgtctgngaa aatcttgata 400  
 gacatcatcg gagtggactt tgcctttgca gaactctgtg ttgttccttt 450

gcggatcttc tcctttcttcc cagttccagt cacagtgagg gcgcattctca 500

cgggtgggt gatgacactg aagaaaacct tcgtc 535

<210> 9

<211> 434

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 32, 54, 80, 111, 117, 122, 139, 193, 205, 221, 226, 228, 273, 293, 296, 305, 336, 358, 361

<223> unknown base

<400> 9

tgacggaatc cggggtggg tatcctgggt tngacaagat aaacccccag 50

caanaaattg gggagcaggg caaaacagtn acgggcagcc cacatcaaga 100

agttcacctt ngtttgnatg gntctgtcaa ctacgctnt gtttcgtgat 150

gttttgagaca cccaaagtgt ttgagaaaat tttgatagac atnatcggag 200

tggantttgc ctttgcagaa ntttgngntg ttcttttgcg gattttctcc 250

tttttccag ttccagtcac agngagggcg catctcaccg ggnggntgat 300

gacantgaag aaaacctttg tccttgcccc cagctntttg gtgcggatca 350

ttgtcctnat ngccagcctt gtggtcctac cctacctggg ggtgcacggt 400

gcgaccctgg gcgtgggttc cctcctggcg ggca 434

<210> 10

<211> 154

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 33, 49, 68, 83, 90, 98, 119

<223> unknown base

<400> 10

tattcccagt tccggtcacg gggagggcgc atntcaccgg gtggctgang 50

acactgaaga aaaccttngt ctttgcccc agntttgtgn tgcgatnat 100

cgtcctcatc gccagcctng tggctctacc ctacctgggg gtgcacggtg 150

agac 154

<210> 11

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 11  
ctgatccggt tcttggtgcc cctg 24

<210> 12  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 12  
gctctgtcac tcacgctc 18

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 13  
tcattctcttc cctctccc 18

<210> 14  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 14  
ccttccgccg cggagttc 18

<210> 15  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 15  
ggcaaagtcc actccgatga tgct 24

<210> 16  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

```

<400> 16
gcctgctgtg gtcacaggtc tccg 24

<210> 17
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 17
tcggggagca ggccttgaac cggggcattg ctgctgtcaa ggagg 45

<210> 18
<211> 1901
<212> DNA
<213> Homo sapiens

<400> 18
gccccgcgcc cggcgccggg cggccgaagc cgggagccac cgccatgggg 50
gcctgcctgg gagcctgtct cctgtctcage tgcgcgtcct gcctctgcgg 100
ctctgcccc tgcattcctgt gcagctgctg ccccgccagc cgcaactcca 150
ccgtgagccg cctcatcttc acgtttcttc tcttctctgg ggtgctggtg 200
tccatcatta tgctgagccc gggcgtggag agtcagctct acaagctgcc 250
ctgggtgtgt gaggaggggg cgggatccc caccgtcctg cagggccaca 300
tcgactgtgg ctccctgctt ggctaccgag ctgtctaccg catgtgcttc 350
gccacggcgg ccttcttctt cttctttttt accctgtctc tgctctgcgt 400
gagcagcagc cgggaccccc gggctgccat ccagaatggg ttttggttct 450
ttaagttcct gatcctggtg ggcctcaccg tgggtgcott ctacatccct 500
gacggctcct tcaccaacat ctggttctac ttggcgctcg tgggctcctt 550
cctcttcctc ctcatccagc tgggtgctgt catcgacttt gcgcactcct 600
ggaaccagcg gtggctgggc aaggccgagg agtgcgattc ccgtgcctgg 650
tacgcaggcc tcttcttctt cactctcttc ttctacttgc tgtcgatcgc 700
ggcgtggcg ctgatgttca tgtactacac tgagcccagc ggctgccacg 750
agggcaaggt cttcatcagc ctcaacctca ccttctgtgt ctgcgtgtcc 800
atcgtgctg tcttgcccaa ggtccaggac gccagccca actcgggtct 850
gctgcaggcc tcggtcatca ccctctacac catgtttgtc acctggtcag 900
ccctatccag tatccctgaa cagaaatgca acccccattt gccaacccag 950

```



ctgggcaacg agacagttgt ggcaggcccc gagggctatg agacccagtg 1000  
gtgggatgcc ccgagcattg tgggcctcat catcttctc ctgtgcaccc 1050  
tcttcatcag tctgcgctcc tcagaccacc ggcaggtgaa cagcctgatg 1100  
cagaccgagg agtgcccacc tatgctagac gccacacagc agcagcagca 1150  
gcagggtggca gcctgtgagg gccgggcctt tgacaacgag caggacggcg 1200  
tcacctacag ctactccttc ttccatttct gcctggtgct ggccctactg 1250  
cacgtcatga tgacgctcac caactggtac aagcccgggtg agacccggaa 1300  
gatgatcagc acgtggaccg ccgtgtgggt gaagatctgt gccagctggg 1350  
cagggctgct cctctacctg tggaccctgg tagccccact cctcctgcgc 1400  
aaccgcgact tcagctgagg cagcctcaca gcctgccatc tggtgccctc 1450  
tgccacctgg tgccctcagg ctcggtgaca gccaacctgc cccctcccca 1500  
caccaatcag ccaggctgag cccccacccc tgccccagct ccaggacctg 1550  
cccctgagcc gggccttcta gtcgtagtgc cttcagggtc cgaggagcat 1600  
caggctcctg cagagcccca tccccccgcc acaccacac ggtggagctg 1650  
cctcttctct cccctcctcc ctgttgccca tactcagcat ctcgatgaa 1700  
agggctccct tgtcctcagg ctccacggga gcggggctgc tggagagagc 1750  
ggggaactcc caccacagtg gggcatccgg cactgaagcc ctggtgttcc 1800  
tggtcacgtc cccagggga cctgcccc ttctggact tcgtgcctta 1850  
ctgagtctct aagacttttt ctaataaaca agccagtgcg tgtaaaaaaa 1900

a 1901

<210> 19

<211> 457

<212> PRT

<213> Homo sapiens

<400> 19

Met Gly Ala Cys Leu Gly Ala Cys Ser Leu Leu Ser Cys Ala Ser  
1 5 10 15

Cys Leu Cys Gly Ser Ala Pro Cys Ile Leu Cys Ser Cys Cys Pro  
20 25 30

Ala Ser Arg Asn Ser Thr Val Ser Arg Leu Ile Phe Thr Phe Phe  
35 40 45

Leu Phe Leu Gly Val Leu Val Ser Ile Ile Met Leu Ser Pro Gly  
50 55 60

Val	Glu	Ser	Gln	Leu	Tyr	Lys	Leu	Pro	Trp	Val	Cys	Glu	Glu	Gly	65	70	75
Ala	Gly	Ile	Pro	Thr	Val	Leu	Gln	Gly	His	Ile	Asp	Cys	Gly	Ser	80	85	90
Leu	Leu	Gly	Tyr	Arg	Ala	Val	Tyr	Arg	Met	Cys	Phe	Ala	Thr	Ala	95	100	105
Ala	Phe	Phe	Phe	Phe	Phe	Phe	Thr	Leu	Leu	Met	Leu	Cys	Val	Ser	110	115	120
Ser	Ser	Arg	Asp	Pro	Arg	Ala	Ala	Ile	Gln	Asn	Gly	Phe	Trp	Phe	125	130	135
Phe	Lys	Phe	Leu	Ile	Leu	Val	Gly	Leu	Thr	Val	Gly	Ala	Phe	Tyr	140	145	150
Ile	Pro	Asp	Gly	Ser	Phe	Thr	Asn	Ile	Trp	Phe	Tyr	Phe	Gly	Val	155	160	165
Val	Gly	Ser	Phe	Leu	Phe	Ile	Leu	Ile	Gln	Leu	Val	Leu	Leu	Ile	170	175	180
Asp	Phe	Ala	His	Ser	Trp	Asn	Gln	Arg	Trp	Leu	Gly	Lys	Ala	Glu	185	190	195
Glu	Cys	Asp	Ser	Arg	Ala	Trp	Tyr	Ala	Gly	Leu	Phe	Phe	Phe	Thr	200	205	210
Leu	Leu	Phe	Tyr	Leu	Leu	Ser	Ile	Ala	Ala	Val	Ala	Leu	Met	Phe	215	220	225
Met	Tyr	Tyr	Thr	Glu	Pro	Ser	Gly	Cys	His	Glu	Gly	Lys	Val	Phe	230	235	240
Ile	Ser	Leu	Asn	Leu	Thr	Phe	Cys	Val	Cys	Val	Ser	Ile	Ala	Ala	245	250	255
Val	Leu	Pro	Lys	Val	Gln	Asp	Ala	Gln	Pro	Asn	Ser	Gly	Leu	Leu	260	265	270
Gln	Ala	Ser	Val	Ile	Thr	Leu	Tyr	Thr	Met	Phe	Val	Thr	Trp	Ser	275	280	285
Ala	Leu	Ser	Ser	Ile	Pro	Glu	Gln	Lys	Cys	Asn	Pro	His	Leu	Pro	290	295	300
Thr	Gln	Leu	Gly	Asn	Glu	Thr	Val	Val	Ala	Gly	Pro	Glu	Gly	Tyr	305	310	315
Glu	Thr	Gln	Trp	Trp	Asp	Ala	Pro	Ser	Ile	Val	Gly	Leu	Ile	Ile	320	325	330
Phe	Leu	Leu	Cys	Thr	Leu	Phe	Ile	Ser	Leu	Arg	Ser	Ser	Asp	His	335	340	345
Arg	Gln	Val	Asn	Ser	Leu	Met	Gln	Thr	Glu	Glu	Cys	Pro	Pro	Met			

09978192-101501

	350		355		360
Leu Asp Ala Thr	Gln Gln Gln Gln Gln	Gln Val Ala Ala Cys	Glu		
	365		370		375
Gly Arg Ala Phe	Asp Asn Glu Gln Asp	Gly Val Thr Tyr Ser	Tyr		
	380		385		390
Ser Phe Phe His	Phe Cys Leu Val Leu	Ala Ser Leu His Val	Met		
	395		400		405
Met Thr Leu Thr	Asn Trp Tyr Lys Pro	Gly Glu Thr Arg Lys	Met		
	410		415		420
Ile Ser Thr Trp	Thr Ala Val Trp Val	Lys Ile Cys Ala Ser	Trp		
	425		430		435
Ala Gly Leu Leu	Leu Tyr Leu Trp Thr	Leu Val Ala Pro Leu	Leu		
	440		445		450
Leu Arg Asn Arg	Asp Phe Ser				
	455				

<210> 20  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 20  
 gccgcctcat cttcacgttc ttcc 24  
  
 <210> 21  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 21  
 tcatccagct ggtgctgctc 20  
  
 <210> 22  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 22  
 cttcttcac ttctgcctgg 20  
  
 <210> 23  
 <211> 18

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 23  
cctgggcaaa aatgcaac 18

<210> 24  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 24  
caggaatgta gaaggcaccc acgg 24

<210> 25  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 25  
tggcacagat cttcacccac acgg 24

<210> 26  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 26  
tgtccatcat tatgctgagc ccgggcgtgg agagtcagct ctacaagctg 50

<210> 27  
<211> 1351  
<212> DNA  
<213> Homo sapiens

<400> 27  
gagcgaggcc ggggactgaa ggtgtgggtg tcgagccctc tggcagaggg 50  
ttaacctggg tcaaatgcac ggattctcac ctcgtagagt tacgctctcc 100  
cgcggcacgt ccgcgaggac ttgaagtcct gagcgctcaa gtttgtccgt 150  
aggtcgagag aaggccatgg aggtgccgcc accggcaccg cggagctttc 200  
tctgtagagc attgtgccta tttccccgag tctttgctgc cgaagctgtg 250

actgccgatt cggaagtcct tgaggagcgt cagaagcggc ttccctacgt 300  
cccagagccc tattaccggg aatctggatg ggaccgcctc cgggagctgt 350  
ttggcaaaga tgaacagcag agaatttcaa aggaccttgc taatatctgt 400  
aagacggcag ctacagcagg catcattggc tgggtgtatg ggggaatacc 450  
agctttttatt catgctaaac aacaatacat tgagcagagc caggcagaaa 500  
tttatcataa cgggtttgat gctgtgcaat ctgcacatcg tgctgccaca 550  
cgaggcttca ttcgttatgg ctggcgctgg ggttggagaa ctgcagtgtt 600  
tgtgactata ttcaacacag tgaacactag tctgaatgta taccgaaata 650  
aagatgcctt aagccatttt gtaattgcag gagctgtcac gggaagtctt 700  
tttaggataa acgtaggcct gcgtggcctg gtggctggtg gcataattgg 750  
agccttgctg ggcactcctg taggaggcct gctgatggca tttcagaagt 800  
acgctggtga gactgttcag gaaagaaaac agaaggatcg aaaggcactc 850  
catgagctaa aactggaaga gtggaaaggc agactacaag ttactgagca 900  
cctccctgag aaaattgaaa gtagtttacg ggaagatgaa cctgagaatg 950  
atgctaagaa aattgaagca ctgctaaacc ttcctagaaa cccttcagta 1000  
atagataaac aagacaagga ctgaaagtgc tctgaacttg aaactcactg 1050  
gagagctgaa gggagctgcc atgtccgatg aatgccaaca gacaggccac 1100  
tcttttggtca gcctgctgac aaatttaagt gctggtacct gtggtggcag 1150  
tggcttgctc ttgtcttttt cttttctttt taactaagaa tggggctgtt 1200  
gtactctcac tttacttata cttaaattta aatacatact tatgtttgta 1250  
ttaatctatc aatatatgca tacatggata tatccacca cctagatttt 1300  
aagcagtaaa taaaacattt cgcaaaagat taaagttgaa ttttacagtt 1350  
t 1351

<210> 28  
<211> 285  
<212> PRT  
<213> Homo sapiens

<400> 28  
Met Glu Val Pro Pro Pro Ala Pro Arg Ser Phe Leu Cys Arg Ala  
1 5 10 15  
Leu Cys Leu Phe Pro Arg Val Phe Ala Ala Glu Ala Val Thr Ala  
20 25 30

Asp	Ser	Glu	Val	Leu	Glu	Glu	Arg	Gln	Lys	Arg	Leu	Pro	Tyr	Val	35	40	45
Pro	Glu	Pro	Tyr	Tyr	Pro	Glu	Ser	Gly	Trp	Asp	Arg	Leu	Arg	Glu	50	55	60
Leu	Phe	Gly	Lys	Asp	Glu	Gln	Gln	Arg	Ile	Ser	Lys	Asp	Leu	Ala	65	70	75
Asn	Ile	Cys	Lys	Thr	Ala	Ala	Thr	Ala	Gly	Ile	Ile	Gly	Trp	Val	80	85	90
Tyr	Gly	Gly	Ile	Pro	Ala	Phe	Ile	His	Ala	Lys	Gln	Gln	Tyr	Ile	95	100	105
Glu	Gln	Ser	Gln	Ala	Glu	Ile	Tyr	His	Asn	Arg	Phe	Asp	Ala	Val	110	115	120
Gln	Ser	Ala	His	Arg	Ala	Ala	Thr	Arg	Gly	Phe	Ile	Arg	Tyr	Gly	125	130	135
Trp	Arg	Trp	Gly	Trp	Arg	Thr	Ala	Val	Phe	Val	Thr	Ile	Phe	Asn	140	145	150
Thr	Val	Asn	Thr	Ser	Leu	Asn	Val	Tyr	Arg	Asn	Lys	Asp	Ala	Leu	155	160	165
Ser	His	Phe	Val	Ile	Ala	Gly	Ala	Val	Thr	Gly	Ser	Leu	Phe	Arg	170	175	180
Ile	Asn	Val	Gly	Leu	Arg	Gly	Leu	Val	Ala	Gly	Gly	Ile	Ile	Gly	185	190	195
Ala	Leu	Leu	Gly	Thr	Pro	Val	Gly	Gly	Leu	Leu	Met	Ala	Phe	Gln	200	205	210
Lys	Tyr	Ala	Gly	Glu	Thr	Val	Gln	Glu	Arg	Lys	Gln	Lys	Asp	Arg	215	220	225
Lys	Ala	Leu	His	Glu	Leu	Lys	Leu	Glu	Glu	Trp	Lys	Gly	Arg	Leu	230	235	240
Gln	Val	Thr	Glu	His	Leu	Pro	Glu	Lys	Ile	Glu	Ser	Ser	Leu	Arg	245	250	255
Glu	Asp	Glu	Pro	Glu	Asn	Asp	Ala	Lys	Lys	Ile	Glu	Ala	Leu	Leu	260	265	270
Asn	Leu	Pro	Arg	Asn	Pro	Ser	Val	Ile	Asp	Lys	Gln	Asp	Lys	Asp	275	280	285

<210> 29

<211> 324

<212> DNA

<213> Homo sapiens

<400> 29

cggaagtccc ttgaggagcg tcagaagcgg cttccctacg tcccagagcc 50

ctattaccgc gaatctggat gggaccgctc cgggagctgt ttggcaaaga 100  
 tgaacagcag agaatttcaa aggaccttgc taatatctgt aagacggcag 150  
 ctacagcagg catcattggc tgggtgtatg ggggaatacc agcttttatt 200  
 catgctaaac aacaatacat tgagcagagc caggcagaaa tttatcataa 250  
 ccggtttgat gctgtgcaat ctgcacatcg tgctgccaca cgaggcttca 300  
 ttogttcatg gctggcgccg aacc 324

<210> 30  
 <211> 377  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 262, 330, 371  
 <223> unknown base

<400> 30  
 tcaagtttgt ccgtaggtcg agagaaggcc atggaggtgc cgccaccgac 50  
 accgcggagc ttttttctgt agagcattgt gcctatttcc ccgagttttt 100  
 gctgccgaag ctgtgactgc cgattcggaa gtccttgagg agcgtcagaa 150  
 gcggcttccc tacgtcccag agccctatta cccggaattt ggatgggacc 200  
 gcctccggga gctgtttggc aaagatgaac agcagagaat ttcaaaggac 250  
 cttgctgata tntgtaagac ggcagctaca gcaggcatca ttggctgggt 300  
 gtatggggga ataccagctt ttattcatgn taaacaacaa tacattgagc 350  
 agagccaggc agaaatttat nataacc 377

<210> 31  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 31  
 tcgtacagtt acgctctccc 20

<210> 32  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 32  
cttgaggagc gtcagaagcg 20

<210> 33  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 33  
ataacgaatg aagcctcgtg 20

<210> 34  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 34  
gctaataatct gtaagacggc agctacagca ggcatcattg 40

<210> 35  
<211> 1819  
<212> DNA  
<213> Homo sapiens

<400> 35  
gagccgcccgc cgcgcgcgcgc cgcgcgactg cagccccagg ccccgggccc 50  
ccaccacagt ctgcgttgct gccccgcctg ggccaggccc caaaggcaag 100  
gacaaagcag ctgtcaggga acctccgccg gagtcgaatt tacgtgcagc 150  
tgccggcaac cacagggttc aagatggttt gcgggggctt cgcgtgttcc 200  
aagaactgcc tgtgcgcctt caacctgctt tacaccttg ttagtctgct 250  
gctaattgga attgctgcgt ggggcattgg cttcgggctg atttccagtc 300  
tccgagtggc cggcgtgggc attgcagtgg gcattcttctt gttcctgatt 350  
gcttttagtg gtctgattgg agctgtaaaa catcatcagg tgttgctatt 400  
tttttatatg attattctgt tacttgattt tattgttcag ttttctgtat 450  
cttgcgcttg tttagccctg aaccaggagc aacagggtca gcttctggag 500  
gttggttgga acaatacggc aagtgtcga aatgacatcc agagaaatct 550  
aaactgctgt ggggttcgaa gtgttaaccc aatgacacc tgtctggcta 600  
gctgtgttaa aagtgaccac tcgtgctcgc catgtgctcc aatcatagga 650  
gaatatgctg gagaggtttt gagatttgtt ggtggcattg gcctgttctt 700



cagttttaca gagatcctgg gtgtttggct gacctacaga tacaggaacc 750  
 agaaagaccc ccgcgcgaat cctagtgcac tcctttgatg agaaaacaag 800  
 gaagatttcc ttctgtatta tgatcttggt cactttctgt aattttctgt 850  
 taagctccat ttgccagttt aaggaaggaa acactatctg gaaaagtacc 900  
 ttattgatag tggaattata tatttttact ctatgtttct ctacatgttt 950  
 ttttctttcc gttgctgaaa aatatttgaa acttgtgggc tctgaagctc 1000  
 ggtggcacct ggaatttact gtattcattg tcgggcactg tccactgtgg 1050  
 cctttcttag catttttacc tgcagaaaaa ctttgtatgg taccactgtg 1100  
 ttggttatat ggtgaatctg aacgtacatc tcactggtat aattatatgt 1150  
 agcactgtgc tgtgtagata gttcctactg gaaaaagagt ggaaatttat 1200  
 taaaatcaga aagtatgaga tcctgttatg ttaagggaaa tccaaattcc 1250  
 caattttttt tgggtctttt aggaaagatt gttgtggtaa aaagtgttag 1300  
 tataaaaatg ataatttact tgtagtcttt tatgattaca ccaatgtatt 1350  
 ctagaaatag ttatgtctta ggaaattgtg gtttaatttt tgacttttac 1400  
 aggtaagtgc aaaggagaag tggtttcatg aaatgttcta atgtataata 1450  
 acatttacct tcagcctcca tcagaatgga acgagttttg agtaatcagg 1500  
 aagtatatct atatgatctt gatattgttt tataataatt tgaagtctaa 1550  
 aagactgcat ttttaaacaa gttagtatta atgcgttggc ccacgtagca 1600  
 aaaagatatt tgattatctt aaaaattggt aaataccgtt ttcatgaaat 1650  
 ttctcagtat tgtaacagca acttgtcaaa cctaagcata tttgaatatg 1700  
 atctcccata atttgaaatt gaaatcgtat tgtgtggctc tgtatattct 1750  
 gttaaaaaat taaaggacag aaacctttct ttgtgtatgc atgtttgaat 1800  
 taaaagaaag taatggaag 1819

<210> 36  
 <211> 204  
 <212> PRT  
 <213> Homo sapiens

<400> 36  
 Met Val Cys Gly Gly Phe Ala Cys Ser Lys Asn Cys Leu Cys Ala  
 1 5 10 15  
 Leu Asn Leu Leu Tyr Thr Leu Val Ser Leu Leu Leu Ile Gly Ile  
 20 25 30

Ala	Ala	Trp	Gly	Ile	Gly	Phe	Gly	Leu	Ile	Ser	Ser	Leu	Arg	Val
				35					40					45
Val	Gly	Val	Val	Ile	Ala	Val	Gly	Ile	Phe	Leu	Phe	Leu	Ile	Ala
				50					55					60
Leu	Val	Gly	Leu	Ile	Gly	Ala	Val	Lys	His	His	Gln	Val	Leu	Leu
				65					70					75
Phe	Phe	Tyr	Met	Ile	Ile	Leu	Leu	Leu	Val	Phe	Ile	Val	Gln	Phe
				80					85					90
Ser	Val	Ser	Cys	Ala	Cys	Leu	Ala	Leu	Asn	Gln	Glu	Gln	Gln	Gly
				95					100					105
Gln	Leu	Leu	Glu	Val	Gly	Trp	Asn	Asn	Thr	Ala	Ser	Ala	Arg	Asn
				110					115					120
Asp	Ile	Gln	Arg	Asn	Leu	Asn	Cys	Cys	Gly	Phe	Arg	Ser	Val	Asn
				125					130					135
Pro	Asn	Asp	Thr	Cys	Leu	Ala	Ser	Cys	Val	Lys	Ser	Asp	His	Ser
				140					145					150
Cys	Ser	Pro	Cys	Ala	Pro	Ile	Ile	Gly	Glu	Tyr	Ala	Gly	Glu	Val
				155					160					165
Leu	Arg	Phe	Val	Gly	Gly	Ile	Gly	Leu	Phe	Phe	Ser	Phe	Thr	Glu
				170					175					180
Ile	Leu	Gly	Val	Trp	Leu	Thr	Tyr	Arg	Tyr	Arg	Asn	Gln	Lys	Asp
				185					190					195
Pro	Arg	Ala	Asn	Pro	Ser	Ala	Phe	Leu						
				200										

<210> 37  
 <211> 390  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 35, 61, 83, 106, 130, 133, 187, 232, 260, 336  
 <223> unknown base

<400> 37  
 tgattggagc tgtaaaaaan tcttcaggtg ttgtnatttt tttatatgat 50  
 tattctgtaa nttgtattta ttgttcagtt ttntgtatct tgcgcttggt 100  
 tagccttgaa ccaggagcaa cagggtcagn ttntggaggt tggttggaac 150  
 aatacggcaa gtgctcgaaa tgacatccag agaaatntaa actgctgtgg 200  
 gttccgaagt gttaacccaa atgacacctg tntggctagc tgtgttaaaa 250  
 gtgaccactn gtgctcgcca tgtgctccaa tcataggaga atatgctgga 300

gaggttttga gatttggttg tggcattggc ctgttnttca gttttacaga 350  
 gatcctgggt gtttggtga cctacagata caggaaccag 390

<210> 38  
 <211> 566  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 27  
 <223> unknown base

<400> 38  
 aatcccaa at tccccaat ttttggnc tttagggaaa gatgtgtgt 50  
 ggtaaaaagt gttagtataa aaatgataa ttacttgtag tcttttatga 100  
 ttacaccaat gtattctaga atagtattgt cttaggaaat tgtggtttta 150  
 tttttgactt ttacaggtaa gtgcaaagga gaagtgggtt catgaaatgt 200  
 tctaattgtat aataacattt accttcagcc tcccatcaga atggaacgag 250  
 ttttgagtaa tccaggaagt atatctatat gatcttgata ttgttttata 300  
 taatttgaag tctaaaagac tgcattttta aacaagttag tattaatgcg 350  
 ttggcccacg tagcaaaaag atatttgatt atcttaaaaa ttgttaaata 400  
 ccgttttcat gaaagttctc agtattgtaa cagcaacttg tcaaacctaa 450  
 gcatatttga atatgatctc ccataatttg aaattgaaat cgtatttgtgt 500  
 ggaggaaatg gcaatcttat gtgtgctgaa ggacacagta agagcaccaa 550  
 gttgtgcccc acttgc 566

<210> 39  
 <211> 264  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 84-85, 206  
 <223> unknown base

<400> 39  
 atgattattc tgttacttgt atttattggt cagttttatg gtatcttgcg 50  
 cttgttttagc cctgaaacc aggagcaaca gggnnacagc tctggaggt 100  
 tggttggcaa caatcacggc caagtgactc cgcaaatgac atcccagaga 150  
 aatcctaaac tgctgtgggt tccgaagtgt taacccaaat gacacctgtc 200

tggctngctg tgttaaaagt gaccactcgt gctcgccatg tgctccaatc 250

ataggagaat atgc 264

<210> 40

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 40

accacgtct gcgttgctgc c 21

<210> 41

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 41

gagaatatgc tggagagg 18

<210> 42

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 42

aggaatgcac taggattcgc gcgg 24

<210> 43

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 43

ggccccaag gcaaggacaa agcagctgtc agggaacctc cgccg 45

<210> 44

<211> 2061

<212> DNA

<213> Homo sapiens

<400> 44

cagtcacat gaagctgggc tgtgtcctca tggcctgggc cctctacctt 50

tcccttggtg tgctctgggt ggcccagatg ctactggctg ccagttttga 100

09978182660  
TOSTOT" 25182660

gacgctgcag tgtgagggac ctgtctgcac tgaggagagc agctgccaca 150  
 cggaggatga cttgactgat gcaaggggaag ctggcttcca ggtcaaggcc 200  
 tacactttca gtgaaccott ccacctgatt gtgtcctatg actggctgat 250  
 cctccaaggt ccagccaagc cagtttttga aggggacctg ctggttctgc 300  
 gctgccaggc ctggcaagac tggccactga ctcaggtgac cttctaccga 350  
 gatggctcag ctctgggtcc ccccgggcct aacaggggaat tctccatcac 400  
 cgtggtacaa aaggcagaca gcgggcacta ccactgcagt ggcatcttcc 450  
 agagccctgg tcttgggatc ccagaaacag catctgttgt ggctatcaca 500  
 gtccaagaac tgtttccagc gccaatctc agagctgtac cctcagctga 550  
 accccaagca ggaagcccca tgacctgag ttgtcagaca aagttgcccc 600  
 tgcagaggtc agctgcccgc ctctcttct ccttctacaa ggatggaagg 650  
 atagtcaaaa gcagggggct ctctcagaa ttccagatcc ccacagcttc 700  
 agaagatcac tccgggtcat actggtgtga ggcagccact gaggacaacc 750  
 aagtttgaa acagagcccc cagctagaga tcagagtga gggtgcttcc 800  
 agctctgctg cacctccac attgaatcca gctctcaga aatcagctgc 850  
 tccaggaact gctcctgagg agggccctgg gcctctgct ccgcccga 900  
 ccccatcttc tgaggatcca ggcttttct ctctctggg gatgccagat 950  
 cctcatctgt atcaccagat gggccttct ctcaaacaca tgcaggatgt 1000  
 gagagtcctc ctcggtcacc tgctcatgga gttgagggaa ttatctggcc 1050  
 accagaagcc tgggaccaca aaggctactg ctgaatagaa gtaaacagtt 1100  
 catccatgat ctacttaac caccacaata aatctgattc tttattttct 1150  
 cttcctgtcc tgcacatatg cataagtact tttacaagtt gtcccagtgt 1200  
 tttgttagaa taatgtagtt aggtgagtgt aaataaattt atataaagt 1250  
 agaattagag tttagctata attgtgtatt ctctcttaac acaacagaat 1300  
 tctgctgtct agatcaggaa tttctatctg ttatatcgac cagaatgttg 1350  
 tgatttaaag agaactaatg gaagtggatt gaatacagca gtctcaactg 1400  
 ggggcaattt tgccccccag aggacattgg gcaatgtttg gagacatttt 1450  
 ggtcattata cttggggggg tgggggatgg tgggatgtgt gtctactggc 1500  
 atccagtaaa tagaagccag gggtgccgct aaacatccta taatgcacag 1550

ggagtagctacc cacaacgaaa aataatctgg cccaaaatgt cagttgtact 1600  
 gagtttgaga aaccccagcc taatgaaacc ctaggtgttg ggctctggaa 1650  
 tgggactttg tcccttctaa ttattatctc tttccagcct cattcagcta 1700  
 ttcttactga cataccagtc tttagctggt gctatggtct gttctttagt 1750  
 tctagtttgt atcccctcaa aagccattat gttgaaatcc taatcccca 1800  
 ggtgatggca ttaagaatg ggcctttggg aagtgattag atcaggagtg 1850  
 cagagccctc atgattagga ttagtgccct tatttaaaaa ggccccagag 1900  
 agctaactca cccttcacc atatgaggac gtggcaagaa gatgacatgt 1950  
 atgagaacca aaaaacagct gtcgcaaac accgactctg tcgttgccct 2000  
 gatcttgaaac ttccagcctc cagaactatg agaaataaaa ttctggttgt 2050  
 ttgtagccta a 2061

<210> 45  
 <211> 359  
 <212> PRT  
 <213> Homo sapiens

<400> 45  
 Met Lys Leu Gly Cys Val Leu Met Ala Trp Ala Leu Tyr Leu Ser  
 1 5 10 15  
 Leu Gly Val Leu Trp Val Ala Gln Met Leu Leu Ala Ala Ser Phe  
 20 25 30  
 Glu Thr Leu Gln Cys Glu Gly Pro Val Cys Thr Glu Glu Ser Ser  
 35 40 45  
 Cys His Thr Glu Asp Asp Leu Thr Asp Ala Arg Glu Ala Gly Phe  
 50 55 60  
 Gln Val Lys Ala Tyr Thr Phe Ser Glu Pro Phe His Leu Ile Val  
 65 70 75  
 Ser Tyr Asp Trp Leu Ile Leu Gln Gly Pro Ala Lys Pro Val Phe  
 80 85 90  
 Glu Gly Asp Leu Leu Val Leu Arg Cys Gln Ala Trp Gln Asp Trp  
 95 100 105  
 Pro Leu Thr Gln Val Thr Phe Tyr Arg Asp Gly Ser Ala Leu Gly  
 110 115 120  
 Pro Pro Gly Pro Asn Arg Glu Phe Ser Ile Thr Val Val Gln Lys  
 125 130 135  
 Ala Asp Ser Gly His Tyr His Cys Ser Gly Ile Phe Gln Ser Pro  
 140 145 150

Gly	Pro	Gly	Ile	Pro	Glu	Thr	Ala	Ser	Val	Val	Ala	Ile	Thr	Val	
				155					160					165	
Gln	Glu	Leu	Phe	Pro	Ala	Pro	Ile	Leu	Arg	Ala	Val	Pro	Ser	Ala	
				170					175					180	
Glu	Pro	Gln	Ala	Gly	Ser	Pro	Met	Thr	Leu	Ser	Cys	Gln	Thr	Lys	
				185					190					195	
Leu	Pro	Leu	Gln	Arg	Ser	Ala	Ala	Arg	Leu	Leu	Phe	Ser	Phe	Tyr	
				200					205					210	
Lys	Asp	Gly	Arg	Ile	Val	Gln	Ser	Arg	Gly	Leu	Ser	Ser	Glu	Phe	
				215					220					225	
Gln	Ile	Pro	Thr	Ala	Ser	Glu	Asp	His	Ser	Gly	Ser	Tyr	Trp	Cys	
				230					235					240	
Glu	Ala	Ala	Thr	Glu	Asp	Asn	Gln	Val	Trp	Lys	Gln	Ser	Pro	Gln	
				245					250					255	
Leu	Glu	Ile	Arg	Val	Gln	Gly	Ala	Ser	Ser	Ser	Ala	Ala	Pro	Pro	
				260					265					270	
Thr	Leu	Asn	Pro	Ala	Pro	Gln	Lys	Ser	Ala	Ala	Pro	Gly	Thr	Ala	
				275					280					285	
Pro	Glu	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Ser	
				290					295					300	
Ser	Glu	Asp	Pro	Gly	Phe	Ser	Ser	Pro	Leu	Gly	Met	Pro	Asp	Pro	
				305					310					315	
His	Leu	Tyr	His	Gln	Met	Gly	Leu	Leu	Leu	Lys	His	Met	Gln	Asp	
				320					325					330	
Val	Arg	Val	Leu	Leu	Gly	His	Leu	Leu	Met	Glu	Leu	Arg	Glu	Leu	
				335					340					345	
Ser	Gly	His	Gln	Lys	Pro	Gly	Thr	Thr	Lys	Ala	Thr	Ala	Glu		
				350					355						

<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 46

tgggctgtgt cctcatgg 18

<210> 47

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 47  
tttccagcgc caattctc 18

<210> 48  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 48  
agttcttgga ctgtgatagc cac 23

<210> 49  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 49  
aaacttggtt gtcttcagtg gctg 24

<210> 50  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 50  
gtgagggacc tgtctgcact gaggagagca gctgccacac ggagg 45

<210> 51  
<211> 2181  
<212> DNA  
<213> Homo sapiens

<400> 51  
cccacgcgtc cgcccacgcg tccgcccacg ggtccgcca cgcgtccggg 50  
ccaccagaag tttgagcctc tttggtagca ggaggctgga agaaaggaca 100  
gaagtagctc tggctgtgat ggggatctta ctgggcctgc tactcctggg 150  
gcacctaaac gtggacactt atggccgtcc catcctggaa gtgccagaga 200  
gtgtaacagg accttggaag ggggatgtga atcttccttg cacctatgac 250  
cccctgcaag gctacacca agtcttggtg aagtggctgg tacaacgtgg 300  
ctcagaccct gtcaccatct ttctacgtga ctcttctgga gaccatatcc 350



agcaggcaaa gtaccagggc cgccctgcatg tgagccacaa ggttccagga 400  
 gatgtatccc tccaattgag caccctggag atggatgacc ggagccacta 450  
 cacgtgtgaa gtcacctggc agactcctga tggcaaccaa gtcgtgagag 500  
 ataagattac tgagctccgt gtccagaaac tctctgtctc caagcccaca 550  
 gtgacaactg gcagcgggta tggcttcacg gtgccccagg gaatgaggat 600  
 tagccttcaa tgccaggctc ggggttctcc tcccatcagt tatatttggt 650  
 ataagcaaca gactaataac caggaaccca tcaaagtagc aaccctaagt 700  
 accttactct tcaagcctgc ggtgatagcc gactcaggct cctatttctg 750  
 cactgccaag ggccagggtg gctctgagca gcacagcgac attgtgaagt 800  
 ttgtgggtcaa agactcctca aagctactca agaccaagac tgaggcacct 850  
 acaaccatga cataccctt gaaagcaaca tctacagtga agcagtcctg 900  
 ggactggacc actgacatgg atggctacct tggagagacc agtgctgggc 950  
 caggaaagag cctgcctgtc ttgccatca tctcatcat ctcttgtgc 1000  
 tgtatggtgg tttttaccat ggcttatatc atgctctgtc ggaagacatc 1050  
 ccaacaagag catgtctacg aagcagccag gtaagaaagt ctctcctctt 1100  
 ccatttttga ccccgctcct gccctcaatt ttgattactg gcaggaaatg 1150  
 tggaggaagg ggggtgtggc acagacccaa tcttaaggcc ggaggccttc 1200  
 agggtcagga catagctgcc ttccctctct caggcacctt ctgagggttg 1250  
 tttggccctc tgaacacaaa ggataattta gatccatctg ccttctgctt 1300  
 ccagaatccc tgggtggtag gatcctgata attaattggc aagaattgag 1350  
 gcagaagggt gggaaaccag gaccacagcc ccaagtcctt tcttatgggt 1400  
 ggtgggctct tgggcatag ggcacatgcc agagaggcca acgactctgg 1450  
 agaaaccatg aggggtggca tcttcgcaag tggctgtctc agtgatgagc 1500  
 caacttccca gaatctgggc aacaactact ctgatgagcc ctgcatagga 1550  
 caggagtacc agatcatcgc ccagatcaat ggcaactacg cccgcctgct 1600  
 ggacacagtt cctctggatt atgagtttct ggccactgag ggcaaaagtg 1650  
 tctgttaaaa atgccccatt aggccaggat ctgctgacat aattgcctag 1700  
 tcagtccttg ccttctgcat ggccttcttc cctgctacct ctcttctg 1750  
 atagcccaaa gtgtccgcct accaactctg gagccgctgg gagtcactgg 1800

ctttgccttg gaatttgcca gatgcatctc aagtaagcca gctgctggat 1850  
 ttggctctgg gcccttctag tatctctgcc gggggcttct ggtactcctc 1900  
 totaaatacc agagggaaga tgcccatagc actaggactt ggtcatcatg 1950  
 cctacagaca ctattcaact ttggcatctt gccaccagaa gacccgaggg 2000  
 aggctcagct ctgccagctc agaggaccag ctatatccag gatcatttct 2050  
 ctttcttcag ggccagacag cttttaattg aaattgttat ttcacaggcc 2100  
 agggttcagt tctgctcctc cactataagt ctaatgttct gactctctcc 2150  
 tggtgctcaa taaatatcta atcataacag c 2181

<210> 52  
 <211> 321  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Met Gly Ile Leu Leu Gly Leu Leu Leu Gly His Leu Thr Val  
 1 5 10 15  
 Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr  
 20 25 30  
 Gly Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro  
 35 40 45  
 Leu Gln Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg  
 50 55 60  
 Gly Ser Asp Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp  
 65 70 75  
 His Ile Gln Gln Ala Lys Tyr Gln Gly Arg Leu His Val Ser His  
 80 85 90  
 Lys Val Pro Gly Asp Val Ser Leu Gln Leu Ser Thr Leu Glu Met  
 95 100 105  
 Asp Asp Arg Ser His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro  
 110 115 120  
 Asp Gly Asn Gln Val Val Arg Asp Lys Ile Thr Glu Leu Arg Val  
 125 130 135  
 Gln Lys Leu Ser Val Ser Lys Pro Thr Val Thr Thr Gly Ser Gly  
 140 145 150  
 Tyr Gly Phe Thr Val Pro Gln Gly Met Arg Ile Ser Leu Gln Cys  
 155 160 165  
 Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile Trp Tyr Lys Gln  
 170 175 180

Gln Thr Asn Asn	Gln Glu Pro Ile Lys	Val Ala Thr Leu Ser Thr	185	190	195
Leu Leu Phe Lys	Pro Ala Val Ile Ala	Asp Ser Gly Ser Tyr Phe	200	205	210
Cys Thr Ala Lys	Gly Gln Val Gly Ser	Glu Gln His Ser Asp Ile	215	220	225
Val Lys Phe Val	Val Lys Asp Ser Ser	Lys Leu Leu Lys Thr Lys	230	235	240
Thr Glu Ala Pro	Thr Thr Met Thr Tyr	Pro Leu Lys Ala Thr Ser	245	250	255
Thr Val Lys Gln	Ser Trp Asp Trp Thr	Thr Asp Met Asp Gly Tyr	260	265	270
Leu Gly Glu Thr	Ser Ala Gly Pro Gly	Lys Ser Leu Pro Val Phe	275	280	285
Ala Ile Ile Leu	Ile Ile Ser Leu Cys	Cys Met Val Val Phe Thr	290	295	300
Met Ala Tyr Ile	Met Leu Cys Arg Lys	Thr Ser Gln Gln Glu His	305	310	315
Val Tyr Glu Ala	Ala Arg		320		

<210> 53  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 53  
 tatccctcca attgagcacc ctgg 24

<210> 54  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 54  
 gtcggaagac atcccaacaa g 21

<210> 55  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 55

cttcacaatg tcgctgtgct gctc 24

<210> 56

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 56

agccaaatcc agcagctggc ttac 24

<210> 57

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 57

tggatgaccg gagccactac acgtgtgaag tcacctggca gactcctgat 50

<210> 58

<211> 2458

<212> DNA

<213> Homo sapiens

<400> 58

gcgcccgggag cccatctgcc cccaggggca cggggcgcg ggcgggtcc 50

cgccccggcac atggctgcag ccacctgcg cgcaccccga ggccgcgcg 100

ccagctcgcc cgaggtccgt cggaggcgcc cggccgcccc ggagccaagc 150

agcaactgag cggggaagcg cccgcgtccg gggatcggga tgtccctcct 200

ccttctcctc ttgctagttt cctactatgt tggaaccttg gggactcaca 250

ctgagatcaa gagagtggca gaggaaaagg tcactttgcc ctgccaccat 300

caactggggc ttccagaaaa agacactctg gatattgaat ggctgctcac 350

cgataatgaa gggaaccaa aagtgggtgat cacttactcc agtcgtcatg 400

tctacaataa cttgactgag gaacagaagg gccgagtggc ctttgcttcc 450

aatttctctg caggagatgc ctccttgag attgaacctc tgaagcccag 500

tgatgagggc cggtagacct gtaagggttaa gaattcaggg cgctacgtgt 550

ggagccatgt catcttaaaa gtcttagtga gaccatccaa gcccaagtgt 600

gagttggaag gagagctgac agaaggaagt gacctgactt tgcagtgtga 650

gtcatcctct ggcacagagc ccattgtgta ttactggcag cgaatccgag 700  
 agaaagaggg agaggatgaa cgtctgcctc ccaaacttag gattgactac 750  
 aaccaccctg gacgagttct gctgcagaat cttaccatgt cctactctgg 800  
 actgtaccag tgcacagcag gcaacgaagc tgggaaggaa agctgtgtgg 850  
 tgcgagtaac tgtacagtat gtacaaagca tcggcatggg tgcaggagca 900  
 gtgacaggca tagtggctgg agccctgctg attttcctct tgggtgtggct 950  
 gctaataccga aggaaagaca aagaaagata tgaggaagaa gagagaccta 1000  
 atgaaattcg agaagatgct gaagctccaa aagcccgtct tgtgaaaccc 1050  
 agctcctctt cctcaggctc tcggagctca cgctctgggt cttcctccac 1100  
 tcgctccaca gcaaatagtg cctcacgcag ccagcggaca ctgtcaactg 1150  
 acgcagcacc ccagccaggg ctggccaccc aggcatacag cctagtgggg 1200  
 ccagaggtga gaggttctga accaaagaaa gtccaccatg ctaatctgac 1250  
 caaagcagaa accacacca gcatgatccc cagccagagc agagccttcc 1300  
 aaacggctctg aattacaatg gacttgactc ccacgctttc ctaggagtca 1350  
 ggggtctttg actcttctcg tcattggagc tcaagtcacc agccacacaa 1400  
 ccagatgaga ggtcatctaa gtagcagtga gcattgcacg gaacagattc 1450  
 agatgagcat tttccttata caataccaaa caagcaaaag gatgtaagct 1500  
 gattcatctg taaaaaggca tcttattgtg ccttttagacc agagtaaggg 1550  
 aaagcaggag tccaaatcta tttgttgacc aggacctgtg gtgagaaggt 1600  
 tggggaaagg tgaggtgaat atacctaaaa cttttaatgt gggatatttt 1650  
 gtatcagtgc tttgattcac aattttcaag aggaaatggg atgctgtttg 1700  
 taaattttct atgcatttct gcaaacttat tggattatta gttattcaga 1750  
 cagtcaagca gaaccacag cttattaca cctgtctaca ccatgtactg 1800  
 agctaaccac ttctaagaaa ctccaaaaaa ggaaacatgt gtcttctatt 1850  
 ctgacttaac ttcatttgtc ataaggtttg gatattaatt tcaaggggag 1900  
 ttgaaatagt gggagatgga gaagagtga tgagtttctc ccactctata 1950  
 ctaatctcac tatttgtatt gagcccaaaa taactatgaa aggagacaaa 2000  
 aatttgtgac aaaggattgt gaagagcttt ccatcttcat gatgttatga 2050  
 ggattgttga caaacattag aaatatataa tggagcaatt gtggatttcc 2100

cctcaaataca gatgcctcta aggactttcc tgctagatat ttctggaagg 2150  
 agaaaatata acatgtcatt tatcaacgtc cttagaaaga attcttctag 2200  
 agaaaaaggg atctaggaat gctgaaagat tacccaacat accattatag 2250  
 tctcttcttt ctgagaaaat gtgaaaccag aattgcaaga ctgggtggac 2300  
 tagaaagga gattagatca gttttctctt aatatgtcaa ggaaggtagc 2350  
 cgggcatggt gccaggcacc tgtaggaaaa tccagcaggt ggaggttgca 2400  
 gtgagccgag attatgccat tgcactccag cctgggtgac agagcgggac 2450  
 tccgtctc 2458

<210> 59  
 <211> 373  
 <212> PRT  
 <213> Homo sapiens

<400> 59  
 Met Ser Leu Leu Leu Leu Leu Leu Val Ser Tyr Tyr Val Gly  
 1 5 10 15  
 Thr Leu Gly Thr His Thr Glu Ile Lys Arg Val Ala Glu Glu Lys  
 20 25 30  
 Val Thr Leu Pro Cys His His Gln Leu Gly Leu Pro Glu Lys Asp  
 35 40 45  
 Thr Leu Asp Ile Glu Trp Leu Leu Thr Asp Asn Glu Gly Asn Gln  
 50 55 60  
 Lys Val Val Ile Thr Tyr Ser Ser Arg His Val Tyr Asn Asn Leu  
 65 70 75  
 Thr Glu Glu Gln Lys Gly Arg Val Ala Phe Ala Ser Asn Phe Leu  
 80 85 90  
 Ala Gly Asp Ala Ser Leu Gln Ile Glu Pro Leu Lys Pro Ser Asp  
 95 100 105  
 Glu Gly Arg Tyr Thr Cys Lys Val Lys Asn Ser Gly Arg Tyr Val  
 110 115 120  
 Trp Ser His Val Ile Leu Lys Val Leu Val Arg Pro Ser Lys Pro  
 125 130 135  
 Lys Cys Glu Leu Glu Gly Glu Leu Thr Glu Gly Ser Asp Leu Thr  
 140 145 150  
 Leu Gln Cys Glu Ser Ser Ser Gly Thr Glu Pro Ile Val Tyr Tyr  
 155 160 165  
 Trp Gln Arg Ile Arg Glu Lys Glu Gly Glu Asp Glu Arg Leu Pro  
 170 175 180

09978192-101501

Pro Lys Ser Arg Ile Asp Tyr Asn His	Pro Gly Arg Val Leu Leu
185	190 195
Gln Asn Leu Thr Met Ser Tyr Ser Gly	Leu Tyr Gln Cys Thr Ala
200	205 210
Gly Asn Glu Ala Gly Lys Glu Ser Cys	Val Val Arg Val Thr Val
215	220 225
Gln Tyr Val Gln Ser Ile Gly Met Val	Ala Gly Ala Val Thr Gly
230	235 240
Ile Val Ala Gly Ala Leu Leu Ile Phe	Leu Leu Val Trp Leu Leu
245	250 255
Ile Arg Arg Lys Asp Lys Glu Arg Tyr	Glu Glu Glu Glu Arg Pro
260	265 270
Asn Glu Ile Arg Glu Asp Ala Glu Ala	Pro Lys Ala Arg Leu Val
275	280 285
Lys Pro Ser Ser Ser Ser Ser Gly Ser	Arg Ser Ser Arg Ser Gly
290	295 300
Ser Ser Ser Thr Arg Ser Thr Ala Asn	Ser Ala Ser Arg Ser Gln
305	310 315
Arg Thr Leu Ser Thr Asp Ala Ala Pro	Gln Pro Gly Leu Ala Thr
320	325 330
Gln Ala Tyr Ser Leu Val Gly Pro Glu	Val Arg Gly Ser Glu Pro
335	340 345
Lys Lys Val His His Ala Asn Leu Thr	Lys Ala Glu Thr Thr Pro
350	355 360
Ser Met Ile Pro Ser Gln Ser Arg Ala	Phe Gln Thr Val
365	370

<210> 60  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 60  
 ccagtgcaca gcaggcaacg aagc 24

<210> 61  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 61  
actaggctgt atgcctgggt gggc 24

<210> 62  
<211> 43  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 62  
gtatgtacaa agcatcggca tggttgcagg agcagtgaca ggc 43

<210> 63  
<211> 3534  
<212> DNA  
<213> Homo sapiens

<400> 63  
gtcgttcctt tgctctctcg cgcccagtc tctccctgg ttctcctcag 50  
ccgctgtcgg aggagagcac ccggagacgc gggctgcagt cgcggcggct 100  
tctccccgcc tgggcggcct cgccgctggg caggtgctga gcgcccctag 150  
agcctccctt gccgcctccc tctctgccc ggccgcagca gtgcacatgg 200  
ggtgttgagg gtagatgggc tcccggcccg ggaggcggcg gtggatgcgg 250  
cgctgggcag aagcagccgc cgattccagc tgccccgcgc gccccgggcg 300  
cccctgcgag tccccggttc agccatgggg acctctccga gcagcagcac 350  
cgccctcgcc tctgcagcc gcatcgcccg ccgagccaca gccacgatga 400  
tcgcgggctc cttctcctg cttggattcc ttagcaccac cacagctcag 450  
ccagaacaga aggcctcgaa tctcattggc acataccgcc atgttgaccg 500  
tgccaccggc caggtgctaa cctgtgacaa gtgtccagca ggaacctatg 550  
tctctgagca ttgtaccaac acaagcctgc gcgtctgcag cagttgccct 600  
gtggggacct ttaccaggca tgagaatggc atagagaaat gccatgactg 650  
tagtcagcca tgcccatggc caatgattga gaaattacct tgtgctgcct 700  
tgactgaccg agaatgcact tgcccacctg gcatgttcca gtctaaccgt 750  
acctgtgccc cccatacggg gtgtcctgtg ggttggggtg tgcggaagaa 800  
agggacagag actgaggatg tgccgtgtaa gcagtgtgct cgggggtacct 850  
tctcagatgt gccttctagt gtgatgaaat gcaaagcata cacagactgt 900  
ctgagtcaga acctggtggg gatcaagccg gggaccaagg agacagacaa 950



cgtctgtggc acactcccgt ccttctccag ctccacctca ccttcccctg 1000  
 gcacagccat ctttccacgc cctgagcaca tggaaaccca tgaagtccct 1050  
 tcctccactt atgttcccaa aggcattgaac tcaacagaat ccaactcttc 1100  
 tgctctgtt agaccaaagg tactgagtag catccaggaa gggacagtcc 1150  
 ctgacaacac aagctcagca agggggaagg aagacgtgaa caagaccctc 1200  
 ccaaaccctc aggtagtcaa ccaccagcaa ggccccacc acagacacat 1250  
 cctgaagctg ctgccgtcca tggaggccac tgggggagag aagtccagca 1300  
 cgcccatcaa gggccccaag aggggacatc ctagacagaa cctacacaag 1350  
 cattttgaca tcaatgagca tttgccctgg atgattgtgc ttttctgt 1400  
 gctggtgctt gtggtgattg tgggtgtgag tatccgaaa agctcgagga 1450  
 ctctgaaaaa ggggccccgg caggatccca gtgccattgt ggaaaaggca 1500  
 gggctgaaga aatccatgac tccaaccag aaccgggaga aatggatcta 1550  
 ctactgcaat ggccatggtg tcgatatact gaagcttgta gcagcccaag 1600  
 tgggaagcca gtggaaagat atctatcagt ttctttgcaa tgccagtga 1650  
 agggaggttg ctgctttctc caatgggtac acagccgacc acgagcgggc 1700  
 ctacgcagct ctgcagcact ggaccatccg gggccccgag gccagcctcg 1750  
 cccagctaat tagcgccctg cgccagcacc ggagaaacga tgttgaggag 1800  
 aagattcgtg ggctgatgga agacaccacc cagctggaaa ctgacaaact 1850  
 agctctcccg atgagcccca gcccgcttag cccgagcccc atccccagcc 1900  
 ccaacgcgaa acttgagaat tccgctctcc tgacgggtgga gccttccccca 1950  
 caggacaaga acaagggtt cttoctggat gagtcggagc cccttctccg 2000  
 ctgtgactct acatccagcg gctcctccgc gctgagcagg aacggttcct 2050  
 ttattaccaaa agaaaagaag gacacagtgt tgccgcaggt acgcctggac 2100  
 ccctgtgact tgcagcctat ctttgatgac atgctccact ttctaaatcc 2150  
 tgaggagctg cgggtgattg aagagattcc ccaggctgag gacaaactag 2200  
 accggctatt cgaaattatt ggagtcaaga gccaggaagc cagccagacc 2250  
 ctcttgagct ctgtttatag ccatcttctc gacctgctgt agaacatagg 2300  
 gatactgcat tctggaaatt actcaattta gtggcagggt gggtttttta 2350  
 ttttctctctg tttctgattt ttgttggttg ggggtgtgtgt gtgtgtttgt 2400

gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gtttaacaga gaatatggcc 2450  
 agtgcttgag ttctttctcc ttctctctct ctcttttttt tttaaataac 2500  
 tcttctggga agttgggtta taagcctttg ccagggtgtaa ctgttgtgaa 2550  
 ataccaccca ctaaagtttt ttaagttcca tattttctcc attttgcctt 2600  
 cttatgtatt ttcaagatta ttctgtgcac tttaaattta cttaacttac 2650  
 cataaatgca gtgtgacttt tcccacacac tggattgtga ggctcttaac 2700  
 ttcttaaaag tataatggca tcttgtgaat cctataagca gtctttatgt 2750  
 ctcttaacat tcacacctac tttttaaaaa caaatattat tactatTTTT 2800  
 attattgttt gtcttttata aattttctta aagattaaga aaatttaaga 2850  
 ccccatgag ttactgtaat gcaattcaac tttgagttat cttttaaata 2900  
 tgtcttgat agttcatatt catggctgaa acttgaccac actattgctg 2950  
 attgtatggt tttcacctgg acaccgtgta gaatgcttga ttacttgta 3000  
 tcttcttatg ctaatatgct ctgggctgga gaaatgaaat cctcaagcca 3050  
 tcaggatttg ctatttaagt ggcttgacaa ctgggccacc aaagaacttg 3100  
 aacttcacct tttaggattt gagctgttct ggaacacatt gctgcacttt 3150  
 ggaaagtcaa aatcaagtgc cagtggcgcc ctttccatag agaatttgcc 3200  
 cagctttgct ttaaaagatg tcttgTTTT tatatacaca taatcaatag 3250  
 gtccaatctg ctctcaaggc cttggtcctg gtgggattcc ttcaccaatt 3300  
 actttaatta aaaatggctg caactgtaag aacccttgtc tgatatattt 3350  
 gcaactatgc tccattttac aaatgtacct tctaagtctc agttgccagg 3400  
 ttccaatgca aaggtggcgt ggactccctt tgtgtgggtg gggtttgtgg 3450  
 gtagtggtga aggaccgata tcagaaaaat gccttcaagt gtactaattt 3500  
 attaataaac attaggtgtt tgttaaaaaa aaaa 3534

<210> 64  
 <211> 655  
 <212> PRT  
 <213> Homo sapiens

<400> 64  
 Met Gly Thr Ser Pro Ser Ser Ser Thr Ala Leu Ala Ser Cys Ser  
 1 5 10 15  
 Arg Ile Ala Arg Arg Ala Thr Ala Thr Met Ile Ala Gly Ser Leu  
 20 25 30

Leu	Leu	Leu	Gly	Phe	Leu	Ser	Thr	Thr	Thr	Ala	Gln	Pro	Glu	Gln	
				35						40				45	
Lys	Ala	Ser	Asn	Leu	Ile	Gly	Thr	Tyr	Arg	His	Val	Asp	Arg	Ala	
				50					55					60	
Thr	Gly	Gln	Val	Leu	Thr	Cys	Asp	Lys	Cys	Pro	Ala	Gly	Thr	Tyr	
				65					70					75	
Val	Ser	Glu	His	Cys	Thr	Asn	Thr	Ser	Leu	Arg	Val	Cys	Ser	Ser	
				80					85					90	
Cys	Pro	Val	Gly	Thr	Phe	Thr	Arg	His	Glu	Asn	Gly	Ile	Glu	Lys	
				95					100					105	
Cys	His	Asp	Cys	Ser	Gln	Pro	Cys	Pro	Trp	Pro	Met	Ile	Glu	Lys	
				110					115					120	
Leu	Pro	Cys	Ala	Ala	Leu	Thr	Asp	Arg	Glu	Cys	Thr	Cys	Pro	Pro	
				125					130					135	
Gly	Met	Phe	Gln	Ser	Asn	Ala	Thr	Cys	Ala	Pro	His	Thr	Val	Cys	
				140					145					150	
Pro	Val	Gly	Trp	Gly	Val	Arg	Lys	Lys	Gly	Thr	Glu	Thr	Glu	Asp	
				155					160					165	
Val	Arg	Cys	Lys	Gln	Cys	Ala	Arg	Gly	Thr	Phe	Ser	Asp	Val	Pro	
				170					175					180	
Ser	Ser	Val	Met	Lys	Cys	Lys	Ala	Tyr	Thr	Asp	Cys	Leu	Ser	Gln	
				185					190					195	
Asn	Leu	Val	Val	Ile	Lys	Pro	Gly	Thr	Lys	Glu	Thr	Asp	Asn	Val	
				200					205					210	
Cys	Gly	Thr	Leu	Pro	Ser	Phe	Ser	Ser	Ser	Thr	Ser	Pro	Ser	Pro	
				215					220					225	
Gly	Thr	Ala	Ile	Phe	Pro	Arg	Pro	Glu	His	Met	Glu	Thr	His	Glu	
				230					235					240	
Val	Pro	Ser	Ser	Thr	Tyr	Val	Pro	Lys	Gly	Met	Asn	Ser	Thr	Glu	
				245					250					255	
Ser	Asn	Ser	Ser	Ala	Ser	Val	Arg	Pro	Lys	Val	Leu	Ser	Ser	Ile	
				260					265					270	
Gln	Glu	Gly	Thr	Val	Pro	Asp	Asn	Thr	Ser	Ser	Ala	Arg	Gly	Lys	
				275					280					285	
Glu	Asp	Val	Asn	Lys	Thr	Leu	Pro	Asn	Leu	Gln	Val	Val	Asn	His	
				290					295					300	
Gln	Gln	Gly	Pro	His	His	Arg	His	Ile	Leu	Lys	Leu	Leu	Pro	Ser	
				305					310					315	
Met	Glu	Ala	Thr	Gly	Gly	Glu	Lys	Ser	Ser	Thr	Pro	Ile	Lys	Gly	

320	325	330
Pro Lys Arg Gly His 335	Pro Arg Gln Asn Leu His Lys His Phe 340	Asp 345
Ile Asn Glu His 350	Leu Pro Trp Met Ile Val Leu Phe Leu Leu 355	Leu 360
Val Leu Val Val 365	Ile Val Val Cys Ser Ile Arg Lys Ser Ser 370	Arg 375
Thr Leu Lys Lys 380	Gly Pro Arg Gln Asp Pro Ser Ala Ile Val 385	Glu 390
Lys Ala Gly Leu 395	Lys Lys Ser Met Thr Pro Thr Gln Asn Arg 400	Glu 405
Lys Trp Ile Tyr 410	Tyr Cys Asn Gly His Gly Ile Asp Ile Leu 415	Lys 420
Leu Val Ala Ala 425	Gln Val Gly Ser Gln Trp Lys Asp Ile Tyr 430	Gln 435
Phe Leu Cys Asn 440	Ala Ser Glu Arg Glu Val Ala Ala Phe Ser 445	Asn 450
Gly Tyr Thr Ala 455	Asp His Glu Arg Ala Tyr Ala Ala Leu Gln 460	His 465
Trp Thr Ile Arg 470	Gly Pro Glu Ala Ser Leu Ala Gln Leu Ile 475	Ser 480
Ala Leu Arg Gln 485	His Arg Arg Asn Asp Val Val Glu Lys Ile 490	Arg 495
Gly Leu Met Glu 500	Asp Thr Thr Gln Leu Glu Thr Asp Lys Leu 505	Ala 510
Leu Pro Met Ser 515	Pro Ser Pro Leu Ser Pro Ser Pro Ile Pro 520	Ser 525
Pro Asn Ala Lys 530	Leu Glu Asn Ser Ala Leu Leu Thr Val Glu 535	Pro 540
Ser Pro Gln Asp 545	Lys Asn Lys Gly Phe Phe Val Asp Glu Ser 550	Glu 555
Pro Leu Leu Arg 560	Cys Asp Ser Thr Ser Ser Gly Ser Ser Ala 565	Leu 570
Ser Arg Asn Gly 575	Ser Phe Ile Thr Lys Glu Lys Lys Asp Thr 580	Val 585
Leu Arg Gln Val 590	Arg Leu Asp Pro Cys Asp Leu Gln Pro Ile 595	Phe 600
Asp Asp Met Leu 605	His Phe Leu Asn Pro Glu Glu Leu Arg Val 610	Ile 615

Glu Glu Ile Pro Gln Ala Glu Asp Lys Leu Asp Arg Leu Phe Glu  
620 625 630

Ile Ile Gly Val Lys Ser Gln Glu Ala Ser Gln Thr Leu Leu Asp  
635 640 645

Ser Val Tyr Ser His Leu Pro Asp Leu Leu  
650 655

<210> 65  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 65  
gtagcagtgc acatggggtg ttgg 24

<210> 66  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 66  
accgcacatc ctcaagtctct gtcc 24

<210> 67  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 67  
acgatgatcg cgggctccct tctcctgctt ggattcctta gcaccaccac 50

<210> 68  
<211> 2412  
<212> DNA  
<213> Homo sapiens

<400> 68  
atgggaagcc agtaacactg tggcctacta tctcttccgt ggtgccatct 50  
acatTTTTTgg gactcgggaa ttatgaggta gaggtggagg cggagccgga 100  
tgtcagaggt cctgaaatag tcaccatggg ggaaaatgat ccgcctgctg 150  
ttgaagcccc cttctcattc cgatcgcttt ttggccttga tgatttgaaa 200  
ataagtctg ttgcaccaga tgcagatgct gttgctgcac agatcctgtc 250

actgctgcca ttgaagtttt ttccaatcat cgtcattggg atcattgcat 300  
tgatattagc actggccatt ggtctgggca tccacttoga ctgctcaggg 350  
aagtacagat gtcgctcatc ctttaagtgt atcgagctga tagctcgatg 400  
tgacggagtc tcggattgca aagacgggga ggacgagtac cgctgtgtcc 450  
gggtgggtgg tcagaatgcc gtgctocagg tgttcacagc tgcttcgtgg 500  
aagaccatgt gctccgatga ctggaagggg cactacgcaa atgttgctg 550  
tgcccaactg ggtttcccaa gctatgtgag ttcagataac ctcagagtga 600  
gctcgctgga ggggcagttc cgggaggagt ttgtgtccat cgatcacctc 650  
ttgccagatg acaaggtgac tgcattacac cactcagtat atgtgaggga 700  
gggatgtgcc tctggccaag tggttacott gcagtgcaca gcctgtggtc 750  
atagaagggg ctacagctca cgcacgtgg gtggaacat gtccttgctc 800  
tcgcagtggc cctggcaggc cagccttcag ttccagggct accacctgtg 850  
cgggggctct gtcacacgc ccctgtggat catcactgct gcacactgtg 900  
tttatgactt gtacctcccc aagtcattga ccatccaggt gggcttagtt 950  
tcctgtttgg acaatccagc cccatccac ttggtggaga agattgtcta 1000  
ccacagcaag tacaagccaa agaggctggg caatgacatc gcccttatga 1050  
agctggccgg gccactcag ttcaatgaaa tgatccagcc tgtgtgcctg 1100  
cccaactctg aagagaactt ccccgatgga aaagtgtgct ggacgtcagg 1150  
atggggggcc acagaggatg gaggtgacgc ctccctgtc ctgaaccacg 1200  
cggccgtccc tttgatttcc aacaagatct gcaaccacag ggacgtgtac 1250  
ggtggcatca tctccccctc catgctctgc gcgggctacc tgacgggtgg 1300  
cgtggacagc tgccaggggg acagcggggg gccctggtg tgtcaagaga 1350  
ggaggctgtg gaagtttagt ggagcgacca gctttggcat cggctgcgca 1400  
gaggtgaaca agcctggggg gtacaccctg gtcacctcct tcctggactg 1450  
gatccacgag cagatggaga gagacctaaa aacctgaaga ggaaggggac 1500  
aagtagccac ctgagttcct gaggtgatga agacagcccg atcctccct 1550  
ggactcccgt gtaggaacct gcacacgagc agacaccctt ggagctctga 1600  
gttccggcac cagtagcagg cccgaaagag gcacccttcc atctgattcc 1650  
agcacaacct tcaagctgct ttttgttttt tgtttttttg aggtggagtc 1700

tcgctctgtt gccaggtg gagtgcagt gcgaaatccc tgctcactgc 1750  
 agcctccgct tccctgggtc aagcgattct cttgcctcag cttccccagt 1800  
 agctgggacc acaggtgccc gccaccacac ccaactaatt tttgtatttt 1850  
 tagtagagac aggggtttcac catgttggcc aggctgctct caaaccctg 1900  
 acctcaaagt atgtgcctgc ttcagcctcc cacagtgcgt ggattacagg 1950  
 catggggcac cagccttagc ctcagcctcc tttctgatct tctaagaa 2000  
 caaagaagc agcaacttgc aagggcggcc tttccactg gtccatctgg 2050  
 ttttctctcc agggcttgc aaaattcctg acgagataag cagttatgtg 2100  
 acctcacgtg caaagccacc aacagccact cagaaaagac gcaccagccc 2150  
 agaagtgcag aactgcagtc actgcaggtt ttcattctta gggaccagaa 2200  
 ccaaaccac cctttctact tccaagactt atttcacat gtggggaggt 2250  
 taatctagga atgactcgtt taaggcctat tttcatgatt tctttgtagc 2300  
 atttggtgct tgacgtatta ttgtccttg attccaaata atatgtttcc 2350  
 ttccctcatt gtctggcgtg tctgcgtgga ctggtgacgt gaatcaaat 2400  
 catccactga aa 2412

<210> 69  
 <211> 453  
 <212> PRT  
 <213> Homo sapiens

<400> 69  
 Met Gly Glu Asn Asp Pro Pro Ala Val Glu Ala Pro Phe Ser Phe  
 1 5 10 15  
 Arg Ser Leu Phe Gly Leu Asp Asp Leu Lys Ile Ser Pro Val Ala  
 20 25 30  
 Pro Asp Ala Asp Ala Val Ala Ala Gln Ile Leu Ser Leu Leu Pro  
 35 40 45  
 Leu Lys Phe Phe Pro Ile Ile Val Ile Gly Ile Ile Ala Leu Ile  
 50 55 60  
 Leu Ala Leu Ala Ile Gly Leu Gly Ile His Phe Asp Cys Ser Gly  
 65 70 75  
 Lys Tyr Arg Cys Arg Ser Ser Phe Lys Cys Ile Glu Leu Ile Ala  
 80 85 90  
 Arg Cys Asp Gly Val Ser Asp Cys Lys Asp Gly Glu Asp Glu Tyr  
 95 100 105  
 Arg Cys Val Arg Val Gly Gly Gln Asn Ala Val Leu Gln Val Phe

110	115	120
Thr Ala Ala Ser Trp Lys Thr Met Cys	Ser Asp Asp Trp Lys Gly	
125	130	135
His Tyr Ala Asn Val Ala Cys Ala Gln	Leu Gly Phe Pro Ser Tyr	
140	145	150
Val Ser Ser Asp Asn Leu Arg Val Ser	Ser Leu Glu Gly Gln Phe	
155	160	165
Arg Glu Glu Phe Val Ser Ile Asp His	Leu Leu Pro Asp Asp Lys	
170	175	180
Val Thr Ala Leu His His Ser Val Tyr	Val Arg Glu Gly Cys Ala	
185	190	195
Ser Gly His Val Val Thr Leu Gln Cys	Thr Ala Cys Gly His Arg	
200	205	210
Arg Gly Tyr Ser Ser Arg Ile Val Gly	Gly Asn Met Ser Leu Leu	
215	220	225
Ser Gln Trp Pro Trp Gln Ala Ser Leu	Gln Phe Gln Gly Tyr His	
230	235	240
Leu Cys Gly Gly Ser Val Ile Thr Pro	Leu Trp Ile Ile Thr Ala	
245	250	255
Ala His Cys Val Tyr Asp Leu Tyr Leu	Pro Lys Ser Trp Thr Ile	
260	265	270
Gln Val Gly Leu Val Ser Leu Leu Asp	Asn Pro Ala Pro Ser His	
275	280	285
Leu Val Glu Lys Ile Val Tyr His Ser	Lys Tyr Lys Pro Lys Arg	
290	295	300
Leu Gly Asn Asp Ile Ala Leu Met Lys	Leu Ala Gly Pro Leu Thr	
305	310	315
Phe Asn Glu Met Ile Gln Pro Val Cys	Leu Pro Asn Ser Glu Glu	
320	325	330
Asn Phe Pro Asp Gly Lys Val Cys Trp	Thr Ser Gly Trp Gly Ala	
335	340	345
Thr Glu Asp Gly Gly Asp Ala Ser Pro	Val Leu Asn His Ala Ala	
350	355	360
Val Pro Leu Ile Ser Asn Lys Ile Cys	Asn His Arg Asp Val Tyr	
365	370	375
Gly Gly Ile Ile Ser Pro Ser Met Leu	Cys Ala Gly Tyr Leu Thr	
380	385	390
Gly Gly Val Asp Ser Cys Gln Gly Asp	Ser Gly Gly Pro Leu Val	
395	400	405



Cys Gln Glu Arg Arg Leu Trp Lys Leu Val Gly Ala Thr Ser Phe  
 410 415 420

Gly Ile Gly Cys Ala Glu Val Asn Lys Pro Gly Val Tyr Thr Arg  
 425 430 435

Val Thr Ser Phe Leu Asp Trp Ile His Glu Gln Met Glu Arg Asp  
 440 445 450

Leu Lys Thr

<210> 70  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 70  
 tgacatcgcc cttatgaagc tggc 24

<210> 71  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 71  
 tacacgtccc tgtggttgca gatc 24

<210> 72  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 72  
 cggttcaatgc agaaatgatc cagcctgtgt gcttgcccaa ctctgaagag 50

<210> 73  
 <211> 3305  
 <212> DNA  
 <213> Homo sapiens

<400> 73  
 cccacgcgtc cgtcctagtc ccggggccaa ctgggacagt ttgctcattt 50  
 attgcaacgg tcaaggctgg cttgtgccag aacggcgcg gcgcgcgcac 100  
 gcacgcacac acacgggggg aaactttttt aaaaatgaaa ggctagaaga 150  
 gctcagcggc ggcgcggggc ctgcgcgagg gctccggagc tgactcgccg 200

aggcaggaaa tccctccggt cgcgacgccc ggccccggct cggcgcccg 250  
gtgggatggt gcagcgctcg ccgccccggc cgagagctgc tgcactgaag 300  
gccccgacg atggcagcgc gcccgtgcc cgtgtcccc gccccgccc 350  
tctgtctcg cctggccggt gctctgctcg cgcctgcga ggccccaggg 400  
gtgagcttat ggaaccaagg aagagctgat gaagttgtca gtgcctctgt 450  
tcggagtggg gacctctgga tcccagtga gagcttcgac tccaagaatc 500  
atccagaagt gctgaatatt cgactacaac gggaaagcaa agaactgac 550  
ataaatctgg aaagaaatga aggtctcatt gccagcagtt tcacggaaac 600  
ccactatctg caagacggta ctgatgtctc cctcgctcga aattacacgg 650  
gtcactgtta ctacatgga catgtacggg gatattctga ttcagcagtc 700  
agtctcagca cgtgttctgg tctcagggga cttattgtgt ttgaaaatga 750  
aagctatgtc ttagaaccaa tgaaaagtgc aaccaacaga taaaactct 800  
tcccagcgaa gaagctgaaa agcgtccggg gatcatgtgg atcacatcac 850  
aacacaccaa acctcgctgc aaagaatgtg tttccaccac cctctcagac 900  
atgggcaaga aggcataaaa gagagaccct caaggcaact aagtatgtgg 950  
agctggtgat cgtggcagac aaccgagagt ttcagaggca aggaaaagat 1000  
ctggaaaaag ttaagcagcg attaatagag attgctaata acgttgacaa 1050  
gttttacaga ccactgaaca ttcggtatgt gttggtaggc gtggaagtgt 1100  
ggaatgacat ggacaaatgc tctgtaagtc aggaccatt caccagcctc 1150  
catgaatttc tggactggag gaagatgaag cttctacctc gcaaatocca 1200  
tgacaatgcg cagcttgtca gtggggttta tttccaagg accaccatcg 1250  
gcatggcccc aatcatgagc atgtgcacgg cagaccagtc tgggggaatt 1300  
gtcatggacc attcagacaa tccccttggg gcagccgtga cctggcaca 1350  
tgagctgggc cacaatttcg ggatgaatca tgacacactg gacaggggct 1400  
gtagctgtca aatggcggtt gagaaaggag gctgcatcat gaacgcttc 1450  
accgggtacc ctttcccat ggtgttcagc agttgcagca ggaaggactt 1500  
ggagaccagc ctggagaaaag gaatgggggt gtgcctgttt aacctgccgg 1550  
aagtcaggga gtctttcggg ggccagaagt gtgggaacag atttgtggaa 1600  
gaaggagagg agtgtgactg tggggagcca gaggaatgta tgaatcgctg 1650

ctgcaatgcc accacctgta cctgaagcc ggacgctgtg tgcgcacatg 1700  
ggctgtgctg tgaagactgc cagctgaagc ctgcaggaac agcgtgcagg 1750  
gactccagca actcctgtga cctcccagag ttctgcacag gggccagccc 1800  
tcaactgccc gccaatgtgt acctgcacga tgggcactca tgtcaggatg 1850  
tggacggcta ctgctacaat ggcatctgcc agactcacga gcagcagtgt 1900  
gtcacgctct ggggaccagg tgctaaacct gccoctggga tctgctttga 1950  
gagagtcaat tctgcagggtg atccttatgg caactgtggc aaagtctcga 2000  
agagttcctt tgccaaatgc gagatgagag atgctaaatg tggaaaaatc 2050  
cagtgtcaag gaggtgccag ccggccagtc attggtacca atgccgtttc 2100  
catagaaaca aacatccctc tgcagcaagg aggccggatt ctgtgccggg 2150  
ggaccacagt gtacttgggc gatgacatgc cggaccagg gcttgtgctt 2200  
gcaggcacia agtgtgcaga tggaaaaatc tgctgaatc gtcaatgtca 2250  
aaatattagt gtctttgggg ttcacgagtg tgcaatgcag tgccacggca 2300  
gaggggtgtg caacaacagg aagaactgcc actgcgaggc ccaactgggca 2350  
cctcccttct gtgacaagtt tggctttgga ggaagcacag acagcggccc 2400  
catccggcaa gcagaagcaa ggcaggaagc tgcagagtcc aacagggagc 2450  
gcggccaggg ccaggagccc gtgggatcgc aggagcatgc gtctactgcc 2500  
tcaactgacac tcatctgagc octcccatga catggagacc gtgaccagtg 2550  
ctgctgcaga ggaggtcacg cgtccccaag gcctcctgtg actggcagca 2600  
ttgactctgt ggctttgcca tcgtttccat gacaacagac acaacacagt 2650  
tctcggggct caggagggga agtccagcct accaggcacg tctgcagaaa 2700  
cagtgcaggg aagggcagcg acttcctggt tgagcttctg ctaaaacatg 2750  
gacatgcttc agtgctgctc ctgagagagt agcaggttac cactctggca 2800  
ggccccagcc ctgcagcaag gaggaagagg actcaaaagt ctggcctttc 2850  
actgagcctc cacagcagtg ggggagaagc aagggttggg ccagtggtcc 2900  
cctttcccca gtgacacctc agccttggca gccctgatga ctggtctctg 2950  
gctgcaactt aatgctctga tatggctttt agcatttatt atatgaaaat 3000  
agcagggttt tagtttttaa tttatcagag accctgccac ccattccatc 3050  
tccatccaag caaactgaat ggcaatgaaa caaactggag aagaaggtag 3100

gagaaagggc ggtgaactct ggctctttgc tgtggacatg cgtgaccagc 3150  
 agtactcagg tttgagggtt tgcagaaagc caggggaaccc acagagtcac 3200  
 caacccttca ttttaacaagt aagaatgtta aaaagtgaaa acaatgtaag 3250  
 agcctaactc catccccccgt ggccattact gcataaaata gagtgcattt 3300  
 gaaat 3305

<210> 74  
 <211> 735  
 <212> PRT  
 <213> Homo sapiens

<400> 74  
 Met Ala Ala Arg Pro Leu Pro Val Ser Pro Ala Arg Ala Leu Leu  
 1 5 10 15  
 Leu Ala Leu Ala Gly Ala Leu Leu Ala Pro Cys Glu Ala Arg Gly  
 20 25 30  
 Val Ser Leu Trp Asn Gln Gly Arg Ala Asp Glu Val Val Ser Ala  
 35 40 45  
 Ser Val Arg Ser Gly Asp Leu Trp Ile Pro Val Lys Ser Phe Asp  
 50 55 60  
 Ser Lys Asn His Pro Glu Val Leu Asn Ile Arg Leu Gln Arg Glu  
 65 70 75  
 Ser Lys Glu Leu Ile Ile Asn Leu Glu Arg Asn Glu Gly Leu Ile  
 80 85 90  
 Ala Ser Ser Phe Thr Glu Thr His Tyr Leu Gln Asp Gly Thr Asp  
 95 100 105  
 Val Ser Leu Ala Arg Asn Tyr Thr Gly His Cys Tyr Tyr His Gly  
 110 115 120  
 His Val Arg Gly Tyr Ser Asp Ser Ala Val Ser Leu Ser Thr Cys  
 125 130 135  
 Ser Gly Leu Arg Gly Leu Ile Val Phe Glu Asn Glu Ser Tyr Val  
 140 145 150  
 Leu Glu Pro Met Lys Ser Ala Thr Asn Arg Tyr Lys Leu Phe Pro  
 155 160 165  
 Ala Lys Lys Leu Lys Ser Val Arg Gly Ser Cys Gly Ser His His  
 170 175 180  
 Asn Thr Pro Asn Leu Ala Ala Lys Asn Val Phe Pro Pro Pro Ser  
 185 190 195  
 Gln Thr Trp Ala Arg Arg His Lys Arg Glu Thr Leu Lys Ala Thr  
 200 205 210

09978192-101504

Lys Tyr Val Glu	Leu Val Ile Val Ala	Asp Asn Arg Glu Phe Gln
215	220	225
Arg Gln Gly Lys	Asp Leu Glu Lys Val	Lys Gln Arg Leu Ile Glu
230	235	240
Ile Ala Asn His	Val Asp Lys Phe Tyr	Arg Pro Leu Asn Ile Arg
245	250	255
Ile Val Leu Val	Gly Val Glu Val Trp	Asn Asp Met Asp Lys Cys
260	265	270
Ser Val Ser Gln	Asp Pro Phe Thr Ser	Leu His Glu Phe Leu Asp
275	280	285
Trp Arg Lys Met	Lys Leu Leu Pro Arg	Lys Ser His Asp Asn Ala
290	295	300
Gln Leu Val Ser	Gly Val Tyr Phe Gln	Gly Thr Thr Ile Gly Met
305	310	315
Ala Pro Ile Met	Ser Met Cys Thr Ala	Asp Gln Ser Gly Gly Ile
320	325	330
Val Met Asp His	Ser Asp Asn Pro Leu	Gly Ala Ala Val Thr Leu
335	340	345
Ala His Glu Leu	Gly His Asn Phe Gly	Met Asn His Asp Thr Leu
350	355	360
Asp Arg Gly Cys	Ser Cys Gln Met Ala	Val Glu Lys Gly Gly Cys
365	370	375
Ile Met Asn Ala	Ser Thr Gly Tyr Pro	Phe Pro Met Val Phe Ser
380	385	390
Ser Cys Ser Arg	Lys Asp Leu Glu Thr	Ser Leu Glu Lys Gly Met
395	400	405
Gly Val Cys Leu	Phe Asn Leu Pro Glu	Val Arg Glu Ser Phe Gly
410	415	420
Gly Gln Lys Cys	Gly Asn Arg Phe Val	Glu Glu Gly Glu Glu Cys
425	430	435
Asp Cys Gly Glu	Pro Glu Glu Cys Met	Asn Arg Cys Cys Asn Ala
440	445	450
Thr Thr Cys Thr	Leu Lys Pro Asp Ala	Val Cys Ala His Gly Leu
455	460	465
Cys Cys Glu Asp	Cys Gln Leu Lys Pro	Ala Gly Thr Ala Cys Arg
470	475	480
Asp Ser Ser Asn	Ser Cys Asp Leu Pro	Glu Phe Cys Thr Gly Ala
485	490	495
Ser Pro His Cys	Pro Ala Asn Val Tyr	Leu His Asp Gly His Ser

500	505	510
Cys Gln Asp Val Asp Gly Tyr Cys Tyr	Asn Gly Ile Cys Gln Thr	
515	520	525
His Glu Gln Gln Cys Val Thr Leu Trp	Gly Pro Gly Ala Lys Pro	
530	535	540
Ala Pro Gly Ile Cys Phe Glu Arg Val	Asn Ser Ala Gly Asp Pro	
545	550	555
Tyr Gly Asn Cys Gly Lys Val Ser Lys	Ser Ser Phe Ala Lys Cys	
560	565	570
Glu Met Arg Asp Ala Lys Cys Gly Lys	Ile Gln Cys Gln Gly Gly	
575	580	585
Ala Ser Arg Pro Val Ile Gly Thr Asn	Ala Val Ser Ile Glu Thr	
590	595	600
Asn Ile Pro Leu Gln Gln Gly Gly Arg	Ile Leu Cys Arg Gly Thr	
605	610	615
His Val Tyr Leu Gly Asp Asp Met Pro	Asp Pro Gly Leu Val Leu	
620	625	630
Ala Gly Thr Lys Cys Ala Asp Gly Lys	Ile Cys Leu Asn Arg Gln	
635	640	645
Cys Gln Asn Ile Ser Val Phe Gly Val	His Glu Cys Ala Met Gln	
650	655	660
Cys His Gly Arg Gly Val Cys Asn Asn	Arg Lys Asn Cys His Cys	
665	670	675
Glu Ala His Trp Ala Pro Pro Phe Cys	Asp Lys Phe Gly Phe Gly	
680	685	690
Gly Ser Thr Asp Ser Gly Pro Ile Arg	Gln Ala Glu Ala Arg Gln	
695	700	705
Glu Ala Ala Glu Ser Asn Arg Glu Arg	Gly Gln Gly Gln Glu Pro	
710	715	720
Val Gly Ser Gln Glu His Ala Ser Thr	Ala Ser Leu Thr Leu Ile	
725	730	735

<210> 75  
 <211> 483  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> unsure  
 <222> 30, 94, 143, 156, 163, 179, 193, 369, 371, 381, 390, 473  
 <223> unknown base  
  
 <400> 75

tccaaggct tcttgatgg cagatgattn tggggttttg cattgtttcc 50  
 ctgacaacga aaacaaaaca gttttggggg ttcaggaggg gaantccagc 100  
 ctaccagga agtttgaga aacagtgcaa ggaagggcag ganttcctgg 150  
 ttgagntttt tgntaaaaca tggacatgnt tcagtgtctg tcntgagaga 200  
 gtagcagggtt accacttttg gcaggcccca gccctgcagc aaggaggaag 250  
 aggactcaaa agtttggcct ttcactgagc ctccacagca gtgggggaga 300  
 agcaagggtt gggcccagtg tcccctttcc ccagtgcacac ctcagccttg 350  
 gcagccctga taactggtnt ntggctgcaa nttaatgctn tgatatggct 400  
 tttagcattt attatatgaa aatagcaggg ttttagtttt taatttatca 450  
 gagaccctgc caccattcc atntccatcc aag 483

<210> 76  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 76  
 gtctcagcac gtgttctggt ctcaggg 27

<210> 77  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 77  
 catgagcatg tgcacggc 18

<210> 78  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 78  
 tacctgcacg atgggcac 18

<210> 79  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 79  
cactgggcac ctcccttc 18

<210> 80  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 80  
ctccaggctg gtctccaagt cttcc 26

<210> 81  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 81  
tccctgttgg actctgcagc ttcc 24

<210> 82  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 82  
cttcgctggg aagagtttg 19

<210> 83  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 83  
gtgcaaccaa cagatacaaa ctcttcccag cgaagaagct gaaaagcgtc 50

<210> 84  
<211> 1714  
<212> DNA  
<213> Homo sapiens

<400> 84  
catcctgcaa catggtgaaa ccacgcctgg ctaattttgt tgtatttttg 50



gtagagatgg gatttcaccg tgtagccag gattgtctca atctgacctc 100  
 atgatctgcc cgcctcggcc tcccaaagtg ctgggattac aggcgagtgc 150  
 aaccacaccc ggccacaaac tttttaagaa gttaatgaaa ccataccttt 200  
 tacattttta atgacaggaa aatgctcaca ataattgtta acccaaaatt 250  
 ctggatacaa aagtacaatc ttactgtgt aaatacatgt atatgtacta 300  
 tatgaaaata taccaaatat caataatact tatctctggg taaaaacctc 350  
 ttctcatacc ctgtgctaac aacttttaac aaaaaatttg catcactttt 400  
 aagaatcaag aaaaatttct gaaggtcata tgggacagaa aaaaaacca 450  
 agggaaaaat cacgccactt gggaaaaaaa gattcgaaat ctgccttttt 500  
 atagatttgt aattaataag gtccaggctt tctaagcaac ttaaatgttt 550  
 tgtttcgaaa caaagtactt gtctggatgt aggaggaaag ggagtgatgt 600  
 cactgccatt atgatgcccc ttgaatataa gaccctactt gctatctccc 650  
 ctgcaccagc caggagccac ccactctcca gcacactgag cagcaagctg 700  
 gacacacggc aactgatcc aaatgggtaa ggggatggtg gcgatgctca 750  
 ttctgggtct gctacttctg gcgctgctcc taccctgca ggtttcttca 800  
 tttgttcctt taaccagtat gccggaagct actgcagccg aaaccacaaa 850  
 gccctccaac agtgcctac agcctacagc cggctctcct gtggtcttgc 900  
 ttgcccttct acatctctac cattaagagg caggtaaga aacagctaca 950  
 gttctccaac ccatacacta aaaccgaatc caaatgggtc ctagaagtgc 1000  
 aatgtggcaa ggaaaaaac caggtcttca tcaaactctac taatttact 1050  
 ccttattaac agagaaacgc ttgagagtct caaactggac tggtttaaag 1100  
 agcatctgaa ggatttgact agatgataaa tgctgtact ccagttactt 1150  
 tgggaggcct aggcggcgg atcacctgag gtcaggagtt tgagactaac 1200  
 ctggccaaaa tggtgaaacc ccactgttac taaaataca aatattgact 1250  
 gggcgtgggt gtgagtgcct gtgatccag ctactcaggt ggctgaagca 1300  
 ggacaatcac ttgaactcag gaggcagagg ttgcagtgag ctgagatcgc 1350  
 gctactgcac tctagcctag cctgggcaac agagtgagac ttcgtctcaa 1400  
 aaaaaaaaaa gccaagtgca gtggctcacg cctgtaatcc cggcactttg 1450  
 ggaggccgag gtgggcggat cacgaggtca ggagatcaag accatcctgg 1500

ctaatacagt gaaacccctgt ctctactaaa aatacaaaaa attagccggg 1550  
 gatggtggca ggcacctgga gtcccagcta ctcgggaggc tgaggcagga 1600  
 gaatagcgtg aactcaggag gcggagcttg cagtgagccg agattgcgct 1650  
 actgcactcc agcctgggcg acagcgcgag actccgtctc aaaaaaaaaa 1700  
 aaaaaaaaaa aaaa 1714

<210> 85  
 <211> 67  
 <212> PRT  
 <213> Homo sapiens

<400> 85  
 Met Gly Lys Gly Met Val Ala Met Leu Ile Leu Gly Leu Leu Leu  
 1 5 10 15  
 Leu Ala Leu Leu Leu Pro Val Gln Val Ser Ser Phe Val Pro Leu  
 20 25 30  
 Thr Ser Met Pro Glu Ala Thr Ala Ala Glu Thr Thr Lys Pro Ser  
 35 40 45  
 Asn Ser Ala Leu Gln Pro Thr Ala Gly Leu Leu Val Val Leu Leu  
 50 55 60  
 Ala Leu Leu His Leu Tyr His  
 65

<210> 86  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 86  
 acgggcacac tggatcccaa atg 23

<210> 87  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 87  
 ggtagagatg tagaaggga agcaagacc 29

<210> 88  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 88

gctccctacc cgtgcaggtt tcttcatttg ttcctttaac cagtatgccg 50

<210> 89

<211> 2956

<212> DNA

<213> Homo sapiens

<400> 89

gccgcggcga gagcgcgccc agccccgccg cgatgccccg gcgcccagga 50

cgctcctcc cgctgctggc ccggccggcg gccctgactg cgctgctgct 100

gctgctgctg ggccatggcg gcggcggggc ctggggcgcc cgggcccagg 150

aggcggcggc ggccggcggc gacgggcccc ccgcggcaga cggcgaggac 200

ggacaggacc cgcacagcaa gcacctgtac acggccgaca tgttcacgca 250

cgggatccag agcgcgcgcg acttcgtcat gttcttcgcg ccttgggtgtg 300

gacactgcca gcggctgcag ccgacttgga atgacctggg agacaaatac 350

aacagcatgg aagatgcca agtctatgtg gctaaagtgg actgcacggc 400

ccactccgac gtgtgctccg cccagggggg gcgaggatac cccaccttaa 450

agcttttcaa gccaggccaa gaagctgtga agtaccaggg tcctcgggac 500

ttccagacac tggaaaactg gatgctgcag aactgaacg aggagccagt 550

gacaccagag ccggaagtgg aaccgcccag tgcccccgag ctcaagcaag 600

ggctgtatga gctctcagca agcaactttg agctgcacgt tgcacaaggc 650

gaccacttta tcaagttctt cgctccgtgg tgtgggtcact gcaaagccct 700

ggctccaacc tgggagcagc tggctctggg ccttgaacat tccgaaactg 750

tcaagattgg caaggttgat tgtacacagc actatgaact ctgctccgga 800

aaccagggtt gtggctatcc cactcttctc tggttccgag atgggaaaaa 850

ggtggatcag tacaaggga agcgggattt ggagtcactg agggagtacg 900

tggagtcgca gctgcagcgc acagagactg gagcgacgga gaccgtcacg 950

ccctcagagg ccccggtgct ggcagctgag cccgaggctg acaagggcac 1000

tgtgttggca ctactgaaa ataacttoga tgacaccatt gcagaaggaa 1050

taaccttcat caagttttat gctccatggt gtggtcattg taagactctg 1100

gctcctactt gggaggaact ctctaaaaag gaattccctg gtctggcggg 1150

09978192-101501

ggtcaagatc gccgaagtag actgcactgc tgaacggaat atctgcagca 1200  
 agtattcggg acgaggctac cccacgttat tgcttttccg aggagggaa 1250  
 aaagtcaagt agcacagtgg aggcagagac cttgactcgt tacaccgctt 1300  
 tgtcctgagc caagcgaaa acgaacttta ggaacacagt tggaggtcac 1350  
 ctctcctgcc cagctcccg accctgcgtt taggagttca gtcccacaga 1400  
 ggccactggg ttcccagtgg tggctgttca gaaagcagaa cataactaagc 1450  
 gtgaggtatc ttcttttgtgt gtgtgttttc caagccaaca cactctacag 1500  
 attctttatt aagttaagtt tctctaagta aatgtgtaac tcatggtcac 1550  
 tgtgtaaaca ttttcagtgg cgatataatcc cctttgacct tctcttgatg 1600  
 aaatttacat ggtttccttt gagactaaaa tagcgttgag ggaaatgaaa 1650  
 ttgctggact atttgtggct cctgagttga gtgatttttg tgaaagaaa 1700  
 cacatccaaa gcatagttta cctgcccacg agttctggaa aggtggcctt 1750  
 gtggcagtat tgacgttcct ctgatcttaa ggtcacagtt gactcaatac 1800  
 tgtgttggtc cgtagcatgg agcagattga aatgcaaaaa cccacacctc 1850  
 tggagatac cttcacggcc gctgctggag cttctgttgc tgtgaatact 1900  
 tctctcagtg tgagaggtta gccgtgatga aagcagcgtt acttctgacc 1950  
 gtgcctgagt aagagaatgc tgatgccata actttatgtg tcgatacttg 2000  
 tcaaatcagt tactgttcag gggatccttc tgtttctcac ggggtgaaac 2050  
 atgtcttttag ttctcatgt taacacgaag ccagagccca catgaactgt 2100  
 tggatgtctt ccttagaaaag ggtaggcatg gaaaattcca cgaggctcat 2150  
 tctcagtatc tcattaactc attgaaagat tccagttgta tttgtcacct 2200  
 ggggtgacaa gaccagacag gctttccag gcctgggtat ccaggaggc 2250  
 tctgcagccc tgctgaaggg ccctaactag agttctagag tttctgattc 2300  
 tgtttctcag tagtctttt agaggcttgc tatacttggt ctgcttcaag 2350  
 gaggtcgacc ttctaagtga tgaagaatgg gatgcatttg atctcaagac 2400  
 caaagacaga tgtcagtggg ctgctctggc cctggtgtgc acggctgtgg 2450  
 cagctgttga tgccagtgtc ctctaactca tgctgtcctt gtgattaaac 2500  
 acctctatct cccttgggaa taagcacata caggcttaag ctctaagata 2550  
 gataggtgtt tgtcctttta ccatcgagct acttcccata ataaccactt 2600

tgcattcaac actcttcacc cacctcccat acgcaagggg atgtggatac 2650  
 ttggcccaaa gtaactgggtg gtaggaatct tagaaacaag accacttata 2700  
 ctgtctgtct gaggcagaag ataacagcag catctcgacc agcctctgcc 2750  
 ttaaaggaaa tctttattaa tcacgtatgg ttcacagata attctttttt 2800  
 taaaaaaacc caacctccta gagaagcaca actgtcaaga gtcttgtaca 2850  
 cacaacttca gctttgcatac acgagtcttg tattccaaga aaatcaaagt 2900  
 ggtacaattt gtttggtttac actatgatac tttctaaata aactcttttt 2950  
 ttttaa 2956

<210> 90  
 <211> 432  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
 Met Pro Ala Arg Pro Gly Arg Leu Leu Pro Leu Leu Ala Arg Pro  
 1 5 10 15  
 Ala Ala Leu Thr Ala Leu Leu Leu Leu Leu Leu Gly His Gly Gly  
 20 25 30  
 Gly Gly Arg Trp Gly Ala Arg Ala Gln Glu Ala Ala Ala Ala Ala  
 35 40 45  
 Ala Asp Gly Pro Pro Ala Ala Asp Gly Glu Asp Gly Gln Asp Pro  
 50 55 60  
 His Ser Lys His Leu Tyr Thr Ala Asp Met Phe Thr His Gly Ile  
 65 70 75  
 Gln Ser Ala Ala His Phe Val Met Phe Phe Ala Pro Trp Cys Gly  
 80 85 90  
 His Cys Gln Arg Leu Gln Pro Thr Trp Asn Asp Leu Gly Asp Lys  
 95 100 105  
 Tyr Asn Ser Met Glu Asp Ala Lys Val Tyr Val Ala Lys Val Asp  
 110 115 120  
 Cys Thr Ala His Ser Asp Val Cys Ser Ala Gln Gly Val Arg Gly  
 125 130 135  
 Tyr Pro Thr Leu Lys Leu Phe Lys Pro Gly Gln Glu Ala Val Lys  
 140 145 150  
 Tyr Gln Gly Pro Arg Asp Phe Gln Thr Leu Glu Asn Trp Met Leu  
 155 160 165  
 Gln Thr Leu Asn Glu Glu Pro Val Thr Pro Glu Pro Glu Val Glu  
 170 175 180

Pro	Pro	Ser	Ala	Pro	Glu	Leu	Lys	Gln	Gly	Leu	Tyr	Glu	Leu	Ser	185	190	195
Ala	Ser	Asn	Phe	Glu	Leu	His	Val	Ala	Gln	Gly	Asp	His	Phe	Ile	200	205	210
Lys	Phe	Phe	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Ala	Leu	Ala	Pro	215	220	225
Thr	Trp	Glu	Gln	Leu	Ala	Leu	Gly	Leu	Glu	His	Ser	Glu	Thr	Val	230	235	240
Lys	Ile	Gly	Lys	Val	Asp	Cys	Thr	Gln	His	Tyr	Glu	Leu	Cys	Ser	245	250	255
Gly	Asn	Gln	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Trp	Phe	Arg	Asp	260	265	270
Gly	Lys	Lys	Val	Asp	Gln	Tyr	Lys	Gly	Lys	Arg	Asp	Leu	Glu	Ser	275	280	285
Leu	Arg	Glu	Tyr	Val	Glu	Ser	Gln	Leu	Gln	Arg	Thr	Glu	Thr	Gly	290	295	300
Ala	Thr	Glu	Thr	Val	Thr	Pro	Ser	Glu	Ala	Pro	Val	Leu	Ala	Ala	305	310	315
Glu	Pro	Glu	Ala	Asp	Lys	Gly	Thr	Val	Leu	Ala	Leu	Thr	Glu	Asn	320	325	330
Asn	Phe	Asp	Asp	Thr	Ile	Ala	Glu	Gly	Ile	Thr	Phe	Ile	Lys	Phe	335	340	345
Tyr	Ala	Pro	Trp	Cys	Gly	His	Cys	Lys	Thr	Leu	Ala	Pro	Thr	Trp	350	355	360
Glu	Glu	Leu	Ser	Lys	Lys	Glu	Phe	Pro	Gly	Leu	Ala	Gly	Val	Lys	365	370	375
Ile	Ala	Glu	Val	Asp	Cys	Thr	Ala	Glu	Arg	Asn	Ile	Cys	Ser	Lys	380	385	390
Tyr	Ser	Val	Arg	Gly	Tyr	Pro	Thr	Leu	Leu	Leu	Phe	Arg	Gly	Gly	395	400	405
Lys	Lys	Val	Ser	Glu	His	Ser	Gly	Gly	Arg	Asp	Leu	Asp	Ser	Leu	410	415	420
His	Arg	Phe	Val	Leu	Ser	Gln	Ala	Lys	Asp	Glu	Leu				425	430	

<210> 91

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 91  
atgttcttcg cgccctggtg 20

<210> 92  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 92  
ccaagccaac acactctaca g 21

<210> 93  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 93  
aagtggtcgc cttgtgcaac gtgc 24

<210> 94  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 94  
ggtcaaaggg gatatatcgc cac 23

<210> 95  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 95  
gcatggaaga tgccaaagtc tatgtggcta aagtggactg cacggccca 49

<210> 96  
<211> 1016  
<212> DNA  
<213> Homo sapiens

<400> 96  
cttttctgag gaaccacagc aatgaatggc tttgcatcct tgcttogaag 50  
aaaccaattt atcctcctgg tactatttct tttgcaaatt cagagtctgg 100  
gtctggatat tgatagccgt cctaccgctg aagtctgtgc cacacacaca 150

atttcaccag gacccaaagg agatgatggt gaaaaaggag atccaggaga 200  
agagggaaag catggcaaag tgggacgcat ggggccgaaa ggaattaaag 250  
gagaactggg tgatatggga gatcagggca atattggcaa gactgggccc 300  
attgggaaga aggggtgacaa aggggaaaaa ggtttgcttg gaatacctgg 350  
agaaaaaggc aaagcaggta ctgtctgtga ttgtggaaga taccggaaat 400  
ttgttggaaga actggatatt agtattgctc ggctcaagac atctatgaag 450  
tttgtcaaga atgtgatagc agggattagg gaaactgaag agaaattcta 500  
ctacatcgtg caggaagaga agaactacag ggaatcccta acccactgca 550  
ggattcgggg tggaatgcta gccatgcca aggatgaagc tgccaacaca 600  
ctcatcgctg actatgttgc caagagtggc ttctttcggg tgttcattgg 650  
cgtgaatgac cttgaaaggg agggacagta catgtccaca gacaacactc 700  
cactgcagaa ctatagcaac tggaatgagg gggaaccag cgaccctat 750  
ggatcatgagg actgtgtgga gatgctgagc tctggcagat ggaatgacac 800  
agagtgccat cttaccatgt actttgtctg tgagttcatc aagaagaaaa 850  
agtaacttcc ctcatcctac gtatttgcta ttttcctgtg accgtcatta 900  
cagttattgt tatccatcct ttttttcctg attgtactac atttgatctg 950  
agtcaacata gctagaaaat gctaaactga ggtatggagc ctccatcatc 1000  
aaaaaaaaa aaaaaa 1016

<210> 97  
<211> 277  
<212> PRT  
<213> Homo sapiens

<400> 97  
Met Asn Gly Phe Ala Ser Leu Leu Arg Arg Asn Gln Phe Ile Leu  
1 5 10 15  
Leu Val Leu Phe Leu Leu Gln Ile Gln Ser Leu Gly Leu Asp Ile  
20 25 30  
Asp Ser Arg Pro Thr Ala Glu Val Cys Ala Thr His Thr Ile Ser  
35 40 45  
Pro Gly Pro Lys Gly Asp Asp Gly Glu Lys Gly Asp Pro Gly Glu  
50 55 60  
Glu Gly Lys His Gly Lys Val Gly Arg Met Gly Pro Lys Gly Ile  
65 70 75  
Lys Gly Glu Leu Gly Asp Met Gly Asp Gln Gly Asn Ile Gly Lys



80	85	90
Thr Gly Pro Ile Gly Lys Lys Gly Asp	Lys Gly Glu Lys Gly Leu	
95	100	105
Leu Gly Ile Pro Gly Glu Lys Gly Lys	Ala Gly Thr Val Cys Asp	
110	115	120
Cys Gly Arg Tyr Arg Lys Phe Val Gly	Gln Leu Asp Ile Ser Ile	
125	130	135
Ala Arg Leu Lys Thr Ser Met Lys Phe	Val Lys Asn Val Ile Ala	
140	145	150
Gly Ile Arg Glu Thr Glu Glu Lys Phe	Tyr Tyr Ile Val Gln Glu	
155	160	165
Glu Lys Asn Tyr Arg Glu Ser Leu Thr	His Cys Arg Ile Arg Gly	
170	175	180
Gly Met Leu Ala Met Pro Lys Asp Glu	Ala Ala Asn Thr Leu Ile	
185	190	195
Ala Asp Tyr Val Ala Lys Ser Gly Phe	Phe Arg Val Phe Ile Gly	
200	205	210
Val Asn Asp Leu Glu Arg Glu Gly Gln	Tyr Met Ser Thr Asp Asn	
215	220	225
Thr Pro Leu Gln Asn Tyr Ser Asn Trp	Asn Glu Gly Glu Pro Ser	
230	235	240
Asp Pro Tyr Gly His Glu Asp Cys Val	Glu Met Leu Ser Ser Gly	
245	250	255
Arg Trp Asn Asp Thr Glu Cys His Leu	Thr Met Tyr Phe Val Cys	
260	265	270
Glu Phe Ile Lys Lys Lys Lys		
275		

<210> 98  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 98  
 cgctgactat gttgcccaaga gtgg 24

<210> 99  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 99

gatgatggag gctccatacc tcag 24

<210> 100

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 100

gtgttcattg gcgtgaatga ccttgaaagg gagggacagt acatgttcac 50

<210> 101

<211> 2574

<212> DNA

<213> Homo sapiens

<400> 101

ggttctatcg attcgaattc ggccacactg gccggatcct ctagagatcc 50

ctcgacctcg acccacgcgt ccgctgctct ccgcccgtgt ggagtgggtg 100

gggcctgggt gggaatgggc gtgtgccagc gcacgcgcgc tccctggaag 150

gagaagtctc agctagaacg agcggcccta ggttttcgga agggaggatc 200

agggatgttt gcgagcggct ggaaccagac ggtgccgata gaggaagcgg 250

gctccatggc tgccctcctg ctgctgcccc tgctgctggt gctaccgctg 300

ctgctgctga agctacacct ctggccgcag ttgcgctggc ttccggcgga 350

cttggccttt gcggtgcgag ctctgtgctg caaaagggtt cttcgagctc 400

gcgccctggc cgcggctgcc gccgaccggg aagggtcccga ggggggctgc 450

agcctggcct ggcgccctgc ggaactggcc cagcagcgcg ccgcgcacac 500

ctttctcatt cacggctcgc ggcgcttttag ctactcagag gcggagcgcg 550

agagtaacag ggctgcacgc gccttcctac gtgcgctagg ctgggactgg 600

ggacccgacg gcggcgacag cggcgagggg agcgcctggag aaggcgagcg 650

ggcagcgccg ggagccggag atgcagcggc cggaagcggc gcggagtttg 700

ccggagggga cgggtgccgc agaggtggag gagccgccgc ccctctgtca 750

cctggagcaa ctgtggcgct gctcctcccc gctggcccag agtttctgtg 800

gctctggttc gggctggcca aggcggcct gcgcactgcc tttgtgcca 850

ccgccctgcg ccggggcccc ctgctgcact gcctccgcag ctgcggcgcg 900

cgcgcgctgg tgctggcgcc agagtttctg gaggccctgg agccggacct 950  
 gcccgccctg agagccatgg ggctccacct gtgggctgca ggcccaggaa 1000  
 cccaccctgc tggaattagc gatttgctgg ctgaagtgtc cgctgaagtg 1050  
 gatgggcccag tgccaggata cctctcttcc cccagagca taacagacac 1100  
 gtgcctgtac atcttcacct ctggcaccac gggcctcccc aaggctgctc 1150  
 ggatcagtca tctgaagatc ctgcaatgcc agggcttcta tcagctgtgt 1200  
 ggtgtccacc aggaagatgt gatctacctc gccctccac tctaccacat 1250  
 gtccggttcc ctgctgggca tcgtgggctg catgggcatt ggggccacag 1300  
 tgggtgctgaa atccaagttc tcggctggtc agttctggga agattgccag 1350  
 cagcacaggg tgacggtgtt ccagtacatt ggggagctgt gccgatacct 1400  
 tgtcaaccag ccccgagca aggcagaacg tggccataag gtccggctgg 1450  
 cagtgggcag cgggctgcgc ccagatacct gggagcggtt tgtgcggcgc 1500  
 ttcgggcccc tgcaggtgct ggagacatat ggactgacag agggcaacgt 1550  
 ggccaccatc aactacacag gacagcgggg cgctgtgggg cgtgcttctc 1600  
 ggctttacaa gcatactctc cccttctcct tgattcgcta tgatgtcacc 1650  
 acaggagagc caattcgga ccccgaggg cactgtatgg ccacatctcc 1700  
 aggtgagcca gggctgctgg tggccccggg aagccagcag tccccattcc 1750  
 tgggctatgc tggcgggcca gagctggccc aggggaagtt gctaaaggat 1800  
 gtcttccggc ctggggatgt tttcttcaac actggggacc tgctggtctg 1850  
 cgatgaccaa ggttttctcc gcttccatga tcgtactgga gacaccttca 1900  
 ggtggaaggg ggagaatgtg gccacaaccg aggtggcaga ggtcttcgag 1950  
 gccctagatt ttcttcagga ggtgaacgtc tatggagtca ctgtgccagg 2000  
 gcatgaaggc agggctggaa tggcagccct agttctgcgt cccccccacg 2050  
 ctttggacct tatgcagctc tacacccacg tgtctgagaa cttgccacct 2100  
 tatgcccggc cccgattcct caggctccag gagtctttgg ccaccacaga 2150  
 gaccttcaaa cagcagaaag ttcggatggc aatgagggc ttcgaccca 2200  
 gcacctgtc tgacctactg tacgttctgg accaggctgt aggtgcctac 2250  
 ctgccccca caactgccc gtacagcgcc ctctggcag gaaaccttcg 2300  
 aatctgagaa cttccacacc tgaggcacct gagagaggaa ctctgtgggg 2350

tgggggccgt tgcaggtgta ctgggctgtc agggatcttt tctataccag 2400  
 aactgcggtc actatTTTTgt aataaatgtg gctggagctg atccagctgt 2450  
 ctctgaccta aaaaaaaaaa aaaaaaaaaa aaaaaaaaag ggcggccgcg 2500  
 actctagagt cgacctgcag tagggataac agggtaataa gcttggccgc 2550  
 catggcccaa cttgtttatt gcag 2574

<210> 102  
 <211> 730  
 <212> PRT  
 <213> Homo sapiens

<400> 102  
 Met Gly Val Cys Gln Arg Thr Arg Ala Pro Trp Lys Glu Lys Ser  
 1 5 10 15  
 Gln Leu Glu Arg Ala Ala Leu Gly Phe Arg Lys Gly Gly Ser Gly  
 20 25 30  
 Met Phe Ala Ser Gly Trp Asn Gln Thr Val Pro Ile Glu Glu Ala  
 35 40 45  
 Gly Ser Met Ala Ala Leu Leu Leu Leu Pro Leu Leu Leu Leu Leu  
 50 55 60  
 Pro Leu Leu Leu Leu Lys Leu His Leu Trp Pro Gln Leu Arg Trp  
 65 70 75  
 Leu Pro Ala Asp Leu Ala Phe Ala Val Arg Ala Leu Cys Cys Lys  
 80 85 90  
 Arg Ala Leu Arg Ala Arg Ala Leu Ala Ala Ala Ala Asp Pro  
 95 100 105  
 Glu Gly Pro Glu Gly Gly Cys Ser Leu Ala Trp Arg Leu Ala Glu  
 110 115 120  
 Leu Ala Gln Gln Arg Ala Ala His Thr Phe Leu Ile His Gly Ser  
 125 130 135  
 Arg Arg Phe Ser Tyr Ser Glu Ala Glu Arg Glu Ser Asn Arg Ala  
 140 145 150  
 Ala Arg Ala Phe Leu Arg Ala Leu Gly Trp Asp Trp Gly Pro Asp  
 155 160 165  
 Gly Gly Asp Ser Gly Glu Gly Ser Ala Gly Glu Gly Glu Arg Ala  
 170 175 180  
 Ala Pro Gly Ala Gly Asp Ala Ala Ala Gly Ser Gly Ala Glu Phe  
 185 190 195  
 Ala Gly Gly Asp Gly Ala Ala Arg Gly Gly Gly Ala Ala Ala Pro  
 200 205 210

09978192-101501

Leu Ser Pro Gly	Ala Thr Val Ala	Leu Leu Leu Pro	Ala Gly Pro	215	220	225
Glu Phe Leu Trp	Leu Trp Phe Gly	Leu Ala Lys Ala	Gly Leu Arg	230	235	240
Thr Ala Phe Val	Pro Thr Ala Leu	Arg Arg Gly Pro	Leu Leu His	245	250	255
Cys Leu Arg Ser	Cys Gly Ala Arg	Ala Leu Val Leu	Ala Pro Glu	260	265	270
Phe Leu Glu Ser	Leu Glu Pro Asp	Leu Pro Ala Leu	Arg Ala Met	275	280	285
Gly Leu His Leu	Trp Ala Ala Gly	Pro Gly Thr His	Pro Ala Gly	290	295	300
Ile Ser Asp Leu	Leu Ala Glu Val	Ser Ala Glu Val	Asp Gly Pro	305	310	315
Val Pro Gly Tyr	Leu Ser Ser Pro	Gln Ser Ile Thr	Asp Thr Cys	320	325	330
Leu Tyr Ile Phe	Thr Ser Gly Thr	Thr Gly Leu Pro	Lys Ala Ala	335	340	345
Arg Ile Ser His	Leu Lys Ile Leu	Gln Cys Gln Gly	Phe Tyr Gln	350	355	360
Leu Cys Gly Val	His Gln Glu Asp	Val Ile Tyr Leu	Ala Leu Pro	365	370	375
Leu Tyr His Met	Ser Gly Ser Leu	Leu Gly Ile Val	Gly Cys Met	380	385	390
Gly Ile Gly Ala	Thr Val Val Leu	Lys Ser Lys Phe	Ser Ala Gly	395	400	405
Gln Phe Trp Glu	Asp Cys Gln Gln	His Arg Val Thr	Val Phe Gln	410	415	420
Tyr Ile Gly Glu	Leu Cys Arg Tyr	Leu Val Asn Gln	Pro Pro Ser	425	430	435
Lys Ala Glu Arg	Gly His Lys Val	Arg Leu Ala Val	Gly Ser Gly	440	445	450
Leu Arg Pro Asp	Thr Trp Glu Arg	Phe Val Arg Arg	Phe Gly Pro	455	460	465
Leu Gln Val Leu	Glu Thr Tyr Gly	Leu Thr Glu Gly	Asn Val Ala	470	475	480
Thr Ile Asn Tyr	Thr Gly Gln Arg	Gly Ala Val Gly	Arg Ala Ser	485	490	495
Trp Leu Tyr Lys	His Ile Phe Pro	Phe Ser Leu Ile	Arg Tyr Asp			

500	505	510
Val Thr Thr Gly Glu Pro Ile Arg Asp	Pro Gln Gly His Cys Met	
515	520	525
Ala Thr Ser Pro Gly Glu Pro Gly Leu	Leu Val Ala Pro Val Ser	
530	535	540
Gln Gln Ser Pro Phe Leu Gly Tyr Ala	Gly Gly Pro Glu Leu Ala	
545	550	555
Gln Gly Lys Leu Leu Lys Asp Val Phe	Arg Pro Gly Asp Val Phe	
560	565	570
Phe Asn Thr Gly Asp Leu Leu Val Cys	Asp Asp Gln Gly Phe Leu	
575	580	585
Arg Phe His Asp Arg Thr Gly Asp Thr	Phe Arg Trp Lys Gly Glu	
590	595	600
Asn Val Ala Thr Thr Glu Val Ala Glu	Val Phe Glu Ala Leu Asp	
605	610	615
Phe Leu Gln Glu Val Asn Val Tyr Gly	Val Thr Val Pro Gly His	
620	625	630
Glu Gly Arg Ala Gly Met Ala Ala Leu	Val Leu Arg Pro Pro His	
635	640	645
Ala Leu Asp Leu Met Gln Leu Tyr Thr	His Val Ser Glu Asn Leu	
650	655	660
Pro Pro Tyr Ala Arg Pro Arg Phe Leu	Arg Leu Gln Glu Ser Leu	
665	670	675
Ala Thr Thr Glu Thr Phe Lys Gln Gln	Lys Val Arg Met Ala Asn	
680	685	690
Glu Gly Phe Asp Pro Ser Thr Leu Ser	Asp Pro Leu Tyr Val Leu	
695	700	705
Asp Gln Ala Val Gly Ala Tyr Leu Pro	Leu Thr Thr Ala Arg Tyr	
710	715	720
Ser Ala Leu Leu Ala Gly Asn Leu Arg	Ile	
725	730	

<210> 103

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 103

gagagccatg gggctccacc tg 22

<210> 104  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 104  
ggagaatgtg gccacaac 18

<210> 105  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 105  
gccctggcac agtgactcca tagacg 26

<210> 106  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 106  
atccacttca gcggacac 18

<210> 107  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 107  
ccagtgccag gatacctctc ttccccccag agcataacag acacg 45

<210> 108  
<211> 2579  
<212> DNA  
<213> Homo sapiens

<400> 108  
cctgtgttaa gctgaggttt ccctagatc tcgtatatcc ccaacacata 50  
cctccacgca cacacatccc caagaacctc gagctcacac caacagacac 100  
acgcgcgcac acacactcgc tctcgcttgc ccatctccct cccgggggag 150  
ccggcgcgcg ctcccacatt tgccgcacac tccggcgagc cgagcccgcg 200

gcgctccagg attctgcggc tcggaactcg gattgcagct ctgaaccccc 250  
atggtgggttt tttaaacact tcttttcctt ctcttcctcg ttttgattgc 300  
accgtttcca tctgggggct agaggagcaa ggcagcagcc ttcccagcca 350  
gcccttggtg gcttgccatc gtccatctgg cttataaaaag tttgctgagc 400  
gcagtccaga gggctgcgct gctcgtcccc tcggctggca gaaggggggtg 450  
acgctgggca gcggcgagga gcgcgccgct gcctctggcg ggctttcggc 500  
ttgaggggca aggtgaagag cgcaccggcc gtgggggttta ccgagctgga 550  
tttgatatgtt gcaccatgcc ttcttgatc ggggctgtga ttcttcccct 600  
cttggggctg ctgctctccc tccccgccgg gccggatgtg aaggctcggg 650  
gctgcggaga ggtccgccag gcgtacgggtg ccaagggatt cagcctggcg 700  
gacatcccct accaggagat cgcaggggaa cacttaagaa tctgtcctca 750  
ggaatataca tgctgcacca cagaaatgga agacaagtta agccaacaaa 800  
gcaaactcga atttgaaaac cttgtggaag agacaagcca ttttgctgcg 850  
accacttttg tgtccaggca taagaaattt gacgaatttt tccgagagct 900  
cctggagaat gcagaaaagt cactaaatga tatgtttgta cggacctatg 950  
gcatgctgta catgcagaat tcagaagtct tccaggacct cttcacagag 1000  
ctgaaaagggt actacactgg gggtaatgtg aatctggagg aaatgctcaa 1050  
tgacttttgg gctcggctcc tggaacggat gtttcagctg ataaaccctc 1100  
agtatcactt cagtgaagac tacctggaat gtgtgagcaa atacactgac 1150  
cagctcaagc catttgagga cgtgccccgg aaactgaaga ttcagggttac 1200  
ccgcgccttc attgctgcca ggacctttgt ccaggggctg actgtgggca 1250  
gagaagttgc aaaccgagtt tccaagggtca gcccaacccc aggggtgtatc 1300  
cgtgcctca tgaagatgct gtactgcca tactgtcggg ggcttccac 1350  
tgtgaggccc tgcaacaact actgtctcaa cgtcatgaag ggctgcttgg 1400  
caaatacaggc tgacctgac acagagtga atctgtttat agatgcaatg 1450  
ctcttggtgg cagagcgact ggaggggcca ttcaacattg agtcgggtcat 1500  
ggaccgata gatgtcaaga tttctgaagc cattatgaac atgcaagaaa 1550  
acagcatgca ggtgtctgca aaggtctttc agggatgtgg tcagcccaaa 1600  
cctgctccag cctcagatc tgcccgtca gctcctgaaa attttaatac 1650



acgtttcagg ccctacaatc ctgaggaaag accaacaact gctgcaggca 1700  
 caagcttggga ccggctgggtc acagacataa aagagaaatt gaagctctct 1750  
 aaaaagggtct gggtcagcatt accctacact atctgcaagg acgagagcgt 1800  
 gacagcggggc acgtccaacg aggaggaatg ctggaacggg cacagcaaag 1850  
 ccagatactt gcctgagatc atgaatgatg ggctcaccaa ccagatcaac 1900  
 aatccccgagg tggatgtgga catcactcgg cctgacactt tcatcagaca 1950  
 gcagattatg gctctccgtg tgatgaccaa caaactaaaa aacgcctaca 2000  
 atggcaatga tgtcaatttc caggacacaa gtgatgaatc cagtgggtca 2050  
 gggagtggca gtgggtgcat ggatgacgtg tgtcccacgg agtttgagtt 2100  
 tgtcaccaca gagggccccg cagtggatcc cgaccggaga gaggtggact 2150  
 cttctgcagc ccagcgtggc cactccctgc tctcctgggc tctcacctgc 2200  
 attgtcctgg cactgcagag actgtgcaga taatcttggg tttttggtca 2250  
 gatgaaactg catttttagct atctgaatgg ccaactcact tcttttctta 2300  
 cactcttggga caatggacca tgccacaaaa acttaccgtt ttctatgaga 2350  
 agagagcagt aatgcaatct gcctcccttt ttgttttccc aaagagtacc 2400  
 gggtgccaga ctgaactgct tcctctttcc ttcagctatc tgtggggacc 2450  
 ttgtttattc tagagagaat tcttactcaa atttttcgta ccaggagatt 2500  
 ttcttacctt catttgcttt tatgctgcag aagtaaagga atctcacgtt 2550  
 gtgagggttt tttttttctc atttaaaat 2579

<210> 109  
 <211> 555  
 <212> PRT  
 <213> Homo sapiens

<400> 109  
 Met Pro Ser Trp Ile Gly Ala Val Ile Leu Pro Leu Leu Gly Leu  
 1 5 10 15  
 Leu Leu Ser Leu Pro Ala Gly Ala Asp Val Lys Ala Arg Ser Cys  
 20 25 30  
 Gly Glu Val Arg Gln Ala Tyr Gly Ala Lys Gly Phe Ser Leu Ala  
 35 40 45  
 Asp Ile Pro Tyr Gln Glu Ile Ala Gly Glu His Leu Arg Ile Cys  
 50 55 60  
 Pro Gln Glu Tyr Thr Cys Cys Thr Thr Glu Met Glu Asp Lys Leu  
 65 70 75

Ser	Gln	Gln	Ser	Lys	Leu	Glu	Phe	Glu	Asn	Leu	Val	Glu	Glu	Thr	80	85	90
Ser	His	Phe	Val	Arg	Thr	Thr	Phe	Val	Ser	Arg	His	Lys	Lys	Phe	95	100	105
Asp	Glu	Phe	Phe	Arg	Glu	Leu	Leu	Glu	Asn	Ala	Glu	Lys	Ser	Leu	110	115	120
Asn	Asp	Met	Phe	Val	Arg	Thr	Tyr	Gly	Met	Leu	Tyr	Met	Gln	Asn	125	130	135
Ser	Glu	Val	Phe	Gln	Asp	Leu	Phe	Thr	Glu	Leu	Lys	Arg	Tyr	Tyr	140	145	150
Thr	Gly	Gly	Asn	Val	Asn	Leu	Glu	Glu	Met	Leu	Asn	Asp	Phe	Trp	155	160	165
Ala	Arg	Leu	Leu	Glu	Arg	Met	Phe	Gln	Leu	Ile	Asn	Pro	Gln	Tyr	170	175	180
His	Phe	Ser	Glu	Asp	Tyr	Leu	Glu	Cys	Val	Ser	Lys	Tyr	Thr	Asp	185	190	195
Gln	Leu	Lys	Pro	Phe	Gly	Asp	Val	Pro	Arg	Lys	Leu	Lys	Ile	Gln	200	205	210
Val	Thr	Arg	Ala	Phe	Ile	Ala	Ala	Arg	Thr	Phe	Val	Gln	Gly	Leu	215	220	225
Thr	Val	Gly	Arg	Glu	Val	Ala	Asn	Arg	Val	Ser	Lys	Val	Ser	Pro	230	235	240
Thr	Pro	Gly	Cys	Ile	Arg	Ala	Leu	Met	Lys	Met	Leu	Tyr	Cys	Pro	245	250	255
Tyr	Cys	Arg	Gly	Leu	Pro	Thr	Val	Arg	Pro	Cys	Asn	Asn	Tyr	Cys	260	265	270
Leu	Asn	Val	Met	Lys	Gly	Cys	Leu	Ala	Asn	Gln	Ala	Asp	Leu	Asp	275	280	285
Thr	Glu	Trp	Asn	Leu	Phe	Ile	Asp	Ala	Met	Leu	Leu	Val	Ala	Glu	290	295	300
Arg	Leu	Glu	Gly	Pro	Phe	Asn	Ile	Glu	Ser	Val	Met	Asp	Pro	Ile	305	310	315
Asp	Val	Lys	Ile	Ser	Glu	Ala	Ile	Met	Asn	Met	Gln	Glu	Asn	Ser	320	325	330
Met	Gln	Val	Ser	Ala	Lys	Val	Phe	Gln	Gly	Cys	Gly	Gln	Pro	Lys	335	340	345
Pro	Ala	Pro	Ala	Leu	Arg	Ser	Ala	Arg	Ser	Ala	Pro	Glu	Asn	Phe	350	355	360
Asn	Thr	Arg	Phe	Arg	Pro	Tyr	Asn	Pro	Glu	Glu	Arg	Pro	Thr	Thr			

365	370	375
Ala Ala Gly Thr Ser Leu Asp Arg Leu	Val Thr Asp Ile Lys Glu	
380	385	390
Lys Leu Lys Leu Ser Lys Lys Val Trp	Ser Ala Leu Pro Tyr Thr	
395	400	405
Ile Cys Lys Asp Glu Ser Val Thr Ala	Gly Thr Ser Asn Glu Glu	
410	415	420
Glu Cys Trp Asn Gly His Ser Lys Ala	Arg Tyr Leu Pro Glu Ile	
425	430	435
Met Asn Asp Gly Leu Thr Asn Gln Ile	Asn Asn Pro Glu Val Asp	
440	445	450
Val Asp Ile Thr Arg Pro Asp Thr Phe	Ile Arg Gln Gln Ile Met	
455	460	465
Ala Leu Arg Val Met Thr Asn Lys Leu	Lys Asn Ala Tyr Asn Gly	
470	475	480
Asn Asp Val Asn Phe Gln Asp Thr Ser	Asp Glu Ser Ser Gly Ser	
485	490	495
Gly Ser Gly Ser Gly Cys Met Asp Asp	Val Cys Pro Thr Glu Phe	
500	505	510
Glu Phe Val Thr Thr Glu Ala Pro Ala	Val Asp Pro Asp Arg Arg	
515	520	525
Glu Val Asp Ser Ser Ala Ala Gln Arg	Gly His Ser Leu Leu Ser	
530	535	540
Trp Ser Leu Thr Cys Ile Val Leu Ala	Leu Gln Arg Leu Cys Arg	
545	550	555

<210> 110  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 110  
 aagcgtgaca gcgggcacgt c 21

<210> 111  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 111

tgcacagtct ctgcagtgcc cagg 24

<210> 112

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 112

gaatgctgga acgggcacag caaagccaga tacttgcttg 40

<210> 113

<211> 4649

<212> DNA

<213> Homo sapiens

<400> 113

cggacgcgtg ggcggacgcg tgggcaaaag aactcggagt gccaaagcta 50

aataagtttag ctgagaaaac gcacgcagtt tgcagcgcct gcgcccgggtg 100

cgccaactac gcaaagacca agcgggctcc gcgcggaaccg gccgcggggc 150

tagggacccg gctttggcct tcaggctccc tagcagcggg gaaaaggaat 200

tgtgtcccgg agttttctgc gaggtggagg gagatcagga aacggcttct 250

tcctcacttc gccgcctggt gagtgtcggg gagattggca aacgcctagg 300

aaaggactgg ggaaaatagc cctgggaaag tggagaaggt gatcaggagg 350

ccggtccact acggcagttt atctgtctga tcagagccag acgcgacgcg 400

tccacttcgc agttctttcc aggtgtgggg accgcaggac agacggccga 450

tcccgcgcgc ctccgtacca gcaactccag gagagtcagc ctgcgtcccc 500

aacgtcgagg gcgctctggc cacgaaaagt tcctgtccac tgtgattctc 550

aattccttgc ttggtttttt tctccagaga acttttgggt ggagatatta 600

acttttttct tttttttttt ccttggtgga agctgctcta gggagggggg 650

aggaggagga gaaagtgaaa tgtgctggag aagagcgagc cctccttggt 700

cttccggagt cccatccatt aagccatcac ttctggaaga ttaaagttgt 750

cggacatggt gacagctgag aggagaggag gatttcttgc caggtggaga 800

gtcttcaccg tctgttgggt gcatgtgtgc gcccgcagcg gcgcccggcg 850

cgtgggttctc cgcgtggagt ctacactggg acctgagtga atggctccca 900

ggggctgtgc ggggcatccg cctccgcctt ctccacaggc ctgtgtctgt 950

cctggaaaga tgctagcaat gggggcgctg gcaggattct ggatcctctg 1000

cctcctcact tatgggttacc tgtcctgggg ccaggcctta gaagaggagg 1050  
aagaaggggc cttactagct caagctggag agaaactaga gcccagcaca 1100  
acttccacct cccagcccca tctcattttc atcctagcgg atgatcaggg 1150  
atttagagat gtgggttacc acggatctga gattaaaaca cctactcttg 1200  
acaagctcgc tgccgaagga gttaaactgg agaactacta tgtccagcct 1250  
at ttgcacac catccaggag tcagttttatt actggaaagt atcagataca 1300  
caccggactt caacattcta tcataagacc tacccaaccc aactgtttac 1350  
ctctggacaa tgccacccta cctcagaaac tgaaggaggt tggatattca 1400  
acgcatatgg tcggaaaatg gcacttgggt tttaacagaa aagaatgcat 1450  
gcccaccaga agaggatttg ataccttttt tggttccctt ttgggaagtg 1500  
gggattacta tacacactac aaatgtgaca gtcctgggat gtgtggctat 1550  
gacttgtatg aaaacgacaa tgctgcctgg gactatgaca atggcatata 1600  
ctccacacag atgtacactc agagagtaca gcaaactcta gcttcccata 1650  
accccacaaa gcctatatatt ttatatactg cctatcaagc tgttcattca 1700  
ccactgcaag ctctggcag gtatttcgaa cactaccgat ccattatcaa 1750  
cataaacagg agaagatatg ctgccatgct ttcttgctta gatgaagcaa 1800  
tcaacaacgt gacattggct ctaaagactt atggtttcta taacaacagc 1850  
attatcattt actcttcaga taatggtggc cagcctacgg caggaggagg 1900  
taactggcct ctgagaggta gcaaaggaac atattgggaa ggagggatcc 1950  
gggctgtagg ctttgtgcat agcccacttc tgaaaaacaa gggaacagtg 2000  
tgtaaggaac ttgtgcacat cactgactgg taccctactc tcatttcact 2050  
ggctgaagga cagattgatg aggacattca actagatggc tatgatattct 2100  
gggagaccat aagtgagggt ctctgctcac cccgagtaga tattttgcat 2150  
aacattgacc cctatacacc aaggcaaaaa atggctcctg ggcagcaggc 2200  
tatgggatct ggaacactgc aatccagtca gccatcagag tgcagcactg 2250  
gaaattgctt acaggaaatc ctggctacag cgactgggtc cccctcagt 2300  
ctttcagcaa cctgggaccg aaccggtggc acaatgaacg gatcaccttg 2350  
tcaactggca aaagtgtatg gcttttcaac atcacagccg acccatatga 2400  
gagggtggac ctatctaaca ggtatccagg aatcgtgaag aagctcctac 2450

ggaggctctc acagttcaac aaaactgcag tgccgggtcag gtatcccccc 2500  
 aaagacccca gaagtaaccc taggctcaat ggaggggtct ggggaccatg 2550  
 gtataaagag gaaaccaaga aaaagaagcc aagcaaaaat caggctgaga 2600  
 aaaagcaaaa gaaaagcaaa aaaaagaaga agaaacagca gaaagcagtc 2650  
 tcaggtaaac cagcaaattt ggctcgataa tatcgctggc ctaagcgtca 2700  
 ggcttggttt catgctgtgc cactccagag acttctgcc cctggccgcc 2750  
 aactgaaaa ctgtcctgct cagtgccaa gtgctactct tgcaagccac 2800  
 acttagagag agtggagatg tttatttctc tcgctccttt agaaaacgtg 2850  
 gtgagtcctg agttccactg ctgtgcttca gtcaactgac caaactgc 2900  
 tttgaattat aggaggagaa caataaccta ccatccgcaa gcatgctaata 2950  
 ttgatggaag ttacagggtg gcatgattaa aactaccttt gataaattac 3000  
 agtcaaagat tgtgtcacct caaaggcctt gaagaatata tttcttggt 3050  
 gaatttttgt atgtctgtca tatgacactt gggtttttta attaatctta 3100  
 ttttatatat ataatatat gtttcttttc ctgtgaaaag ctgtttttct 3150  
 cacatgtgaa cagcttgac ctcattttac catgcgtgag ggaatggcaa 3200  
 ataagaatgt ttgagcacac tgcccacaat gaatgtaact attttctaaa 3250  
 cactttacta gaagaacatt tcagtataaa aaacctaatt tatttttaca 3300  
 gaaaaatatt ttgttggttt tataaaaagt tatgcaaatg acttttattt 3350  
 ttatttcctg cataccatta gaagaatttt atttcatttc ttcaaattat 3400  
 caagcactgt aatactataa attaatgtaa tactgtgtga attcagacta 3450  
 taaaaaacat cattcagaaa actttataat cgtcattggt caatcaagat 3500  
 tttgaatgta ataagatgaa tatattcctt acaaattact tggaaattca 3550  
 atgtttgtgc agagttgaga caactttatt gtttctatca taaactattt 3600  
 atgtatctta attattaaaa tgatttactt tatggcacta gaaaatttac 3650  
 tgtggctttt ctgatctaac ttctagctaa aattgtatca ttggtcctaa 3700  
 aaaataaaaa tctttactaa taggcaattg aaggaatggt ttgctaacaa 3750  
 ccacagtaat ataatatgat ttacagata gatgcttccc cttggctatg 3800  
 acatggagaa agattttccc ataataataa ctaatattta tattaggttg 3850  
 gtgcaaaact agttgcggtt tttccatta aaagtaataa ccttactctt 3900

atacaaagtg gacactgtgg ggagatacag agaaatggaa gatacggatc 3950  
 ctgcctggag taggtaacct tgcttggaaa cccacatgc aaacgtcatg 4000  
 aggagaatta aaggagtatt atcagtaatg aagtttatca tgggtcatca 4050  
 atgagcatag attggtgtgg atcctgtaga ccctggtggtt ttctttgaag 4100  
 tgccctctcc taatgcagag gccttgaagc ttacagtata cacttgaaaa 4150  
 gtcacagata gctagaatta tgatctttga agttataact gtgatctgaa 4200  
 aatgtgtgtg gtggtatgac agcataccat taaatacatt tacatcacag 4250  
 ctcaaaggac tgtgatataa tccatttata tcacaactca aaggactgtg 4300  
 atataatcca tttatatcac agctcacagt ttctgaaaat gtataaaaga 4350  
 atctataatc tagtactgaa attactaaat tgggtaagat gatttaaag 4400  
 attttaattt taacatttta tttctagaat atatggctcc attttatttt 4450  
 atagtgtaaa gttgtatttc ctaaagtttg tgttttgtcg acagtatctt 4500  
 ttaaatgagt cttaaaaata aaggcatatt gttcatgttt aaaaaaaaaa 4550  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4600  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4649

<210> 114  
 <211> 515  
 <212> PRT  
 <213> Homo sapiens

<400> 114  
 Met Ala Pro Arg Gly Cys Ala Gly His Pro Pro Pro Pro Ser Pro  
 1 5 10 15  
 Gln Ala Cys Val Cys Pro Gly Lys Met Leu Ala Met Gly Ala Leu  
 20 25 30  
 Ala Gly Phe Trp Ile Leu Cys Leu Leu Thr Tyr Gly Tyr Leu Ser  
 35 40 45  
 Trp Gly Gln Ala Leu Glu Glu Glu Glu Gly Ala Leu Leu Ala  
 50 55 60  
 Gln Ala Gly Glu Lys Leu Glu Pro Ser Thr Thr Ser Thr Ser Gln  
 65 70 75  
 Pro His Leu Ile Phe Ile Leu Ala Asp Asp Gln Gly Phe Arg Asp  
 80 85 90  
 Val Gly Tyr His Gly Ser Glu Ile Lys Thr Pro Thr Leu Asp Lys  
 95 100 105  
 Leu Ala Ala Glu Gly Val Lys Leu Glu Asn Tyr Tyr Val Gln Pro

110	115	120
Ile Cys Thr Pro Ser Arg Ser Gln Phe	Ile Thr Gly Lys Tyr Gln	
125	130	135
Ile His Thr Gly Leu Gln His Ser Ile	Ile Arg Pro Thr Gln Pro	
140	145	150
Asn Cys Leu Pro Leu Asp Asn Ala Thr	Leu Pro Gln Lys Leu Lys	
155	160	165
Glu Val Gly Tyr Ser Thr His Met Val	Gly Lys Trp His Leu Gly	
170	175	180
Phe Asn Arg Lys Glu Cys Met Pro Thr	Arg Arg Gly Phe Asp Thr	
185	190	195
Phe Phe Gly Ser Leu Leu Gly Ser Gly	Asp Tyr Tyr Thr His Tyr	
200	205	210
Lys Cys Asp Ser Pro Gly Met Cys Gly	Tyr Asp Leu Tyr Glu Asn	
215	220	225
Asp Asn Ala Ala Trp Asp Tyr Asp Asn	Gly Ile Tyr Ser Thr Gln	
230	235	240
Met Tyr Thr Gln Arg Val Gln Gln Ile	Leu Ala Ser His Asn Pro	
245	250	255
Thr Lys Pro Ile Phe Leu Tyr Thr Ala	Tyr Gln Ala Val His Ser	
260	265	270
Pro Leu Gln Ala Pro Gly Arg Tyr Phe	Glu His Tyr Arg Ser Ile	
275	280	285
Ile Asn Ile Asn Arg Arg Arg Tyr Ala	Ala Met Leu Ser Cys Leu	
290	295	300
Asp Glu Ala Ile Asn Asn Val Thr Leu	Ala Leu Lys Thr Tyr Gly	
305	310	315
Phe Tyr Asn Asn Ser Ile Ile Ile Tyr	Ser Ser Asp Asn Gly Gly	
320	325	330
Gln Pro Thr Ala Gly Gly Ser Asn Trp	Pro Leu Arg Gly Ser Lys	
335	340	345
Gly Thr Tyr Trp Glu Gly Gly Ile Arg	Ala Val Gly Phe Val His	
350	355	360
Ser Pro Leu Leu Lys Asn Lys Gly Thr	Val Cys Lys Glu Leu Val	
365	370	375
His Ile Thr Asp Trp Tyr Pro Thr Leu	Ile Ser Leu Ala Glu Gly	
380	385	390
Gln Ile Asp Glu Asp Ile Gln Leu Asp	Gly Tyr Asp Ile Trp Glu	
395	400	405



Thr	Ile	Ser	Glu	Gly	Leu	Arg	Ser	Pro	Arg	Val	Asp	Ile	Leu	His
				410					415					420
Asn	Ile	Asp	Pro	Tyr	Thr	Pro	Arg	Gln	Lys	Met	Ala	Pro	Gly	Gln
				425					430					435
Gln	Ala	Met	Gly	Ser	Gly	Thr	Leu	Gln	Ser	Ser	Gln	Pro	Ser	Glu
				440					445					450
Cys	Ser	Thr	Gly	Asn	Cys	Leu	Gln	Glu	Ile	Leu	Ala	Thr	Ala	Thr
				455					460					465
Gly	Ser	Pro	Leu	Ser	Leu	Ser	Ala	Thr	Trp	Asp	Arg	Thr	Gly	Gly
				470					475					480
Thr	Met	Asn	Gly	Ser	Pro	Cys	Gln	Leu	Ala	Lys	Val	Tyr	Gly	Phe
				485					490					495
Ser	Thr	Ser	Gln	Pro	Thr	His	Met	Arg	Gly	Trp	Thr	Tyr	Leu	Thr
				500					505					510
Gly	Ile	Gln	Glu	Ser										
				515										

<210> 115  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 115  
 cccaaccocaa ctgtttacct ctgg 24

<210> 116  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 116  
 ctctctgagt gtacatctgt gtgg 24

<210> 117  
 <211> 53  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<220>  
 <221> unsure  
 <222> 33  
 <223> unknown base

<400> 117  
gccaccctac ctcagaaact gaaggaggtt ggntattcaa cgcatatggt 50  
cgg 53

<210> 118  
<211> 2260  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2009, 2026, 2033, 2055, 2074, 2078, 2086  
<223> unknown base

<400> 118  
cggacgcgtg ggtgcgagtg gagcggagga cccgagcggc tgaggagaga 50  
ggaggcggcg gcttagctgc tacgggggtcc ggccggcgcc ctcccagggg 100  
gggctcagga ggaggaagga ggaccctgc gagaatgcct ctgccctgga 150  
gccttgccgt cccgctgctg ctctcctggg tggcaggtgg tttcggaac 200  
gcggccagtg caaggcatca cgggttgta gcatcggcac gtcagcctgg 250  
ggtctgtcac tatggaacta aactggcctg ctgctacggc tggagaagaa 300  
acagcaaggg agtctgtgaa gctacatgcg aacctggatg taagtttggt 350  
gagtgcgtgg gaccaaacia atgcagatgc tttccaggat acaccgggaa 400  
aacctgcagt caagatgtga atgagtgtgg aatgaaaccc cggccatgcc 450  
aacacagatg tgtgaataca cacggaagct acaagtgtt ttgcctcagt 500  
ggccacatgc tcatgccaga tgctacgtgt gtgaactcta ggacatgtgc 550  
catgataaac tgtcagtaca gctgtgaaga cacagaagaa gggccacagt 600  
gcctgtgtcc atcctcagga ctccgcctgg ccccaaattg aagagactgt 650  
ctagatattg atgaatgtgc ctctggtaaa gtcactctgtc cctacaatcg 700  
aagatgtgtg aacacatttg gaagctacta ctgcaaattg cacatttggt 750  
tcgaactgca atatatcagt ggacgatatg actgtataga tataaatgaa 800  
tgtactatgg atagccatac gtgcagccac catgccaatt gcttcaatac 850  
ccaaggggcc ttcaagtgtg aatgcaagca gggatataaa ggcaatggac 900  
ttcgggtgtc tgctatccct gaaaattctg tgaaggaagt cctcagagca 950  
cctggtacca tcaaagacag aatcaagaag ttgcttgctc aaaaaacag 1000  
catgaaaaag aaggcaaaaa ttaaaaatgt taccccagaa cccaccagga 1050

ctcctacccc taaggtgaac ttgcagccct tcaactatga agagatagtt 1100  
 tccagaggcg ggaactctca tggaggtaaa aaagggatg aagagaaatg 1150  
 aaagaggggc ttgaggatga gaaaagagaa gagaaagccc tgaagaatga 1200  
 catagaggag cgaagcctgc gaggagatgt gtttttccct aaggtgaatg 1250  
 aagcaggtga attcggcctg attctggtcc aaaggaaagc gctaacttcc 1300  
 aaactggaac ataaagattt aaatatctcg gttgactgca gcttcaatca 1350  
 tgggatctgt gactggaaac aggatagaga agatgatttt gactggaatc 1400  
 ctgctgatcg agataatgct attggcttct atatggcagt tccggccttg 1450  
 gcaggtcaca agaaagacat tggccgattg aaacttctcc tacctgacct 1500  
 gcaaccccaa agcaacttct gtttgcctt tgattaccgg ctggccggag 1550  
 acaaagtcgg gaaacttcga gtgtttgtga aaaacagtaa caatgccctg 1600  
 gcatgggaga agaccacgag tgaggatgaa aagtggaaga cagggaaaat 1650  
 tcagttgtat caaggaactg atgctaccaa aagcatcatt tttgaagcag 1700  
 aacgtggcaa gggcaaaacc ggcgaaatcg cagtggatgg cgtcttgctt 1750  
 gtttcaggct tatgtccaga tagcctttta tctgtggatg actgaatggt 1800  
 actatcttta tatttgactt tgtatgtcag ttccctgggt tttttgatat 1850  
 tgcacatag gacctctggc attttagaat tactagctga aaaattgtaa 1900  
 tgtaccaaca gaaatattat tgtaagatgc ctttcttgta taagatatgc 1950  
 caatatattgc tttaaataatc atatcactgt atcttctcag tcatttctga 2000  
 atctttccnc attatattat aaaatntgga aangtcagtt tatctcccct 2050  
 cctcngtata tctgatttgt atangtangt tgatgngctt ctctctacaa 2100  
 catttctaga aaatagaaaa aaaagcacag agaaatgttt aactgtttga 2150  
 ctcttatgat acttcttgga aactatgaca tcaaagatag acttttgctt 2200  
 aagtggctta gctgggtctt tcatagccaa acttgtatat ttaattcttt 2250  
 gtaataataa 2260

<210> 119

<211> 338

<212> PRT

<213> Homo sapiens

<400> 119

Met	Pro	Leu	Pro	Trp	Ser	Leu	Ala	Leu	Pro	Leu	Leu	Leu	Ser	Trp
1				5					10				15	

Val	Ala	Gly	Gly	Phe	Gly	Asn	Ala	Ala	Ser	Ala	Arg	His	His	Gly	
				20					25					30	
Leu	Leu	Ala	Ser	Ala	Arg	Gln	Pro	Gly	Val	Cys	His	Tyr	Gly	Thr	
				35					40					45	
Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	Val	
				50					55					60	
Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
				65					70					75	
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	
				80					85					90	
Cys	Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	
				95					100					105	
Gln	His	Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	
				110					115					120	
Leu	Ser	Gly	His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	
				125					130					135	
Arg	Thr	Cys	Ala	Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	
				140					145					150	
Glu	Glu	Gly	Pro	Gln	Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	
				155					160					165	
Ala	Pro	Asn	Gly	Arg	Asp	Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	
				170					175					180	
Gly	Lys	Val	Ile	Cys	Pro	Tyr	Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	
				185					190					195	
Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	Ile	Gly	Phe	Glu	Leu	Gln	Tyr	
				200					205					210	
Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	Ile	Asn	Glu	Cys	Thr	Met	
				215					220					225	
Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	Cys	Phe	Asn	Thr	Gln	
				230					235					240	
Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	Lys	Gly	Asn	Gly	
				245					250					255	
Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	Glu	Val	Leu	
				260					265					270	
Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	Leu	Ala	
				275					280					285	
His	Lys	Asn	Ser	Met	Lys	Lys	Lys	Ala	Lys	Ile	Lys	Asn	Val	Thr	
				290					295					300	
Pro	Glu	Pro	Thr	Arg	Thr	Pro	Thr	Pro	Lys	Val	Asn	Leu	Gln	Pro	

09978192-101501

305

310

315

Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly  
320 325 330

Gly Lys Lys Gly Asn Glu Glu Lys  
335

<210> 120

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 120

cctcagtggc cacatgctca tg 22

<210> 121

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 121

ggctgcacgt atggctatcc atag 24

<210> 122

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 122

gataaactgt cagtacagct gtgaagacac agaagaagg ccacagtgcc 50

<210> 123

<211> 1199

<212> DNA

<213> Homo sapiens

<400> 123

gggagctgct gctgtggctg ctggtgctgt gcgcgctgct cctgctcttg 50

gtgcagctgc tgcgcttcct gagggctgac ggcgacctga cgctactatg 100

ggccgagtgg cagggacgac gcccagaatg ggagctgact gatatggtgg 150

tgtgggtgac tggagcctcg agtgaattg gtgaggagct ggcttaccag 200

ttgtctaaac taggagtttc tcttgtgctg tcagccagaa gagtgcata 250

gctggaaagg gtgaaaagaa gatgcctaga gaatggcaat ttaaaagaaa 300

aagatatact tgttttggcc cttgacctga ccgacactgg ttcccatgaa 350  
 gcggttacca aagctgttct ccaggagttt ggtagaatcg acattctggt 400  
 caacaatggt ggaatgtccc agcgttctct gtgcatggat accagcttgg 450  
 atgtctacag aaagctaata gagcttaact acttagggac ggtgtccttg 500  
 acaaaatgtg ttctgcctca catgatcgag aggaagcaag gaaagattgt 550  
 tactgtgaat agcatcctgg gtatcatatc tgtacctctt tccattggat 600  
 actgtgctag caagcatgct ctccgggggt tttttaatgg ccttcgaaca 650  
 gaacttgcca catacccagg tataatagtt tctaacattt gcccaggacc 700  
 tgtgcaatca aatattgtgg agaattccct agctggagaa gtcacaaaga 750  
 ctataggcaa taatggagac cagtcccaca agatgacaac cagtcgttgt 800  
 gtgcggctga tgttaatcag catggccaat gatttgaaag aagtttggat 850  
 ctcagaacaa cctttcttgt tagtaacata tttgtggcaa tacatgcaa 900  
 cctgggcctg gtggataacc aacaagatgg ggaagaaaag gattgagaac 950  
 ttttaagagt gtgtggatgc agactcttct tattttaaaa tctttaagac 1000  
 aaaacatgac tgaaaagagc acctgtactt ttcaagccac tggagggaga 1050  
 aatggaaaac atgaaaacag caatcttctt atgcttctga ataataaag 1100  
 actaatttgt gattttactt tttaatagat atgactttgc ttccaacatg 1150  
 gaatgaaata aaaaataaat aataaaagat tgccatgaat cttgcaaaa 1199

<210> 124  
 <211> 289  
 <212> PRT  
 <213> Homo sapiens

<400> 124  
 Met Val Val Trp Val Thr Gly Ala Ser Ser Gly Ile Gly Glu Glu  
 1 5 10 15  
 Leu Ala Tyr Gln Leu Ser Lys Leu Gly Val Ser Leu Val Leu Ser  
 20 25 30  
 Ala Arg Arg Val His Glu Leu Glu Arg Val Lys Arg Arg Cys Leu  
 35 40 45  
 Glu Asn Gly Asn Leu Lys Glu Lys Asp Ile Leu Val Leu Pro Leu  
 50 55 60  
 Asp Leu Thr Asp Thr Gly Ser His Glu Ala Ala Thr Lys Ala Val  
 65 70 75  
 Leu Gln Glu Phe Gly Arg Ile Asp Ile Leu Val Asn Asn Gly Gly

80

85

90

Met Ser Gln Arg Ser Leu Cys Met Asp Thr Ser Leu Asp Val Tyr  
95 100 105

Arg Lys Leu Ile Glu Leu Asn Tyr Leu Gly Thr Val Ser Leu Thr  
110 115 120

Lys Cys Val Leu Pro His Met Ile Glu Arg Lys Gln Gly Lys Ile  
125 130 135

Val Thr Val Asn Ser Ile Leu Gly Ile Ile Ser Val Pro Leu Ser  
140 145 150

Ile Gly Tyr Cys Ala Ser Lys His Ala Leu Arg Gly Phe Phe Asn  
155 160 165

Gly Leu Arg Thr Glu Leu Ala Thr Tyr Pro Gly Ile Ile Val Ser  
170 175 180

Asn Ile Cys Pro Gly Pro Val Gln Ser Asn Ile Val Glu Asn Ser  
185 190 195

Leu Ala Gly Glu Val Thr Lys Thr Ile Gly Asn Asn Gly Asp Gln  
200 205 210

Ser His Lys Met Thr Thr Ser Arg Cys Val Arg Leu Met Leu Ile  
215 220 225

Ser Met Ala Asn Asp Leu Lys Glu Val Trp Ile Ser Glu Gln Pro  
230 235 240

Phe Leu Leu Val Thr Tyr Leu Trp Gln Tyr Met Pro Thr Trp Ala  
245 250 255

Trp Trp Ile Thr Asn Lys Met Gly Lys Lys Arg Ile Glu Asn Phe  
260 265 270

Lys Ser Gly Val Asp Ala Asp Ser Ser Tyr Phe Lys Ile Phe Lys  
275 280 285

Thr Lys His Asp

<210> 125

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 125

gcaatgaact gggagctgc 19

<210> 126

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 126  
ctgtgaatag catcctggg 19

<210> 127  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 127  
cttttcaagc cactggaggg 20

<210> 128  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 128  
ctgtagacat ccaagctggg atcc 24

<210> 129  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 129  
aagagtctgc atccacacca ctc 23

<210> 130  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 130  
acctgacgct actatgggcc gaggggcagg gacgacgccc agaattg 46

<210> 131  
<211> 2365  
<212> DNA  
<213> Homo sapiens

<400> 131



gcgacgtggg caccgccatc agctgttcgc gcgtcttctc ctccaggtgg 50  
ggcagggggtt tcgggctggt ggagcatgtg ctgggacagg acagcatcct 100  
caatcaatcc aacagcatat tcggttgcat cttctacaca ctacagctat 150  
tgttaggttg cctgcggaca cgctgggcct ctgtcctgat gctgctgagc 200  
tccttggtgt ctctcgctgg ttctgtctac ctggcctgga tcctgttctt 250  
cgtgctctat gatttctgca ttgtttgtat caccacctat gctatcaacg 300  
tgagcctgat gtggctcagt ttccggaagg tccaagaacc ccagggcaag 350  
gctaagaggc actgagccct caacccaagc caggctgacc tcatctgctt 400  
tgctttggtc ttcaagccgc tcagcgtgcc tgtggacagc gtggccccgg 450  
ccccccaag cctcaggagg gcaacacagt ccctggcgag tggccctggc 500  
aggccagtgt gaggaggcaa ggagcccaca tctgcagcgg ctccctggtg 550  
gcagacacct gggctctcac tgctgcccac tgctttgaaa aggcagcagc 600  
aacagaactg aattcctggt cagtggctct gggttctctg cagcgtgagg 650  
gactcagccc tggggccgaa gaggtggggg tggctgccct gcagttgccc 700  
agggcctata accactacag ccagggtca gacctggccc tgctgcagct 750  
cgcccccccc acgacccaca caccctctg cctgccccag cccgccccatc 800  
gcttccccct tggagcctcc tgctgggcca ctggctggga tcaggacacc 850  
agtgatgctc ctgggacctc acgcaatctg cgctgcgtc tcatcagtcg 900  
ccccacatgt aactgtatct acaaccagct gcaccagcga cacctgtcca 950  
acccggcccc gcctgggatg ctatgtgggg gccccagcc tggggtgcag 1000  
ggccccctgtc aggagattc cgggggccct gtgctgtgcc tcgagcctga 1050  
cggacactgg gttcaggctg gcatcatcag ctttgcatca agctgtgccc 1100  
aggaggacgc tcctgtgctg ctgaccaaca cagctgctca cagttcctgg 1150  
ctgcaggctc gagttcaggg ggcagctttc ctggcccaga gccagagac 1200  
cccgagatg agtgatgagg acagctgtgt agcctgtgga tccttgagga 1250  
cagcaggtcc ccaggcagga gcaccctccc catggccctg ggaggccagg 1300  
ctgatgcacc agggacagct ggccctgtggc ggagccctgg tgtcagagga 1350  
ggcgtgcta actgctgcc actgcttcat tgggcgccag gccccagagg 1400  
aatggagcgt agggctgggg accagaccgg aggagtgggg cctgaagcag 1450

ctcactcctgc atggagccta caccaccct gaggggggct acgacatggc 1500  
 cctcctgctg ctggcccagc ctgtgacact gggagccagc ctgcggcccc 1550  
 tctgcctgcc ctatcctgac caccacctgc ctgatgggga gcgtggctgg 1600  
 gttctgggac gggcccgcgc aggagcaggc atcagctccc tccagacagt 1650  
 gcccgtagacc ctctggggc ctagggcctg cagccggctg catgcagctc 1700  
 ctgggggtga tggcagccct attctgccgg ggatggtgtg taccagtgt 1750  
 gtgggtgagc tgcccagctg tgagggcctg tctggggcac cactggtgca 1800  
 tgaggtgagg ggcacatggt tcttgccgg gctgcacagc ttcggagatg 1850  
 cttgccaaagg ccccgccagg ccggcgggtct tcaccgcgct ccctgcctat 1900  
 gaggaactggg tcagcagttt ggactggcag gtctacttcg ccgaggaacc 1950  
 agagcccag gctgagcctg gaagctgcct ggccaacata agccaaccaa 2000  
 ccagctgctg acaggggacc tggccattct caggacaaga gaatgcaggc 2050  
 aggcaaattg cattactgcc cctgtcctcc ccaccctgtc atgtgtgatt 2100  
 ccaggcacca gggcaggccc agaagcccag cagctgtggg aaggaacctg 2150  
 cctggggcca caggtgcca ctccccacc tgcaggacag gggtgtctgt 2200  
 ggacactccc acacccaact ctgctaccaa gcaggcgtct cagctttcct 2250  
 cctcctttac tctttcagat acaatcacgc cagccacgtt gttttgaaaa 2300  
 tttctttttt tggggggcag cagttttcct ttttttaaac ttaaataaat 2350  
 tgttacaaaa taaaa 2365

<210> 132  
 <211> 571  
 <212> PRT  
 <213> Homo sapiens

<400> 132  
 Met Leu Leu Ser Ser Leu Val Ser Leu Ala Gly Ser Val Tyr Leu  
 1 5 10 15  
 Ala Trp Ile Leu Phe Phe Val Leu Tyr Asp Phe Cys Ile Val Cys  
 20 25 30  
 Ile Thr Thr Tyr Ala Ile Asn Val Ser Leu Met Trp Leu Ser Phe  
 35 40 45  
 Arg Lys Val Gln Glu Pro Gln Gly Lys Ala Lys Arg His Gly Asn  
 50 55 60  
 Thr Val Pro Gly Glu Trp Pro Trp Gln Ala Ser Val Arg Arg Gln  
 65 70 75

Gly	Ala	His	Ile	Cys	Ser	Gly	Ser	Leu	Val	Ala	Asp	Thr	Trp	Val	
				80					85					90	
Leu	Thr	Ala	Ala	His	Cys	Phe	Glu	Lys	Ala	Ala	Ala	Thr	Glu	Leu	
				95					100					105	
Asn	Ser	Trp	Ser	Val	Val	Leu	Gly	Ser	Leu	Gln	Arg	Glu	Gly	Leu	
				110					115					120	
Ser	Pro	Gly	Ala	Glu	Glu	Val	Gly	Val	Ala	Ala	Leu	Gln	Leu	Pro	
				125					130					135	
Arg	Ala	Tyr	Asn	His	Tyr	Ser	Gln	Gly	Ser	Asp	Leu	Ala	Leu	Leu	
				140					145					150	
Gln	Leu	Ala	His	Pro	Thr	Thr	His	Thr	Pro	Leu	Cys	Leu	Pro	Gln	
				155					160					165	
Pro	Ala	His	Arg	Phe	Pro	Phe	Gly	Ala	Ser	Cys	Trp	Ala	Thr	Gly	
				170					175					180	
Trp	Asp	Gln	Asp	Thr	Ser	Asp	Ala	Pro	Gly	Thr	Leu	Arg	Asn	Leu	
				185					190					195	
Arg	Leu	Arg	Leu	Ile	Ser	Arg	Pro	Thr	Cys	Asn	Cys	Ile	Tyr	Asn	
				200					205					210	
Gln	Leu	His	Gln	Arg	His	Leu	Ser	Asn	Pro	Ala	Arg	Pro	Gly	Met	
				215					220					225	
Leu	Cys	Gly	Gly	Pro	Gln	Pro	Gly	Val	Gln	Gly	Pro	Cys	Gln	Gly	
				230					235					240	
Asp	Ser	Gly	Gly	Pro	Val	Leu	Cys	Leu	Glu	Pro	Asp	Gly	His	Trp	
				245					250					255	
Val	Gln	Ala	Gly	Ile	Ile	Ser	Phe	Ala	Ser	Ser	Cys	Ala	Gln	Glu	
				260					265					270	
Asp	Ala	Pro	Val	Leu	Leu	Thr	Asn	Thr	Ala	Ala	His	Ser	Ser	Trp	
				275					280					285	
Leu	Gln	Ala	Arg	Val	Gln	Gly	Ala	Ala	Phe	Leu	Ala	Gln	Ser	Pro	
				290					295					300	
Glu	Thr	Pro	Glu	Met	Ser	Asp	Glu	Asp	Ser	Cys	Val	Ala	Cys	Gly	
				305					310					315	
Ser	Leu	Arg	Thr	Ala	Gly	Pro	Gln	Ala	Gly	Ala	Pro	Ser	Pro	Trp	
				320					325					330	
Pro	Trp	Glu	Ala	Arg	Leu	Met	His	Gln	Gly	Gln	Leu	Ala	Cys	Gly	
				335					340					345	
Gly	Ala	Leu	Val	Ser	Glu	Glu	Ala	Val	Leu	Thr	Ala	Ala	His	Cys	
				350					355					360	
Phe	Ile	Gly	Arg	Gln	Ala	Pro	Glu	Glu	Trp	Ser	Val	Gly	Leu	Gly	

	365		370		375
Thr Arg Pro Glu	Glu Trp Gly Leu Lys	Gln Leu Ile Leu His	Gly		
	380	385	390		
Ala Tyr Thr His	Pro Glu Gly Gly Tyr	Asp Met Ala Leu Leu	Leu		
	395	400	405		
Leu Ala Gln Pro	Val Thr Leu Gly Ala	Ser Leu Arg Pro Leu	Cys		
	410	415	420		
Leu Pro Tyr Pro	Asp His His Leu Pro	Asp Gly Glu Arg Gly	Trp		
	425	430	435		
Val Leu Gly Arg	Ala Arg Pro Gly Ala	Gly Ile Ser Ser Leu	Gln		
	440	445	450		
Thr Val Pro Val	Thr Leu Leu Gly Pro	Arg Ala Cys Ser Arg	Leu		
	455	460	465		
His Ala Ala Pro	Gly Gly Asp Gly Ser	Pro Ile Leu Pro Gly	Met		
	470	475	480		
Val Cys Thr Ser	Ala Val Gly Glu Leu	Pro Ser Cys Glu Gly	Leu		
	485	490	495		
Ser Gly Ala Pro	Leu Val His Glu Val	Arg Gly Thr Trp Phe	Leu		
	500	505	510		
Ala Gly Leu His	Ser Phe Gly Asp Ala	Cys Gln Gly Pro Ala	Arg		
	515	520	525		
Pro Ala Val Phe	Thr Ala Leu Pro Ala	Tyr Glu Asp Trp Val	Ser		
	530	535	540		
Ser Leu Asp Trp	Gln Val Tyr Phe Ala	Glu Glu Pro Glu Pro	Glu		
	545	550	555		
Ala Glu Pro Gly	Ser Cys Leu Ala Asn	Ile Ser Gln Pro Thr	Ser		
	560	565	570		

Cys

<210> 133

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 133

cctgtgctgt gcctcgagcc tgac 24

<210> 134

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 134

gtgggcagca gttagcaccg cctc 24

<210> 135

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 135

ggctggcatc atcagctttg catcaagctg tgcccaggag gacgc 45

<210> 136

<211> 1998

<212> DNA

<213> Homo sapiens

<400> 136

cgggcccgc cccgccccca ttccggccgg gcctcgctgc ggcggcgact 50

gagccaggct gggccgcgtc cctgagtcac agagtcggcg cggcgcgga 100

ggggcagcct tccaccacgg ggagcccagc tgtcagccgc ctccaggaa 150

gatgctgcgt cggcggggca gccctggcat ggggtgtgat gtgggtgcag 200

ccctgggagc actgtggttc tgcctcacag gagccctgga ggtccaggtc 250

cctgaagacc cagtgggtgg actggtgggc accgatgcca ccctgtgctg 300

ctccttctcc cctgagcctg gcttcagcct ggcacagctc aacctcatct 350

ggcagctgac agatacaaaa cagctgggtgc acagctttgc tgaggggcag 400

gaccagggca gcgcctatgc caaccgcacg gccctcttcc cggacctgct 450

ggcacagggc aaogcatccc tgaggctgca gcgcgtgcgt gtggcgagac 500

agggcagctt cacctgcttc gtgagcatcc gggatttcgg cagcgctgcc 550

gtcagcctgc aggtggccgc tccctactcg aagcccagca tgaccctgga 600

gcccacaag gacctgcggc caggggacac ggtgaccatc acgtgctcca 650

gctaccaggg ctaccctgag gctgaggtgt tctggcagga tgggcagggt 700

gtgcccctga ctggcaacgt gaccacgtcg cagatggcca acgagcaggg 750

cttggttgat gtgcacagcg tctgcggggt ggtgctgggt gcgaatggca 800

cctacagctg cctggtgcgc aaccccgctg tgcagcagga tgcgcacrgc 850

tctgtcacca tcacagggca gcctatgaca ttccccccag aggccctgtg 900  
 ggtgaccgtg gggctgtctg tctgtctcat tgcactgctg gtggccctgg 950  
 ctttcgtgtg ctggagaaag atcaaacaga gctgtgagga ggagaatgca 1000  
 ggagctgagg accaggatgg ggagggagaa ggctccaaga cagccctgca 1050  
 gcctctgaaa cactctgaca gcaaagaaga tgatggacaa gaaatagcct 1100  
 gaccatgagg accagggagc tgctaccctt ccctacagct cctaccctct 1150  
 ggctgcaatg gggctgcact gtgagccctg cccccaacag atgcatcctg 1200  
 ctctgacagg tgggctcctt ctccaaagga tgcgatacac agaccactgt 1250  
 gcagccttat ttctccaatg gacatgattc ccaagtcata ctgctgcctt 1300  
 ttttcttata gacacaatga acagaccacc cacaacctta gttctctaag 1350  
 tcatcctgcc tgctgcctta tttcacagta catacatttc ttagggacac 1400  
 agtacactga ccacatcacc accctcttct tccagtgtgt cgtggaccat 1450  
 ctggctgcct tttttctcca aaagatgcaa tattcagact gactgacccc 1500  
 ctgccttatt tcaccaaaga cagcatgcat agtcaccccg gccttgtttc 1550  
 tccaatggcc gtgatacact agtgatcatg ttcagccctg cttccacctg 1600  
 catagaatct tttcttctca gacagggaca gtgcggcctc aacatctcct 1650  
 ggagtctaga agctgtttcc tttccctcc ttcctccctg cccaagtga 1700  
 agacagggca gggccaggaa tgctttgggg acaccgaggg gactgcccc 1750  
 cccccccacc atggtgctat tctggggctg gggcagtcct ttctggctt 1800  
 gcctctggcc agctcctggc ctctggtaga gtgagacttc agacgttctg 1850  
 atgccttccg gatgtcatct ctccctgccc caggaatgga agatgtgagg 1900  
 acttctaatt taaatgtggg actcggaggg attttgtaaa ctgggggtat 1950  
 attttgggga aaataaatgt ctttgtaaaa aaaaaaaaaa aaaaaaaaa 1998

<210> 137  
 <211> 316  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 233  
 <223> unknown amino acid

<400> 137  
 Met Leu Arg Arg Arg Gly Ser Pro Gly Met Gly Val His Val Gly

1	5	10	15
Ala Ala Leu Gly	Ala Leu Trp Phe Cys	Leu Thr Gly Ala Leu	Glu
20		25	30
Val Gln Val Pro	Glu Asp Pro Val Val	Ala Leu Val Gly Thr	Asp
35		40	45
Ala Thr Leu Cys	Cys Ser Phe Ser Pro	Glu Pro Gly Phe Ser	Leu
50		55	60
Ala Gln Leu Asn	Leu Ile Trp Gln Leu	Thr Asp Thr Lys Gln	Leu
65		70	75
Val His Ser Phe	Ala Glu Gly Gln Asp	Gln Gly Ser Ala Tyr	Ala
80		85	90
Asn Arg Thr Ala	Leu Phe Pro Asp Leu	Leu Ala Gln Gly Asn	Ala
95		100	105
Ser Leu Arg Leu	Gln Arg Val Arg Val	Ala Asp Glu Gly Ser	Phe
110		115	120
Thr Cys Phe Val	Ser Ile Arg Asp Phe	Gly Ser Ala Ala Val	Ser
125		130	135
Leu Gln Val Ala	Ala Pro Tyr Ser Lys	Pro Ser Met Thr Leu	Glu
140		145	150
Pro Asn Lys Asp	Leu Arg Pro Gly Asp	Thr Val Thr Ile Thr	Cys
155		160	165
Ser Ser Tyr Gln	Gly Tyr Pro Glu Ala	Glu Val Phe Trp Gln	Asp
170		175	180
Gly Gln Gly Val	Pro Leu Thr Gly Asn	Val Thr Thr Ser Gln	Met
185		190	195
Ala Asn Glu Gln	Gly Leu Phe Asp Val	His Ser Val Leu Arg	Val
200		205	210
Val Leu Gly Ala	Asn Gly Thr Tyr Ser	Cys Leu Val Arg Asn	Pro
215		220	225
Val Leu Gln Gln	Asp Ala His Xaa Ser	Val Thr Ile Thr Gly	Gln
230		235	240
Pro Met Thr Phe	Pro Pro Glu Ala Leu	Trp Val Thr Val Gly	Leu
245		250	255
Ser Val Cys Leu	Ile Ala Leu Leu Val	Ala Leu Ala Phe Val	Cys
260		265	270
Trp Arg Lys Ile	Lys Gln Ser Cys Glu	Glu Glu Asn Ala Gly	Ala
275		280	285
Glu Asp Gln Asp	Gly Glu Gly Glu Gly	Ser Lys Thr Ala Leu	Gln
290		295	300

Pro	Leu	Lys	His	Ser	Asp	Ser	Lys	Glu	Asp	Asp	Gly	Gln	Glu	Ile
				305					310					315

Ala

<210> 138  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 138  
 ctggcacagc tcaacctcat ctgg 24

<210> 139  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 139  
 gctgtctgtc tgtctcattg 20

<210> 140  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 140  
 ggacacagta tactgaccac 20

<210> 141  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 141  
 tgcgaaccag gcagctgtaa gtgc 24

<210> 142  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe



<400> 142  
tggaagaaga ggggtggtgat gtgg 24

<210> 143  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 143  
cagctgacag acaccaaaca gctggtgcac agtttcaccg aaggc 45

<210> 144  
<211> 2336  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 1620, 1673  
<223> unknown base

<400> 144  
ttcgtgaccc ttgagaaaag agttggtggt aaatgtgcc cgtcttctaa 50  
gaagggggag tcctgaactt gtctgaagcc cttgtccgta agccttgaac 100  
tacgttctta aatctatgaa gtogagggac ctttcgctgc tttttagagg 150  
acttctttcc ttgcttcagc aacatgaggc ttttcttgtg gaacgcggtc 200  
ttgactctgt tcgtcacttc tttgattggg gctttgatcc ctgaaccaga 250  
agtgaaaatt gaagttctcc agaagccatt catctgccat cgcaagacca 300  
aaggagggga tttgatgttg gtccactatg aaggctactt agaaaaggac 350  
ggctccttat ttcaactccac tcacaaacat aacaatggtc agcccatttg 400  
gtttaccctg ggcatcctgg aggctctcaa aggttgggac cagggcttga 450  
aaggaatgtg tgtaggagag aagagaaagc tcatcattcc tcctgctctg 500  
ggctatggaa aagaaggaaa aggtaaaatt cccccagaaa gtacactgat 550  
atttaatat gatctcctgg agattcgaaa tggaccaaga tcccatgaat 600  
cattccaaga aatggatctt aatgatgact ggaaactctc taaagatgag 650  
gttaaagcat atttaaagaa ggagtttgaa aaacatggtg cgggtggtgaa 700  
tgaaagtcac catgatgctt tgggtggagga tatttttgat aaagaagatg 750  
aagacaaaga tgggtttata tctgccagag aatttacata taaacacgat 800  
gagttataga gatacatcta cccttttaat atagcactca tctttcaaga 850

gagggcagtc atcttttaaag aacattttat ttttatacaa tggtctttct 900  
tgctttgttt tttattttta tatatttttt ctgactccta tttaaagaac 950  
cccttagggt tctaagtacc catttctttc tgataagtta ttgggaagaa 1000  
aaagctaatt ggtctttgaa tagaagactt ctggacaatt tttcactttc 1050  
acagatatga agctttgttt tacttttctca cttataaatt taaaatgttg 1100  
caactgggaa tataccacga catgagacca gggtatagca caaattagca 1150  
ccctatattt ctgcttccct ctattttctc caagttagag gtcaacattt 1200  
gaaaagcctt ttgcaatagc ccaaggcttg ctattttcat gttataatga 1250  
aatagtttat gtgtaactgg ctctgagtct ctgcttgagg accagaggaa 1300  
aatggttggt ggacctgact tggttaatggc tactgtctta ctaaggagat 1350  
gtgcaatgct gaagttagaa acaagggttaa tagccaggca tgggtggctca 1400  
tgcttgtaat cccagcactt tgggaggctg aggcggggcg atcacctgag 1450  
gttgggagtt cgagaccagc ctgaccaaca cggagaaacc ctatctctac 1500  
taaaaataca aagtagcccg gcgtggtgat gcgtgcctgt aatcccagct 1550  
accaggaag gctgaggcgg cagaatcact tgaacccgag gccgagggtg 1600  
cggtaagccg agatcacctn cagcctggac actctgtctc gaaaaaagaa 1650  
aagaacacgg ttaataccat atnaatatgt atgcattgag acatgctacc 1700  
taggacttaa gctgatgaag cttggctcct agtgattggt ggcctattat 1750  
gataaatagg acaaatcatt tatgtgtgag tttctttgta ataaaatgta 1800  
tcaatatggt atagatgagg tagaaagtta tatttatatt caatatttac 1850  
ttcttaaggc tagcgaata tccttctctg ttctttaatg ggtagtctat 1900  
agtatattat actacaataa cattgtatca taagataaag tagtaaacca 1950  
gtctacattt tcccatttct gtctcatcaa aaactgaagt tagctgggtg 2000  
tgggtggctca tgcttgtaat cccagcactt tggggggcaa ggagggtgga 2050  
tcacttgaga tcaggagttc aagaccagcc tggccaacat ggtgaaacct 2100  
tgtctctact aaaaatacaa aaattagcca ggcgtggtgg tgcacacctg 2150  
tagtcccagc tactcgggag gctgagacag gagatttgct tgaacccggg 2200  
aggcggaggt tgcagtgagc caagattgtg ccaactgcact ccagcctggg 2250  
tgacagagca agactccatc tcaaaaaaaaa aaaaaagaag cagacctaca 2300

gcagctacta ttgaataaat acctatcctg gatttt 2336

<210> 145  
 <211> 211  
 <212> PRT  
 <213> Homo sapiens

<400> 145  
 Met Arg Leu Phe Leu Trp Asn Ala Val Leu Thr Leu Phe Val Thr  
   1                  5                  10                  15  
 Ser Leu Ile Gly Ala Leu Ile Pro Glu Pro Glu Val Lys Ile Glu  
                   20                  25                  30  
 Val Leu Gln Lys Pro Phe Ile Cys His Arg Lys Thr Lys Gly Gly  
                   35                  40                  45  
 Asp Leu Met Leu Val His Tyr Glu Gly Tyr Leu Glu Lys Asp Gly  
                   50                  55                  60  
 Ser Leu Phe His Ser Thr His Lys His Asn Asn Gly Gln Pro Ile  
                   65                  70                  75  
 Trp Phe Thr Leu Gly Ile Leu Glu Ala Leu Lys Gly Trp Asp Gln  
                   80                  85                  90  
 Gly Leu Lys Gly Met Cys Val Gly Glu Lys Arg Lys Leu Ile Ile  
                   95                  100                  105  
 Pro Pro Ala Leu Gly Tyr Gly Lys Glu Gly Lys Gly Lys Ile Pro  
                   110                  115                  120  
 Pro Glu Ser Thr Leu Ile Phe Asn Ile Asp Leu Leu Glu Ile Arg  
                   125                  130                  135  
 Asn Gly Pro Arg Ser His Glu Ser Phe Gln Glu Met Asp Leu Asn  
                   140                  145                  150  
 Asp Asp Trp Lys Leu Ser Lys Asp Glu Val Lys Ala Tyr Leu Lys  
                   155                  160                  165  
 Lys Glu Phe Glu Lys His Gly Ala Val Val Asn Glu Ser His His  
                   170                  175                  180  
 Asp Ala Leu Val Glu Asp Ile Phe Asp Lys Glu Asp Glu Asp Lys  
                   185                  190                  195  
 Asp Gly Phe Ile Ser Ala Arg Glu Phe Thr Tyr Lys His Asp Glu  
                   200                  205                  210

Leu

<210> 146  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 146  
ctttccttgc ttcagcaaca tgaggc 26

<210> 147  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 147  
gccagagca ggaggaatga tgagc 25

<210> 148  
<211> 49  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 148  
gtggaacgcg gtcttgactc tgctcgctcac ttctttgatt ggggctttg 49

<210> 149  
<211> 2196  
<212> DNA  
<213> Homo sapiens

<400> 149  
aataaagctt ccttaatggt gtatatgtct ttgaagtaca tccgtgcatt 50  
tttttttagc atccaaccat tctcccttg tagttctcgc cccctcaa 100  
cacctctcc cgtagccac ccgactaaca tctcagctc tgaaaatgca 150  
cagagatgcc tggctacctc gccctgcctt cagcctcagc gggctcagtc 200  
tctttttctc tttggtgcc ccaggacgga gcatggaggt cacagtacct 250  
gccacctca acgtctcaa tggctctgac gccgcctgc cctgcacctt 300  
caactcctgc tacacagtga accacaaaca gttctccctg aactggactt 350  
accaggagtg caacaactgc tctgaggaga tgttctcca gttccgcatg 400  
aagatcatta acctgaagct ggagcgggtt caagaccgcg tggagttctc 450  
aggggaacccc agcaagtacg atgtgtcggg gatgctgaga aacgtgcagc 500  
cggaggatga ggggatttac aactgctaca tcatgaaccc ccctgaccgc 550  
cacctgggcc atggcaagat ccatctgcag gtcctcatgg aagagccccc 600

tgagcgggac tccacggtgg ccgtgattgt ggggtgcctcc gtcgggggct 650  
 tcctggctgt ggtcatcttg gtgctgatgg tggccaagtg tgtgaggaga 700  
 aaaaaagagc agaagctgag cacagatgac ctgaagaccg aggaggaggg 750  
 caagacggac ggtgaaggca acccgatga tggcgccaag tagtgggtgg 800  
 ccggccctgc agcctcccggt gtcccggtctc ctccctctc cgccctgtac 850  
 agtgaccctg cctgctcgct cttggtgtgc ttcccgtagc ctaggacccc 900  
 agggcccacc tggggcctcc tgaacccccg acttcgtatc tcccaccctg 950  
 caccaagagt gacccactct cttccatccg agaaacctgc catgctctgg 1000  
 gacgtgtggg ccctggggag aggagagaaa gggctccac ctgccagtcc 1050  
 ctggggggag gcaggaggca catgtgaggg tcccagaga gaagggagtg 1100  
 ggtgggcagg ggtagaggag gggccgctgt cacctgccca gtgcttgct 1150  
 ggcagtggct tcagagagga cctgggtggg agggagggtt ttctgtgtgt 1200  
 gacagcgctc cctcaggagg gccttgccct ggcacggctg tgctcctccc 1250  
 ctgctcccag ccagagcag ccatcagggt ggaggtgacg atgagttcct 1300  
 gaaacttgga ggggcatgtt aaagggatga ctgtgcattc cagggcactg 1350  
 acggaaagcc agggctgcag gcaaagctgg acatgtgcc tggcccagga 1400  
 ggccatgttg ggccctcggt tccattgcta gtggcctcct tggggctcct 1450  
 gttggctcct aatcccttag gactgtggat gaggccagac tggaagagca 1500  
 gctccaggta gggggccatg tttcccagcg gggaccacc aacagaggcc 1550  
 agtttcaaag tcagctgagg ggctgagggg tggggctcca tggatgaatgc 1600  
 aggttgctgc aggcctctgcc ttctccatgg ggtaaccacc ctgcctggg 1650  
 caggggcagc caaggctggg aaatgaggag gccatgcaca gggggggca 1700  
 gctttctttg gggcttcagt gagaactctc ccagttgcc ttggtggggt 1750  
 ttccacctgg cttttggcta cagagagga agggaaagcc tgaggccggc 1800  
 ataaggggag gccttggaac ctgagctgcc aatgccagcc ctgtcccatc 1850  
 tgcggccacg ctactcgctc ctctcccaac aactcccttc gtggggacaa 1900  
 aagtgacaat tgtaggccag gcacagtggc tcacgcctgt aatcccagca 1950  
 ctttgggagg ccaaggcggg tggattacct ccatctgttt agtagaaatg 2000  
 ggcaaaaccc catctctact aaaaatacaa gaattagctg ggcgtgggtg 2050

cgtgtgacctg taatcccagc tatttgggag gctgaggcag gagaatcgct 2100  
 tgagccccggg aagcagaggt tgcagtgaac tgagatagtg atagtgccac 2150  
 tgcaattcag cctgggtgac atagagagac tccatctcaa aaaaaa 2196

<210> 150  
 <211> 215  
 <212> PRT  
 <213> Homo sapiens

<400> 150  
 Met His Arg Asp Ala Trp Leu Pro Arg Pro Ala Phe Ser Leu Thr  
 1 5 10 15  
 Gly Leu Ser Leu Phe Phe Ser Leu Val Pro Pro Gly Arg Ser Met  
 20 25 30  
 Glu Val Thr Val Pro Ala Thr Leu Asn Val Leu Asn Gly Ser Asp  
 35 40 45  
 Ala Arg Leu Pro Cys Thr Phe Asn Ser Cys Tyr Thr Val Asn His  
 50 55 60  
 Lys Gln Phe Ser Leu Asn Trp Thr Tyr Gln Glu Cys Asn Asn Cys  
 65 70 75  
 Ser Glu Glu Met Phe Leu Gln Phe Arg Met Lys Ile Ile Asn Leu  
 80 85 90  
 Lys Leu Glu Arg Phe Gln Asp Arg Val Glu Phe Ser Gly Asn Pro  
 95 100 105  
 Ser Lys Tyr Asp Val Ser Val Met Leu Arg Asn Val Gln Pro Glu  
 110 115 120  
 Asp Glu Gly Ile Tyr Asn Cys Tyr Ile Met Asn Pro Pro Asp Arg  
 125 130 135  
 His Arg Gly His Gly Lys Ile His Leu Gln Val Leu Met Glu Glu  
 140 145 150  
 Pro Pro Glu Arg Asp Ser Thr Val Ala Val Ile Val Gly Ala Ser  
 155 160 165  
 Val Gly Gly Phe Leu Ala Val Val Ile Leu Val Leu Met Val Val  
 170 175 180  
 Lys Cys Val Arg Arg Lys Lys Glu Gln Lys Leu Ser Thr Asp Asp  
 185 190 195  
 Leu Lys Thr Glu Glu Glu Gly Lys Thr Asp Gly Glu Gly Asn Pro  
 200 205 210  
 Asp Asp Gly Ala Lys  
 215

<210> 151

<211> 524  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 103, 233  
 <223> unknown base

<400> 151  
 gttgtatatg tcttgaagta catccgtgca ttttttttag catccaacca 50  
 tcctcccttg tagttctcgc cccctcaa at caccttctcc cttagccac 100  
 ccnactaaca tctcagtctc tgaaaatgca cagagatgcc tggctacctc 150  
 gccctgcctt cagcctcacg gggctcagtc tctttttctc tttggtgcc 200  
 ccaggacgga gcatggaggt ccacagtacc tgnccaccct caacgtcctc 250  
 aatggctctg acgcccgcct gccctgcct tcaactcctg ctacacagtg 300  
 aaccacaaac agttctccct gaactggaact taccaggagt gcaacaactg 350  
 ctctgaggag atgttctctc agttccgcac gaagatcatt aacctgaagc 400  
 tggagcgggt tcaagaccgc gtggagttct caggggaacc cagcaagtac 450  
 gatgtgtcgg tgatgctgag aaacgtgcag ccggaggatg aggggattta 500  
 caactgctac atcatgaacc cccc 524

<210> 152  
 <211> 368  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 56, 123  
 <223> unknown base

<400> 152  
 tcacgggggt catctctttt tctcttttgt gccaccagg acggagcatg 50  
 gaggtncaca tacctgccac cctcaacgtc ctcaatggct ttgacgccc 100  
 cctgcctctg accttcaact ccngctacac agtgaaccac aaacagttct 150  
 ccctgaactg gatttaccag gactgcaaca actggctctg aggagatgtt 200  
 cctccagttc ccgcatggaa gatcatttaa cctgaaagct ggaagcgggt 250  
 ttcaagaacc gcgtggaagt ttctcagga accccagcaa gtacgatgtg 300  
 tcggtgatgc tgagaaacgt gcagccggag gatgagggga tttacaactg 350  
 ctacatcatg aaccccc 368

<210> 153  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 153  
 acggagcatg gaggtccaca gtac 24

<210> 154  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 154  
 gcacgtttct cagcatcacc gac 23

<210> 155  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 155  
 cgctgcct gcaccttcaa ctctgtctac acagtgaacc acaaacagtt 50

<210> 156  
 <211> 2680  
 <212> DNA  
 <213> Homo sapiens

<400> 156  
 tgcggcgacc gtcgtacacc atgggcctcc acctccgccc ctaccgtgtg 50  
 gggctgctcc cggatggcct cctgttctct ttgctgctgc taatgctgct 100  
 cgcggaccca gcgctcccg cgggacgtca cccccagtg gtgctgggtcc 150  
 ctggtgattt gggtaaccaa ctggaagcca agctggacaa gccgacagt 200  
 gtgcactacc totgctocaa gaagaccgaa agctacttca caatctggct 250  
 gaacctggaa ctgctgctgc ctgtcatcat tgactgctgg attgacaata 300  
 tcaggctggt ttacaacaaa acatccaggg ccaccagtt tcctgatggt 350  
 gtggatgtac gtgtccctgg ctttggaag accttctcac tggagttcct 400  
 ggaccccagc aaaagcagcg tgggttctta tttccacacc atggtggaga 450  
 gccttgtggg ctggggctac aacgggggtg aggatgtccg aggggctccc 500



tatgactggc gccgagcccc aaatgaaaac gggccctact tcctggccct 550  
 ccgcgagatg atcgaggaga tgtaccagct gtatgggggc cccgtggtgc 600  
 tggttgcccc cagtatgggc aacatgtaca cgctctactt tctgcagcgg 650  
 cagccgcagg cctggaagga caagtatatc cgggccttcg tgtcactggg 700  
 tgcgccctgg gggggcggtg ccaagaccct gcgcgtcctg gcttcaggag 750  
 acaacaaccg gatcccagtc atcgggcccc tgaagatccg ggagcagcag 800  
 cggtcagctg tctccaccag ctggctgctg ccctacaact acacatgggtc 850  
 acctgagaag gtgttcgtgc agacaccac aatcaactac aactgcggg 900  
 actaccgcaa gttcttccag gacatcggct ttgaagatgg ctggctcatg 950  
 cggcaggaca cagaagggtg ggtggaagcc acgatgccac ctggcgtgca 1000  
 gctgcactgc ctctatggta ctggcgtccc cacaccagac tccttctact 1050  
 atgagagctt ccctgaccgt gaccctaaaa tctgctttgg tgacggcgat 1100  
 ggtactgtga acttgaagag tgccctgcag tgccaggcct ggcagagccg 1150  
 ccaggagcac caagtgttgc tgcaggagct gccaggcagc gagcacatcg 1200  
 agatgctggc caacgccacc accctggcct atctgaaacg tgtgctcctt 1250  
 gggccctgac tcctgtgcca caggactcct gtggctcggc cgtggacctg 1300  
 ctgttggcct ctggggctgt catggccac gcgttttgca aagtttgtga 1350  
 ctcaccattc aaggccccga gtcttggact gtgaagcatc tgccatgggg 1400  
 aagtgtgtt tgttatcctt tctctgtggc agtgaagaag gaagaaatga 1450  
 gagtctagac tcaagggaca ctggatggca agaagctgc tgatggtgga 1500  
 actgctgtga ccttaggact ggctccacag ggtggactgg ctgggccctg 1550  
 gtcccagtcc ctgcctgggg ccatgtgtcc ccctattcct gtgggctttt 1600  
 catacttgcc tactgggccc tggccccgca gccttcctat gagggatgtt 1650  
 actgggctgt ggtcctgtac ccagaggtcc cagggatcgg ctctggccc 1700  
 ctcggtgac ccttcccaca caccagccac agataggcct gccactggtc 1750  
 atgggtagct agagctgctg gcttccctgt ggcttagctg gtggccagcc 1800  
 tgactggctt cctgggcgag cctagtagct cctgcaggca ggggcagttt 1850  
 gttgcgttct tegtggttcc caggccctgg gacatctcac tccactccta 1900  
 cctcccttac caccaggagc attcaagctc tggattgggc agcagatgtg 1950

ccccagttcc cgcaggctgt gttccagggg ccttgatttc ctcggtatgtg 2000  
ctattggccc caggactgaa gctgcctccc ttcacctgg gactgtgggtt 2050  
ccaaggatga gagcaggggt tggagccatg gccttctggg aacctatgga 2100  
gaaaggggaat ccaaggaagc agccaaggct gctcgcagct tccctgagct 2150  
gcacctcttg ctaacccccc catcacactg ccacctgcc ctaggggtctc 2200  
actagtacca agtgggtcag cacagggctg aggatggggc tcctatccac 2250  
cctggccagc acccagctta gtgctgggac tagcccagaa acttgaatgg 2300  
gacctgaga gagccagggg tcccctgagg cccccctagg ggctttctgt 2350  
ctgccccagg gtgctccatg gatctccctg tggcagcagg catggagagt 2400  
cagggctgcc ttcattggcag taggctctaa gtgggtgact ggccacaggc 2450  
cgagaaaagg gtacagcctc taggtggggg tcccaaagac gccttcaggc 2500  
tggactgagc tgctctccca cagggtttct gtgcagctgg attttctctg 2550  
ttgcatacat gcctggcatc tgtctcccct tgttctgag tggccccaca 2600  
tggggctctg agcaggctgt atctggattc tggcaataaa agtactctgg 2650  
atgctgtaaa aaaaaaaaaa aaaaaaaaaa 2680

<210> 157  
<211> 412  
<212> PRT  
<213> Artificial

<400> 157  
Met Gly Leu His Leu Arg Pro Tyr Arg Val Gly Leu Leu Pro Asp  
1 5 10 15  
Gly Leu Leu Phe Leu Leu Leu Leu Leu Met Leu Leu Ala Asp Pro  
20 25 30  
Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly  
35 40 45  
Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val  
50 55 60  
Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile  
65 70 75  
Trp Leu Asn Leu Glu Leu Leu Leu Pro Val Ile Ile Asp Cys Trp  
80 85 90  
Ile Asp Asn Ile Arg Leu Val Tyr Asn Lys Thr Ser Arg Ala Thr  
95 100 105  
Gln Phe Pro Asp Gly Val Asp Val Arg Val Pro Gly Phe Gly Lys

	110		115		120
Thr Phe Ser Leu	Glu Phe Leu Asp Pro	Ser Lys Ser Ser Val	Gly		
	125	130	135		
Ser Tyr Phe His	Thr Met Val Glu Ser	Leu Val Gly Trp Gly	Tyr		
	140	145	150		
Thr Arg Gly Glu	Asp Val Arg Gly Ala	Pro Tyr Asp Trp Arg	Arg		
	155	160	165		
Ala Pro Asn Glu	Asn Gly Pro Tyr Phe	Leu Ala Leu Arg Glu	Met		
	170	175	180		
Ile Glu Glu Met	Tyr Gln Leu Tyr Gly	Gly Pro Val Val Leu	Val		
	185	190	195		
Ala His Ser Met	Gly Asn Met Tyr Thr	Leu Tyr Phe Leu Gln	Arg		
	200	205	210		
Gln Pro Gln Ala	Trp Lys Asp Lys Tyr	Ile Arg Ala Phe Val	Ser		
	215	220	225		
Leu Gly Ala Pro	Trp Gly Gly Val Ala	Lys Thr Leu Arg Val	Leu		
	230	235	240		
Ala Ser Gly Asp	Asn Asn Arg Ile Pro	Val Ile Gly Pro Leu	Lys		
	245	250	255		
Ile Arg Glu Gln	Gln Arg Ser Ala Val	Ser Thr Ser Trp Leu	Leu		
	260	265	270		
Pro Tyr Asn Tyr	Thr Trp Ser Pro Glu	Lys Val Phe Val Gln	Thr		
	275	280	285		
Pro Thr Ile Asn	Tyr Thr Leu Arg Asp	Tyr Arg Lys Phe Phe	Gln		
	290	295	300		
Asp Ile Gly Phe	Glu Asp Gly Trp Leu	Met Arg Gln Asp Thr	Glu		
	305	310	315		
Gly Leu Val Glu	Ala Thr Met Pro Pro	Gly Val Gln Leu His	Cys		
	320	325	330		
Leu Tyr Gly Thr	Gly Val Pro Thr Pro	Asp Ser Phe Tyr Tyr	Glu		
	335	340	345		
Ser Phe Pro Asp	Arg Asp Pro Lys Ile	Cys Phe Gly Asp Gly	Asp		
	350	355	360		
Gly Thr Val Asn	Leu Lys Ser Ala Leu	Gln Cys Gln Ala Trp	Gln		
	365	370	375		
Ser Arg Gln Glu	His Gln Val Leu Leu	Gln Glu Leu Pro Gly	Ser		
	380	385	390		
Glu His Ile Glu	Met Leu Ala Asn Ala	Thr Thr Leu Ala Tyr	Leu		
	395	400	405		

Lys Arg Val Leu Leu Gly Pro  
410

<210> 158  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 158  
ctggggctac acacggggtg agg 23

<210> 159  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 159  
ggtgccgctg cagaaagtag agcg 24

<210> 160  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 160  
gccccaaatg aaaacgggcc ctacttcctg gccctccgcg agatg 45

<210> 161  
<211> 1512  
<212> DNA  
<213> Homo sapiens

<400> 161  
cgagcgcgtg ggcggacgcg tggggcggcg gcagcggcgg cgacggcgac 50  
atggagagcg gggcctacgg cgcggccaag gcgggcggct ccttcgacct 100  
gcggcgcttc ctgacgcagc cgcaggtggt ggcgcgcgcc gtgtgcttgg 150  
tcttcgcctt gatcgtgttc tcttgcattt atggtgaggg ctacagcaat 200  
gccacagagt ctaagcagat gtactgcgtg ttcaaccgca acgaggatgc 250  
ctgccgctat ggcagtgcca tcgggggtgct ggcccttcctg gcctcggcct 300  
tcttcttgggt ggtcgacgcg tatttccccc agatcagcaa cgccactgac 350  
cgcaagtacc tggtcattgg tgacctgctc ttctcagctc tctggacctt 400

cctgtggttt gttggtttct gcttctcac caaccagtgg gcagtcacca 450  
 acccgaagga cgtgctggtg ggggcogact ctgtgagggc agccatcacc 500  
 ttcagcttct tttccatctt ctctgggggt gtgctggcct ccctggccta 550  
 ccagcgctac aaggctggcg tggacgactt catccagaat tacgttgacc 600  
 ccaactcggga ccccaacact gcctacgcct cctaccaggg tgcattctgtg 650  
 gacaactacc aacagccacc cttcaccag aacgcggaga ccaccgaggg 700  
 ctaccagccg cccctgtgt actgagtggc ggtagcgtg ggaaggggga 750  
 cagagagggc cctccctct gccctggact ttccatcag cctcctggaa 800  
 ctgccagccc ctctctttca cctgttccat cctgtgcagc tgacacacag 850  
 ctaaggagcc tcatagcctg gcgggggctg gcagagccac accccaagt 900  
 cctgtgcccga gagggttca gtcagcgcct cactcctcca gggcactttt 950  
 aggaaagggg ttttagctag tgttttctc cgcttttaac gacctcagcc 1000  
 ccgcctgcag tggctagaag ccagcaggtg cccatgtgct actgacaagt 1050  
 gcctcagctt ccccccggcc cgggtcaggg cgtgggagcc gctattatct 1100  
 gcgttctctg ccaaagactc gtggggggcca tcacacctgc cctgtgcagc 1150  
 ggagccggac caggtctctg tgtcctcact caggtttgct tccctgtgc 1200  
 ccaactgctgt atgatctggg ggcaccacc ctgtgcgggt ggcctctggg 1250  
 ctgcctcccg tgggtgtgagg gcggggctgg tgcctatggc acttctcct 1300  
 tgcctccacc cctggcagca ggaaggggt ttgcctgaca acaccagct 1350  
 ttatgtaaat attctgcagt tgttacttag gaagcctggg gagggcaggg 1400  
 gtgccccatg gctcccagac tctgtctgtg ccgagtgtat tataaaatcg 1450  
 tgggggagat gcccggcctg ggatgctgtt tggagacgga ataatgttt 1500  
 tctcattcaa ag 1512

<210> 162  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Glu Ser Gly Ala Tyr Gly Ala Ala Lys Ala Gly Gly Ser Phe  
 1 5 10 15  
 Asp Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala  
 20 25 30

Val	Cys	Leu	Val	Phe	Ala	Leu	Ile	Val	Phe	Ser	Cys	Ile	Tyr	Gly	35	40	45
Glu	Gly	Tyr	Ser	Asn	Ala	His	Glu	Ser	Lys	Gln	Met	Tyr	Cys	Val	50	55	60
Phe	Asn	Arg	Asn	Glu	Asp	Ala	Cys	Arg	Tyr	Gly	Ser	Ala	Ile	Gly	65	70	75
Val	Leu	Ala	Phe	Leu	Ala	Ser	Ala	Phe	Phe	Leu	Val	Val	Asp	Ala	80	85	90
Tyr	Phe	Pro	Gln	Ile	Ser	Asn	Ala	Thr	Asp	Arg	Lys	Tyr	Leu	Val	95	100	105
Ile	Gly	Asp	Leu	Leu	Phe	Ser	Ala	Leu	Trp	Thr	Phe	Leu	Trp	Phe	110	115	120
Val	Gly	Phe	Cys	Phe	Leu	Thr	Asn	Gln	Trp	Ala	Val	Thr	Asn	Pro	125	130	135
Lys	Asp	Val	Leu	Val	Gly	Ala	Asp	Ser	Val	Arg	Ala	Ala	Ile	Thr	140	145	150
Phe	Ser	Phe	Phe	Ser	Ile	Phe	Ser	Trp	Gly	Val	Leu	Ala	Ser	Leu	155	160	165
Ala	Tyr	Gln	Arg	Tyr	Lys	Ala	Gly	Val	Asp	Asp	Phe	Ile	Gln	Asn	170	175	180
Tyr	Val	Asp	Pro	Thr	Pro	Asp	Pro	Asn	Thr	Ala	Tyr	Ala	Ser	Tyr	185	190	195
Pro	Gly	Ala	Ser	Val	Asp	Asn	Tyr	Gln	Gln	Pro	Pro	Phe	Thr	Gln	200	205	210
Asn	Ala	Glu	Thr	Thr	Glu	Gly	Tyr	Gln	Pro	Pro	Pro	Val	Tyr		215	220	

<210> 163

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 163

tggtcttcgc cttgatcgtg ttct 24

<210> 164

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 164  
gtgtactgag cggcggtag 20

<210> 165  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 165  
ctgaaggtga tggctgcct cac 23

<210> 166  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 166  
ccaggaggct catgggaaag tcc 23

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 167  
ccacgagtct aagcagatgt actgcgtgtt caaccgcaac gaggatgcct 50

<210> 168  
<211> 3143  
<212> DNA  
<213> Homo sapiens

<400> 168  
gagccaccta ccctgctccg aggccaggcc tgcagggcct catcggccag 50  
agggtgatca gtgagcagaa ggatgcccggt ggccgaggcc ccccaggtgg 100  
ctggcgggca gggggacgga ggtgatggcg aggaagcggga gccagagggg 150  
atgttcaagg cctgtgagga ctccaagaga aaagcccggg gctacctccg 200  
cctggtgccc ctgtttgtgc tgctggccct gctcgtgctg gcttcggcgg 250  
gggtgctact ctggtatttc ctagggtaca aggcggaggt gatggtcagc 300  
caggtgtact caggcagtct gcgtgtactc aatcgccact tctcccagga 350  
tcttaccgcg cggaatcta gtgccttccg cagtgaacc gccaaagccc 400

agaagatgct caaggagctc atcaccagca cccgcctggg aacttactac 450  
 aactccagct ccgtctattc ctttgaggag ggacccctca cctgcttctt 500  
 ctggttcatt ctccaaatcc ccgagcaccg ccggctgatg ctgagccccg 550  
 aggtggtgca ggcactgctg gtggaggagc tgctgtccac agtcaacagc 600  
 tcggctgccg tcccctacag ggccgagtac gaagtggacc ccgagggcct 650  
 agtgatcctg gaagccagtg tgaaagacat agctgcattg aattccacgc 700  
 tgggttggtta ccgctacagc tacgtgggcc agggccaggt cctccggctg 750  
 aaggggcctg accacctggc ctccagctgc ctgtggcacc tgcagggccc 800  
 caaggacctc atgctcaaac tccggctgga gtggacgctg gcagagtgcc 850  
 gggaccgact ggccatgtat gacgtggccg ggccccctgga gaagaggctc 900  
 atcacctcgg tgtacggctg cagccgccag gagcccgtgg tggaggttct 950  
 ggcgtcgggg gccatcatgg cggtcgtctg gaagaagggc ctgcacagct 1000  
 actacgaccc ctctgtgctc tccgtgcagc cgggtggtctt ccaggcctgt 1050  
 gaagtgaacc tgacgtgga caacaggctc gactcccagg gcgtcctcag 1100  
 caccocgtac ttccccagct actactcgcc ccaaaccac tgctcctggc 1150  
 acctcacggt gccctctctg gactacggct tggccctctg gtttgatgcc 1200  
 tatgcaactga ggaggcagaa gtatgatattg ccgtgcaccc agggccagt 1250  
 gacgatccag aacaggaggc tgtgtggctt gcgcatcctg cagccctacg 1300  
 ccgagaggat ccccggtggt gccacggccg ggatcaccat caacttcacc 1350  
 tcccagatct ccctcaccgg gcccggtgtg cgggtgcact atggcttgta 1400  
 caaccagtgc gacccctgcc ctggagagtt cctctgttct gtgaatggac 1450  
 tctgtgtccc tgccgtgat ggggtcaagg actgccccaa cggcctggat 1500  
 gagagaaact gcgtttgcag agccacattc cagtgc aaag aggacagcac 1550  
 atgcatctca ctgccccagg tctgtgatgg gcagcctgat tgtctcaacg 1600  
 gcagcgatga agagcagtgc caggaagggg tgccatgtgg gacattcacc 1650  
 ttccagtgtg aggaccggag ctgcgtgaag aagcccaacc cgcagtgtga 1700  
 tgggcggccc gactgcaggg acggctcgga tgaggagcac tgtgactgtg 1750  
 gcctccaggg cccctccagc cgcattgttg gtggagctgt gtcctccgag 1800  
 ggtgagtggc catggcaggc cagcctccag gtccggggtc gacacatctg 1850



tggggggggcc ctcacgctg accgctgggt gataacagct gccactgct 1900  
 tccaggagga cagcatggcc tccacgggtgc tgtggaccgt gttcctgggc 1950  
 aaggtgtggc agaactcgcg ctggcctgga gaggtgtcct tcaaggtgag 2000  
 ccgcctgctc ctgcacccgt accacgaaga ggacagccat gactacgacg 2050  
 tggcgctgct gcagctcgac caccgggtgg tgcgctcggc cgccgtgcgc 2100  
 cccgtctgcc tgcccgcgcg ctcccacttc ttcgagcccg gcctgcactg 2150  
 ctggattacg ggctggggcg ccttgcgcgga gggcgggccc atcagcaacg 2200  
 ctctgcagaa agtggatgtg cagttgatcc cacaggacct gtgcagcgag 2250  
 gcctatcgct accaggtgac gccacgcatg ctgtgtgccc gctaccgcaa 2300  
 gggcaagaag gatgcctgtc agggtgactc aggtggtccg ctggtgtgca 2350  
 aggcactcag tggccgctgg ttcttgccgg ggctgggtcag ctggggcctg 2400  
 ggctgtggcc ggctaacta cttcggcgtc tacacccgca tcacaggtgt 2450  
 gatcagctgg atccagcaag tggtgacctg aggaactgcc cccctgcaaa 2500  
 gcaggggcca cctcctggac tcagagagcc cagggcaact gccaaagcagg 2550  
 gggacaagta ttctggcggg ggggtggggga gagagcaggc cctgtggtgg 2600  
 caggaggtgg catcttgtct cgtccctgat gtctgctcca gtgatggcag 2650  
 gaggatggag aagtgccagc agctgggggt caagacgtcc cctgaggacc 2700  
 caggcccaca cccagccctt ctgcctccca attctctctc ctccgtcccc 2750  
 ttctccact gctgcctaata gcaaggcagt ggctcagcag caagaatgct 2800  
 ggttctacat cccgaggagt gtctgaggtg cgccccactc tgtacagagg 2850  
 ctgtttgggc agccttgccct ccagagagca gattccagct tcggaagccc 2900  
 ctggtctaac ttgggatctg ggaatggaag gtgctcccat cggagggggac 2950  
 cctcagagcc ctggagactg ccaggtgggc ctgctgccac tgtaagccaa 3000  
 aaggtgggga agtcctgact ccaggggtcct tgccccaccc ctgcctgcca 3050  
 cctgggccct cacagcccag accctcactg ggaggtgagc tcagctgccc 3100  
 tttggaataa agctgcctga tcaaaaaaaaa aaaaaaaaaa aaa 3143

<210> 169  
 <211> 802  
 <212> PRT  
 <213> Homo sapiens  
 <400> 169

Met	Pro	Val	Ala	Glu	Ala	Pro	Gln	Val	Ala	Gly	Gly	Gln	Gly	Asp	1	5	10	15
Gly	Gly	Asp	Gly	Glu	Glu	Ala	Glu	Pro	Glu	Gly	Met	Phe	Lys	Ala	20	25	30	
Cys	Glu	Asp	Ser	Lys	Arg	Lys	Ala	Arg	Gly	Tyr	Leu	Arg	Leu	Val	35	40	45	
Pro	Leu	Phe	Val	Leu	Leu	Ala	Leu	Leu	Val	Leu	Ala	Ser	Ala	Gly	50	55	60	
Val	Leu	Leu	Trp	Tyr	Phe	Leu	Gly	Tyr	Lys	Ala	Glu	Val	Met	Val	65	70	75	
Ser	Gln	Val	Tyr	Ser	Gly	Ser	Leu	Arg	Val	Leu	Asn	Arg	His	Phe	80	85	90	
Ser	Gln	Asp	Leu	Thr	Arg	Arg	Glu	Ser	Ser	Ala	Phe	Arg	Ser	Glu	95	100	105	
Thr	Ala	Lys	Ala	Gln	Lys	Met	Leu	Lys	Glu	Leu	Ile	Thr	Ser	Thr	110	115	120	
Arg	Leu	Gly	Thr	Tyr	Tyr	Asn	Ser	Ser	Ser	Val	Tyr	Ser	Phe	Gly	125	130	135	
Glu	Gly	Pro	Leu	Thr	Cys	Phe	Phe	Trp	Phe	Ile	Leu	Gln	Ile	Pro	140	145	150	
Glu	His	Arg	Arg	Leu	Met	Leu	Ser	Pro	Glu	Val	Val	Gln	Ala	Leu	155	160	165	
Leu	Val	Glu	Glu	Leu	Leu	Ser	Thr	Val	Asn	Ser	Ser	Ala	Ala	Val	170	175	180	
Pro	Tyr	Arg	Ala	Glu	Tyr	Glu	Val	Asp	Pro	Glu	Gly	Leu	Val	Ile	185	190	195	
Leu	Glu	Ala	Ser	Val	Lys	Asp	Ile	Ala	Ala	Leu	Asn	Ser	Thr	Leu	200	205	210	
Gly	Cys	Tyr	Arg	Tyr	Ser	Tyr	Val	Gly	Gln	Gly	Gln	Val	Leu	Arg	215	220	225	
Leu	Lys	Gly	Pro	Asp	His	Leu	Ala	Ser	Ser	Cys	Leu	Trp	His	Leu	230	235	240	
Gln	Gly	Pro	Lys	Asp	Leu	Met	Leu	Lys	Leu	Arg	Leu	Glu	Trp	Thr	245	250	255	
Leu	Ala	Glu	Cys	Arg	Asp	Arg	Leu	Ala	Met	Tyr	Asp	Val	Ala	Gly	260	265	270	
Pro	Leu	Glu	Lys	Arg	Leu	Ile	Thr	Ser	Val	Tyr	Gly	Cys	Ser	Arg	275	280	285	
Gln	Glu	Pro	Val	Val	Glu	Val	Leu	Ala	Ser	Gly	Ala	Ile	Met	Ala				

	290		295		300
Val Val Trp Lys	Lys Gly Leu His Ser	Tyr Tyr Asp Pro Phe	Val		
	305		310		315
Leu Ser Val Gln	Pro Val Val Phe Gln	Ala Cys Glu Val Asn	Leu		
	320		325		330
Thr Leu Asp Asn	Arg Leu Asp Ser Gln	Gly Val Leu Ser Thr	Pro		
	335		340		345
Tyr Phe Pro Ser	Tyr Tyr Ser Pro Gln	Thr His Cys Ser Trp	His		
	350		355		360
Leu Thr Val Pro	Ser Leu Asp Tyr Gly	Leu Ala Leu Trp Phe	Asp		
	365		370		375
Ala Tyr Ala Leu	Arg Arg Gln Lys Tyr	Asp Leu Pro Cys Thr	Gln		
	380		385		390
Gly Gln Trp Thr	Ile Gln Asn Arg Arg	Leu Cys Gly Leu Arg	Ile		
	395		400		405
Leu Gln Pro Tyr	Ala Glu Arg Ile Pro	Val Val Ala Thr Ala	Gly		
	410		415		420
Ile Thr Ile Asn	Phe Thr Ser Gln Ile	Ser Leu Thr Gly Pro	Gly		
	425		430		435
Val Arg Val His	Tyr Gly Leu Tyr Asn	Gln Ser Asp Pro Cys	Pro		
	440		445		450
Gly Glu Phe Leu	Cys Ser Val Asn Gly	Leu Cys Val Pro Ala	Cys		
	455		460		465
Asp Gly Val Lys	Asp Cys Pro Asn Gly	Leu Asp Glu Arg Asn	Cys		
	470		475		480
Val Cys Arg Ala	Thr Phe Gln Cys Lys	Glu Asp Ser Thr Cys	Ile		
	485		490		495
Ser Leu Pro Lys	Val Cys Asp Gly Gln	Pro Asp Cys Leu Asn	Gly		
	500		505		510
Ser Asp Glu Glu	Gln Cys Gln Glu Gly	Val Pro Cys Gly Thr	Phe		
	515		520		525
Thr Phe Gln Cys	Glu Asp Arg Ser Cys	Val Lys Lys Pro Asn	Pro		
	530		535		540
Gln Cys Asp Gly	Arg Pro Asp Cys Arg	Asp Gly Ser Asp Glu	Glu		
	545		550		555
His Cys Asp Cys	Gly Leu Gln Gly Pro	Ser Ser Arg Ile Val	Gly		
	560		565		570
Gly Ala Val Ser	Ser Glu Gly Glu Trp	Pro Trp Gln Ala Ser	Leu		
	575		580		585

Gln Val Arg Gly Arg His Ile Cys Gly Gly Ala Leu Ile Ala Asp	590	595	600
Arg Trp Val Ile Thr Ala Ala His Cys Phe Gln Glu Asp Ser Met	605	610	615
Ala Ser Thr Val Leu Trp Thr Val Phe Leu Gly Lys Val Trp Gln	620	625	630
Asn Ser Arg Trp Pro Gly Glu Val Ser Phe Lys Val Ser Arg Leu	635	640	645
Leu Leu His Pro Tyr His Glu Glu Asp Ser His Asp Tyr Asp Val	650	655	660
Ala Leu Leu Gln Leu Asp His Pro Val Val Arg Ser Ala Ala Val	665	670	675
Arg Pro Val Cys Leu Pro Ala Arg Ser His Phe Phe Glu Pro Gly	680	685	690
Leu His Cys Trp Ile Thr Gly Trp Gly Ala Leu Arg Glu Gly Gly	695	700	705
Pro Ile Ser Asn Ala Leu Gln Lys Val Asp Val Gln Leu Ile Pro	710	715	720
Gln Asp Leu Cys Ser Glu Ala Tyr Arg Tyr Gln Val Thr Pro Arg	725	730	735
Met Leu Cys Ala Gly Tyr Arg Lys Gly Lys Lys Asp Ala Cys Gln	740	745	750
Gly Asp Ser Gly Gly Pro Leu Val Cys Lys Ala Leu Ser Gly Arg	755	760	765
Trp Phe Leu Ala Gly Leu Val Ser Trp Gly Leu Gly Cys Gly Arg	770	775	780
Pro Asn Tyr Phe Gly Val Tyr Thr Arg Ile Thr Gly Val Ile Ser	785	790	795
Trp Ile Gln Gln Val Val Thr	800		

<210> 170  
 <211> 1327  
 <212> DNA  
 <213> Homo sapiens

<400> 170  
 gcacccaggg ccagtggacg atccagaaca ggaggctgtg tggcttgccg 50  
 atcctgcagc cctacgccga gaggatcccc gtggtggcca cggccgggat 100  
 caccatcaac ttcacctccc agatctccct caccggggccc ggtgtgcggg 150  
 tgcactatgg cttgtacaac cagtcggacc cctgccctgg agagttcctc 200

tgttctgtga atggactctg tgtccctgcc tgtgatgggg tcaaggactg 250  
 ccccaacggc ctggatgaga gaaactgcgt ttgcagagcc acattccagt 300  
 gcaaagagga cagcacatgc atctcactgc ccaaggtctg tgatgggcag 350  
 cctgattgtc tcaacggcag cgatgaagag cagtgccagg aaggggtgcc 400  
 atgtgggaca ttcaccttcc agtgtgagga ccggagctgc gtgaagaagc 450  
 ccaaccgcga gtgtgatggg cggcccgact gcagggacgg ctccgatgag 500  
 gagcaactgtg actgtggcct ccagggcccc tccagccgca ttgttggtgg 550  
 agctgtgtcc tccgaggggt agtggccatg gcagggcagc ctccaggttc 600  
 ggggtcgaca catctgtggg ggggcccctca tcgctgaccg ctgggtgata 650  
 acagctgccc actgcttcca ggaggacagc atggcctcca cgggtgctgtg 700  
 gaccgtgttc ctgggcaagg tgtggcagaa ctgcgctgg cctggagagg 750  
 tgtccttcaa ggtgagccgc ctgctcctgc acccgtagca cgaagaggac 800  
 agccatgact acgacgtggc gctgctgcag ctgcaccacc cgggtggtgcg 850  
 ctggccgccc gtgcgccccg tctgcctgcc cgcgcgctcc cacttcttcg 900  
 agcccggcct gcaactgctg attacgggtt ggggcgcctt gcgcgagggc 950  
 ggccccatca gcaacgctct gcagaaagtg gatgtgcagt tgatcccaca 1000  
 ggacctgtgc agcgaggcct atcgctacca' ggtgacgcca cgcattgctgt 1050  
 gtgccggcta ccgcaagggc aagaaggatg cctgtcaggg tgactcaggt 1100  
 ggtccgctgg tgtgcaaggc actcagtggc cgctgggttc tggcggggct 1150  
 ggtcagctgg ggcctgggct gtggccggcc taactacttc ggcgtctaca 1200  
 cccgcatcac aggtgtgatc agctggatcc agcaagtggg gacctgagga 1250  
 actgcccccc tgcaaagcag ggcccacctc ctggactcag agagcccagg 1300  
 gcaactgcca agcaggggga caagtat 1327

<210> 171

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 171

taacagctgc ccaactgcttc cagg 24

<210> 172

<211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 172  
 taatccagca gtgcaggccg gg 22

<210> 173  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 173  
 atggcctcca cgggtgctgtg gaccgtgttc ctgggcaagg tgtggcagaa 50

<210> 174  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 174  
 tgcctatgca ctgaggaggc agaag 25

<210> 175  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 175  
 aggcagggac acagagtcca ttcac 25

<210> 176  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 176  
 agtatgattt gccgtgcacc cagggccagt ggacgatcca gaacaggagg 50

<210> 177  
 <211> 1510  
 <212> DNA  
 <213> Homo sapiens

<400> 177

ggacgagggc agatctcggt ctggggcaag ccgttgacac tcgctccctg 50  
ccaccgcccc ggctccgtgc cgccaagttt tcattttcca ctttctctgc 100  
ctccagtcct ccagccccctg gccgagagaa gggctctacc ggccgggatt 150  
gctggaaaca ccaagaggtg gtttttggtt tttaaaactt ctgtttcttg 200  
ggaggggggtg tggcggggca ggatgagcaa ctccgttcct ctgctctgtt 250  
tctggagcct ctgctattgc tttgctgcgg ggagccccgt accttttgg 300  
ccagaggggac ggctggaaga taagctccac aaacccaaag ctacacagac 350  
tgaggtcaaa ccatctgtga ggtttaacct ccgcacctcc aaggaccag 400  
agcatgaagg atgctacctc tccgtcggcc acagccagcc cttagaagac 450  
tgcagtttca acatgacagc taaaaccttt ttcattcttc acggatggac 500  
gatgagcggg atctttgaaa actggctgca caaactcgtg tcagccctgc 550  
acacaagaga gaaagacgcc aatgtagttg tgggtgactg gctccccctg 600  
gccaccagc tttacacgga tgcggtcaat aataccaggg tgggtgggaca 650  
cagcattgcc aggatgctcg actggctgca ggagaaggac gatttttctc 700  
tcgggaatgt ccacttgatc ggctacagcc tcggagcgca cgtggccggg 750  
tatgcaggca acttcgtgaa aggaacggtg ggccgaatca caggtttgga 800  
tcctgcccgg cccatgtttg aaggggcccga catccacaag aggctctctc 850  
cggacgatgc agattttgtg gatgtcctcc acacctacac gcgttccttc 900  
ggcttgagca ttggtattca gatgcctgtg ggccacattg acatctacct 950  
caatgggggt gacttccagc caggctgtgg actcaacgat gtcttgggat 1000  
caattgcata tggaacaatc acagaggtgg taaaatgtga gcatgagcga 1050  
gccgtccacc tctttgttga ctctctggtg aatcaggaca agccgagttt 1100  
tgccttccag tgactgact ccaatcgctt caaaaagggg atctgtctga 1150  
gctgccgcaa gaaccgttgt aatagcattg gctacaatgc caagaaaatg 1200  
aggaacaaga ggaacagcaa aatgtacctt aaaaccggg caggcatgcc 1250  
tttcagaggt aaccttcagt ccctggagtg tccctgagga aggcccttaa 1300  
tacctccttc ttaataccat gctgcagagc agggcacatc ctagcccagg 1350  
agaagtggcc agcacaatcc aatcaaatcg ttgcaaatca gattacactg 1400  
tgcattgcct aggaagggga atctttacaa aataaacagt gtggaccctt 1450

aataaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1500

aaaaaaaaaa 1510

<210> 178

<211> 354

<212> PRT

<213> Homo sapiens

<400> 178

Met	Ser	Asn	Ser	Val	Pro	Leu	Leu	Cys	Phe	Trp	Ser	Leu	Cys	Tyr
1				5					10					15

Cys	Phe	Ala	Ala	Gly	Ser	Pro	Val	Pro	Phe	Gly	Pro	Glu	Gly	Arg
				20					25					30

Leu	Glu	Asp	Lys	Leu	His	Lys	Pro	Lys	Ala	Thr	Gln	Thr	Glu	Val
				35					40					45

Lys	Pro	Ser	Val	Arg	Phe	Asn	Leu	Arg	Thr	Ser	Lys	Asp	Pro	Glu
				50					55					60

His	Glu	Gly	Cys	Tyr	Leu	Ser	Val	Gly	His	Ser	Gln	Pro	Leu	Glu
				65					70					75

Asp	Cys	Ser	Phe	Asn	Met	Thr	Ala	Lys	Thr	Phe	Phe	Ile	Ile	His
				80					85					90

Gly	Trp	Thr	Met	Ser	Gly	Ile	Phe	Glu	Asn	Trp	Leu	His	Lys	Leu
				95					100					105

Val	Ser	Ala	Leu	His	Thr	Arg	Glu	Lys	Asp	Ala	Asn	Val	Val	Val
				110					115					120

Val	Asp	Trp	Leu	Pro	Leu	Ala	His	Gln	Leu	Tyr	Thr	Asp	Ala	Val
				125					130					135

Asn	Asn	Thr	Arg	Val	Val	Gly	His	Ser	Ile	Ala	Arg	Met	Leu	Asp
				140					145					150

Trp	Leu	Gln	Glu	Lys	Asp	Asp	Phe	Ser	Leu	Gly	Asn	Val	His	Leu
				155					160					165

Ile	Gly	Tyr	Ser	Leu	Gly	Ala	His	Val	Ala	Gly	Tyr	Ala	Gly	Asn
				170					175					180

Phe	Val	Lys	Gly	Thr	Val	Gly	Arg	Ile	Thr	Gly	Leu	Asp	Pro	Ala
				185					190					195

Gly	Pro	Met	Phe	Glu	Gly	Ala	Asp	Ile	His	Lys	Arg	Leu	Ser	Pro
				200					205					210

Asp	Asp	Ala	Asp	Phe	Val	Asp	Val	Leu	His	Thr	Tyr	Thr	Arg	Ser
				215					220					225

Phe	Gly	Leu	Ser	Ile	Gly	Ile	Gln	Met	Pro	Val	Gly	His	Ile	Asp
				230					235					240

09978192-101501



Ile	Tyr	Pro	Asn	Gly	Gly	Asp	Phe	Gln	Pro	Gly	Cys	Gly	Leu	Asn
				245					250					255
Asp	Val	Leu	Gly	Ser	Ile	Ala	Tyr	Gly	Thr	Ile	Thr	Glu	Val	Val
				260					265					270
Lys	Cys	Glu	His	Glu	Arg	Ala	Val	His	Leu	Phe	Val	Asp	Ser	Leu
				275					280					285
Val	Asn	Gln	Asp	Lys	Pro	Ser	Phe	Ala	Phe	Gln	Cys	Thr	Asp	Ser
				290					295					300
Asn	Arg	Phe	Lys	Lys	Gly	Ile	Cys	Leu	Ser	Cys	Arg	Lys	Asn	Arg
				305					310					315
Cys	Asn	Ser	Ile	Gly	Tyr	Asn	Ala	Lys	Lys	Met	Arg	Asn	Lys	Arg
				320					325					330
Asn	Ser	Lys	Met	Tyr	Leu	Lys	Thr	Arg	Ala	Gly	Met	Pro	Phe	Arg
				335					340					345
Gly	Asn	Leu	Gln	Ser	Leu	Glu	Cys	Pro						
				350										

<210> 179  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 179  
 gtgagcatga gcgagccgtc cac 23

<210> 180  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 180  
 gctattacaa cggttcttgc ggcagc 26

<210> 181  
 <211> 44  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 181  
 ttgactctct ggtgaatcag gacaagccga gttttgcctt ccag 44

<210> 182

<211> 3240  
 <212> DNA  
 <213> Homo sapiens

<400> 182  
 cggacgcgtg ggcggacgcg tgggcctggg caagggcccg ggcgccgggc 50  
 cgagccacct cttcccctcc cccgcttccc tgtcgcgctc cgctggctgg 100  
 acgcgctgga ggagtggagc agcaccgcgc cggccctggg ggctgacagt 150  
 cggcaaagt tggcccgaag aggaagtggc ctcaaaccac ggcaggtggc 200  
 gaccaggcca gaccaggggc gctcgcctgc tgcgggcggg ctgtaggcga 250  
 gggcgcgccc cagtgccgag acccggggct tcaggagccg gccccgggag 300  
 agaagagtgc ggcggcggac ggagaaaaca actccaaagt tggcgaaagg 350  
 caccgcccct actcccgggc tgccgcgcgc tccccgcccc cagccctggc 400  
 atccagagta cgggtcgagc ccggggccatg gagccccctt ggggagggcg 450  
 caccagggag cctgggcgcc cggggctccg ccgcgacccc atcgggtaga 500  
 ccacagaagc tccgggaccc ttccggcacc tctggacagc ccaggatgct 550  
 gttggccacc ctctcctcc tctccttg aggcgctctg gcccatccag 600  
 accggattat ttttccaaat catgcttggt agggaccccc agcagtgtct 650  
 ttagaagtgc agggcacctt acagaggccc ctgggtccgg acagccgcac 700  
 ctcccctgcc aactgcacct ggctcatcct gggcagcaag gaacagactg 750  
 tcaccatcag gttccagaag ctacacctgg cctgtggctc agagcgctta 800  
 accctacgct cccctctcca gccactgac tccctgtgtg aggcacctcc 850  
 cagccctctg cagctgcccg ggggcaacgt caccatcact tacagctatg 900  
 ctggggccag agcaccatg ggccagggtc tctgtctctc ctacagccaa 950  
 gattggctga tgtgcctgca ggaagagttt cagtgcctga accaccgctg 1000  
 tgtatctgct gtccagcgct gtgatggggt tgatgcctgt ggcgatggct 1050  
 ctgatgaagc aggttgacgc tcagaccctt tccctggcct gacccaaga 1100  
 cccgtcccct ccctgccttg caatgtcacc ttggaggact tctatggggt 1150  
 cttctcctct cctggatata cacacctagc ctcagtctcc caccaccagt 1200  
 cctgccattg gctgctggac ccccatgatg gccggcgggt ggccgtgcgc 1250  
 ttcacagccc tggacttggg ctttggagat gcagtgcctg tgtatgacgg 1300  
 ccctgggccc cctgagagct cccgactact gcgtagtctc accacttca 1350

099819101501

gcaatggcaa ggctgtcact gtggagacac tgtctggcca ggctgttgtg 1400  
 tcctaccaca cagttgcttg gagcaatggt cgtggcttca atgccaccta 1450  
 ccatgtgcgg ggctattgct tgccttggga cagaccctgt ggcttaggct 1500  
 ctggcctggg agctggcgaa ggcctagggt agcgctgcta cagtgaggca 1550  
 cagcgctgtg acggctcatg ggactgtgct gacggcacag atgaggagga 1600  
 ctgcccaggc tgcccacctg gacacttccc ctgtggggct gctggcacct 1650  
 ctggtgccac agcctgctac ctgcctgctg accgctgcaa ctaccagact 1700  
 ttctgtgctg atggagcaga tgagagacgc tgcggcatt gccagcctgg 1750  
 caatttccga tgccgggacg agaagtgcgt gtatgagacg tgggtgtgcg 1800  
 atgggcagcc agactgtgcg gacggcagtg atgagtggga ctgctcctat 1850  
 gttctgcccc gcaaggatcat tacagctgca gtcattggca gcctagtgtg 1900  
 cggcctgctc ctggatcatg ccctgggctg cacctgcaag ctctatgcca 1950  
 ttgcaccca ggagtacagc atctttgccc ccctctccc gatggaggct 2000  
 gagattgtgc agcagcaggc acccccttcc tacgggcagc tcattgcccc 2050  
 gggtgccatc ccacctgtag aagactttcc tacagagaat cctaataata 2100  
 actcagtgtg gggcaacctg cgttctctgc tacagatctt acgccaggat 2150  
 atgactccag gaggtggccc aggtgcccgc cgtcgtcagc ggggccgctt 2200  
 gatgcgacgc ctggtacgcc gtctccgccc ctggggcttg ctccctcgaa 2250  
 ccaacacccc ggctcgggccc tctgaggcca gatcccaggt cacaccttct 2300  
 gctgctcccc ttgaggccct agatggtggc acaggtccag cccgtgaggg 2350  
 cggggcagtg ggtgggcaag atggggagca ggcaccccca ctgcccata 2400  
 aggctcccct cccatctgct agcaogtctc cagccccac tactgtccct 2450  
 gaagccccag ggccactgcc ctactgccc ctagagccat cactattgtc 2500  
 tggagtgggt caggccctgc gaggcgcctt gttgccagc ctggggcccc 2550  
 caggaccaac ccggagcccc cctggacccc acacagcagt cctggccctg 2600  
 gaagatgagg acgatgtgct actggtgcca ctggctgagc cgggggtgtg 2650  
 ggtagctgag gcagaggatg agccactgct tacctgaggg gacctggggg 2700  
 ctctactgag gcctctcccc tgggggctct actcatagtg gcacaacctt 2750  
 ttagaggtgg gtcagcctcc cctccaccac ttccttcctt gtccctggat 2800

ttcagggact tgggtgggcoct cccggttgacc ctatgtagct gctataaagt 2850  
 taagtgtccc tcaggcaggg agaggggtca cagagtctcc tctgtacgtg 2900  
 gccatggcca gacaccccag tcccttcacc accacctgct cccacgcca 2950  
 ccaccatttg ggtggctggtt tttaaaaagt aaagttctta gaggatcata 3000  
 ggtctggaca ctccatcctt gccaaacctc taccctaaaag tggccttaag 3050  
 caccggaatg ccaattaact agagacctc cagcccccaa ggggaggatt 3100  
 tgggcagaac ctgaggtttt gccatccaca atccctccta cagggcctgg 3150  
 ctcacaaaaa gagtgaaca aatgcttcta ttccatagct acggcattgc 3200  
 tcagtaagtt gaggtcaaaa ataaaggaat catacatctc 3240

<210> 183  
 <211> 713  
 <212> PRT  
 <213> Homo sapiens

<400> 183  
 Met Leu Leu Ala Thr Leu Leu Leu Leu Leu Leu Gly Gly Ala Leu  
 1 5 10 15  
 Ala His Pro Asp Arg Ile Ile Phe Pro Asn His Ala Cys Glu Asp  
 20 25 30  
 Pro Pro Ala Val Leu Leu Glu Val Gln Gly Thr Leu Gln Arg Pro  
 35 40 45  
 Leu Val Arg Asp Ser Arg Thr Ser Pro Ala Asn Cys Thr Trp Leu  
 50 55 60  
 Ile Leu Gly Ser Lys Glu Gln Thr Val Thr Ile Arg Phe Gln Lys  
 65 70 75  
 Leu His Leu Ala Cys Gly Ser Glu Arg Leu Thr Leu Arg Ser Pro  
 80 85 90  
 Leu Gln Pro Leu Ile Ser Leu Cys Glu Ala Pro Pro Ser Pro Leu  
 95 100 105  
 Gln Leu Pro Gly Gly Asn Val Thr Ile Thr Tyr Ser Tyr Ala Gly  
 110 115 120  
 Ala Arg Ala Pro Met Gly Gln Gly Phe Leu Leu Ser Tyr Ser Gln  
 125 130 135  
 Asp Trp Leu Met Cys Leu Gln Glu Glu Phe Gln Cys Leu Asn His  
 140 145 150  
 Arg Cys Val Ser Ala Val Gln Arg Cys Asp Gly Val Asp Ala Cys  
 155 160 165  
 Gly Asp Gly Ser Asp Glu Ala Gly Cys Ser Ser Asp Pro Phe Pro

170					175					180				
Gly	Leu	Thr	Pro	Arg	Pro	Val	Pro	Ser	Leu	Pro	Cys	Asn	Val	Thr
				185					190					195
Leu	Glu	Asp	Phe	Tyr	Gly	Val	Phe	Ser	Ser	Pro	Gly	Tyr	Thr	His
				200					205					210
Leu	Ala	Ser	Val	Ser	His	Pro	Gln	Ser	Cys	His	Trp	Leu	Leu	Asp
				215					220					225
Pro	His	Asp	Gly	Arg	Arg	Leu	Ala	Val	Arg	Phe	Thr	Ala	Leu	Asp
				230					235					240
Leu	Gly	Phe	Gly	Asp	Ala	Val	His	Val	Tyr	Asp	Gly	Pro	Gly	Pro
				245					250					255
Pro	Glu	Ser	Ser	Arg	Leu	Leu	Arg	Ser	Leu	Thr	His	Phe	Ser	Asn
				260					265					270
Gly	Lys	Ala	Val	Thr	Val	Glu	Thr	Leu	Ser	Gly	Gln	Ala	Val	Val
				275					280					285
Ser	Tyr	His	Thr	Val	Ala	Trp	Ser	Asn	Gly	Arg	Gly	Phe	Asn	Ala
				290					295					300
Thr	Tyr	His	Val	Arg	Gly	Tyr	Cys	Leu	Pro	Trp	Asp	Arg	Pro	Cys
				305					310					315
Gly	Leu	Gly	Ser	Gly	Leu	Gly	Ala	Gly	Glu	Gly	Leu	Gly	Glu	Arg
				320					325					330
Cys	Tyr	Ser	Glu	Ala	Gln	Arg	Cys	Asp	Gly	Ser	Trp	Asp	Cys	Ala
				335					340					345
Asp	Gly	Thr	Asp	Glu	Glu	Asp	Cys	Pro	Gly	Cys	Pro	Pro	Gly	His
				350					355					360
Phe	Pro	Cys	Gly	Ala	Ala	Gly	Thr	Ser	Gly	Ala	Thr	Ala	Cys	Tyr
				365					370					375
Leu	Pro	Ala	Asp	Arg	Cys	Asn	Tyr	Gln	Thr	Phe	Cys	Ala	Asp	Gly
				380					385					390
Ala	Asp	Glu	Arg	Arg	Cys	Arg	His	Cys	Gln	Pro	Gly	Asn	Phe	Arg
				395					400					405
Cys	Arg	Asp	Glu	Lys	Cys	Val	Tyr	Glu	Thr	Trp	Val	Cys	Asp	Gly
				410					415					420
Gln	Pro	Asp	Cys	Ala	Asp	Gly	Ser	Asp	Glu	Trp	Asp	Cys	Ser	Tyr
				425					430					435
Val	Leu	Pro	Arg	Lys	Val	Ile	Thr	Ala	Ala	Val	Ile	Gly	Ser	Leu
				440					445					450
Val	Cys	Gly	Leu	Leu	Leu	Val	Ile	Ala	Leu	Gly	Cys	Thr	Cys	Lys
				455					460					465

Leu	Tyr	Ala	Ile	Arg	Thr	Gln	Glu	Tyr	Ser	Ile	Phe	Ala	Pro	Leu
				470					475					480
Ser	Arg	Met	Glu	Ala	Glu	Ile	Val	Gln	Gln	Gln	Ala	Pro	Pro	Ser
				485					490					495
Tyr	Gly	Gln	Leu	Ile	Ala	Gln	Gly	Ala	Ile	Pro	Pro	Val	Glu	Asp
				500					505					510
Phe	Pro	Thr	Glu	Asn	Pro	Asn	Asp	Asn	Ser	Val	Leu	Gly	Asn	Leu
				515					520					525
Arg	Ser	Leu	Leu	Gln	Ile	Leu	Arg	Gln	Asp	Met	Thr	Pro	Gly	Gly
				530					535					540
Gly	Pro	Gly	Ala	Arg	Arg	Arg	Gln	Arg	Gly	Arg	Leu	Met	Arg	Arg
				545					550					555
Leu	Val	Arg	Arg	Leu	Arg	Arg	Trp	Gly	Leu	Leu	Pro	Arg	Thr	Asn
				560					565					570
Thr	Pro	Ala	Arg	Ala	Ser	Glu	Ala	Arg	Ser	Gln	Val	Thr	Pro	Ser
				575					580					585
Ala	Ala	Pro	Leu	Glu	Ala	Leu	Asp	Gly	Gly	Thr	Gly	Pro	Ala	Arg
				590					595					600
Glu	Gly	Gly	Ala	Val	Gly	Gly	Gln	Asp	Gly	Glu	Gln	Ala	Pro	Pro
				605					610					615
Leu	Pro	Ile	Lys	Ala	Pro	Leu	Pro	Ser	Ala	Ser	Thr	Ser	Pro	Ala
				620					625					630
Pro	Thr	Thr	Val	Pro	Glu	Ala	Pro	Gly	Pro	Leu	Pro	Ser	Leu	Pro
				635					640					645
Leu	Glu	Pro	Ser	Leu	Leu	Ser	Gly	Val	Val	Gln	Ala	Leu	Arg	Gly
				650					655					660
Arg	Leu	Leu	Pro	Ser	Leu	Gly	Pro	Pro	Gly	Pro	Thr	Arg	Ser	Pro
				665					670					675
Pro	Gly	Pro	His	Thr	Ala	Val	Leu	Ala	Leu	Glu	Asp	Glu	Asp	Asp
				680					685					690
Val	Leu	Leu	Val	Pro	Leu	Ala	Glu	Pro	Gly	Val	Trp	Val	Ala	Glu
				695					700					705
Ala	Glu	Asp	Glu	Pro	Leu	Leu	Thr							
				710										

<210> 184

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 184  
ggctgtcact gtggagacac 20

<210> 185  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 185  
gcaagggtcat tacagctg 18

<210> 186  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 186  
agaacatagg agcagtccca ctc 23

<210> 187  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 187  
tgcttgctgc tgcacaatct cag 23

<210> 188  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 188  
ggctattgct tgccttggga cagaccctgt ggcttaggct ctggc 45

<210> 189  
<211> 663  
<212> DNA  
<213> Homo sapiens

<400> 189  
cgagctgggc gagaagtagg ggagggcggt gctccgccgc ggtggcggtt 50  
gctatcgctt cgcagaacct actcaggcag ccagctgaga agagttgagg 100  
gaaagtgctg ctgctgggtc tgcagacgcg atggataacg tgcagccgaa 150

aataaaacat cgcccttct gcttcagtgt gaaaggccac gtgaagatgc 200  
tgcggctggc actaactgtg acatctatga ccttttttat catcgacaaa 250  
gccccgaac catatattgt tatcactgga tttgaagtca ccgttatctt 300  
atttttcata cttttatatg tactcagact tgatcgatta atgaagtgg 350  
tattttggcc tttgcttgat attatcaact cactggtaac aacagtattc 400  
atgctcatcg tatctgtggt ggcactgata ccagaaacca caacattgac 450  
agttgggtgga ggggtgtttg cacttgtgac agcagtatgc tgtcttgccg 500  
acggggccct tatttaccgg aagcttctgt tcaatcccag cggtccttac 550  
cagaaaaagc ctgtgcatga aaaaaaagaa gttttgtaat tttatattac 600  
tttttagttt gatactaagt attaaacata tttctgtatt cttccaaaaa 650  
aaaaaaaaa aaa 663

<210> 190

<211> 152

<212> PRT

<213> Homo sapiens

<400> 190

Met	Asp	Asn	Val	Gln	Pro	Lys	Ile	Lys	His	Arg	Pro	Phe	Cys	Phe
1				5					10					15

Ser	Val	Lys	Gly	His	Val	Lys	Met	Leu	Arg	Leu	Ala	Leu	Thr	Val
			20						25					30

Thr	Ser	Met	Thr	Phe	Phe	Ile	Ile	Ala	Gln	Ala	Pro	Glu	Pro	Tyr
			35						40					45

Ile	Val	Ile	Thr	Gly	Phe	Glu	Val	Thr	Val	Ile	Leu	Phe	Phe	Ile
			50						55					60

Leu	Leu	Tyr	Val	Leu	Arg	Leu	Asp	Arg	Leu	Met	Lys	Trp	Leu	Phe
			65						70					75

Trp	Pro	Leu	Leu	Asp	Ile	Ile	Asn	Ser	Leu	Val	Thr	Thr	Val	Phe
			80						85					90

Met	Leu	Ile	Val	Ser	Val	Leu	Ala	Leu	Ile	Pro	Glu	Thr	Thr	Thr
			95						100					105

Leu	Thr	Val	Gly	Gly	Gly	Val	Phe	Ala	Leu	Val	Thr	Ala	Val	Cys
			110						115					120

Cys	Leu	Ala	Asp	Gly	Ala	Leu	Ile	Tyr	Arg	Lys	Leu	Leu	Phe	Asn
			125						130					135

Pro	Ser	Gly	Pro	Tyr	Gln	Lys	Lys	Pro	Val	His	Glu	Lys	Lys	Glu
			140						145					150



Val Leu

<210> 191  
<211> 495  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 212, 234, 487  
<223> unknown base

<400> 191  
gggcgagaag taggggaggg cgtgttccgc cgcggtggcg gttgctatcg 50  
ttttgcagaa cctactcagg cagccagntg agaagagttg agggaaagtg 100  
ctgctgctgg gtctgcagac gcgatggata acgtgcagcc gaaaataaaa 150  
catgccccct tctgcttcag tgtgaaaggc cacgtgaaga tgctgcggct 200  
ggcactaact gngacatcta tgaccttttt tatnatogca caagcccctg 250  
aaccatatat tgttatcact ggatttgaag tcaccgttat cttatttttc 300  
atacttttat atgtactcag acttgatcga ttaatgaagt ggttattttg 350  
gcctttgctt gatattatca actcactggg aacaacagta ttcattgctca 400  
tcgtatctgt gttggcactg ataccagaaa ccacaacatt gacagttggg 450  
ggaggggtgt ttgcacttgt gacagcagta tgctgtnttg ccgac 495

<210> 192  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 192  
cgttttgcag aacctactca ggcag 25

<210> 193  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 193  
cctccaccaa ctgtcaatgt tgtgg 25

<210> 194  
<211> 40

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 194  
aaagtgctgc tgctgggtct gcagacgcga tggataacgt 40

<210> 195  
<211> 1879  
<212> DNA  
<213> Homo sapien

<400> 195  
cagccccgcg cgccggccga gtcgctgagc cgcggctgcc ggacgggacg 50  
ggaccggcta ggctgggcgc gccccccggg ccccgccgtg ggcatgggcg 100  
cactggccccg ggcgctgctg ctgcctctgc tggcccagtg gctcctgcgc 150  
gccgcccccg agctggcccc cgcgcccttc acgctgcccc tccgggtggc 200  
cgcggccaacg aaccgcgtag ttgcgcccac cccgggaccc gggacccttg 250  
ccgagcgcca cgccgacggc ttggcgctcg ccctggagcc tgccctggcg 300  
tcccccgcg ggcgcgcca cttcttggcc atggtagaca acctgcaggg 350  
ggactctggc cgcggctact acctggagat gctgatcggg accccccgc 400  
agaagctaca gattctcggt gacactggaa gcagtaactt tgccgtggca 450  
ggaacccgc actcctacat agacacgtac tttgacacag agaggtctag 500  
cacataccgc tccaagggct ttgacgtcac agtgaagtac acacaaggaa 550  
gctggacggg cttcgttggg gaagacctcg tcaccatccc caaaggcttc 600  
aatacttctt ttcttgtcaa cattgccact atttttgaat cagagaattt 650  
ctttttgcct gggattaaat ggaatggaat acttggccta gcttatgcca 700  
cacttgccaa gccatcaagt tctctggaga ccttcttcga ctccctggtg 750  
acacaagcaa acatcccaa cgttttctcc atgcagatgt gtggagccgg 800  
cttgcccgtt gctggatctg ggaccaacgg aggtagtctt gtcttgggtg 850  
gaattgaacc aagtttgtat aaaggagaca tctggtatac ccctattaag 900  
gaagagtggg actaccagat agaaattctg aaattggaaa ttggaggcca 950  
aagccttaat ctggactgca gagagtataa cgcagacaag gccatcgtgg 1000  
acagtggcac cacgctgctg cgcctgcccc agaaggtggt tgatgcggtg 1050  
gtggaagctg tggcccgcgc atctctgatt ccagaattct ctgatggttt 1100

ctggactggg tcccagctgg cgtgctggac gaattcggaa acaccttggg 1150  
 cttacttccc taaaatctcc atctacctga gagacgagaa ctccagcagg 1200  
 tcattccgta tcacaatcct gcctcagctt tacattcagc ccatgatggg 1250  
 ggccggcctg aattatgaat gttaccgatt cggcatttcc ccatccacaa 1300  
 atgcgctggg gatcgggtgcc acggtgatgg agggcttcta cgtcatcttc 1350  
 gacagagccc agaagagggt gggcttcgca gcgagcccct gtgcagaaat 1400  
 tgcagggtgct gcagtgtctg aaatttccgg gccttttcta acagaggatg 1450  
 tagccagcaa ctgtgtcccc gctcagtctt tgagcgagcc cattttgtgg 1500  
 attgtgtcct atgcgctcat gagcgtctgt ggagccatcc tccttgtctt 1550  
 aatcgtcctg ctgctgctgc cgttccgggtg tcagcgtcgc ccccgtagcc 1600  
 ctgaggctgt caatgatgag tcctctctgg tcagacatcg ctggaaatga 1650  
 atagccaggc ctgacctcaa gcaaccatga actcagctat taagaaaatc 1700  
 acatttccag ggcagcagcc gggatcgatg gtggcgcttt ctctgtgcc 1750  
 caccgtctt caatctctgt tctgtctcca gatgccttct agattcactg 1800  
 tcttttgatt cttgattttc aagctttcaa atcctcccta cttccaagaa 1850  
 aaataattaa aaaaaaaact tcattctaa 1879

<210> 196

<211> 518

<212> PRT

<213> Homo sapien

<400> 196

Met	Gly	Ala	Leu	Ala	Arg	Ala	Leu	Leu	Leu	Pro	Leu	Leu	Ala	Gln
1				5					10					15
Trp	Leu	Leu	Arg	Ala	Ala	Pro	Glu	Leu	Ala	Pro	Ala	Pro	Phe	Thr
				20					25					30
Leu	Pro	Leu	Arg	Val	Ala	Ala	Ala	Thr	Asn	Arg	Val	Val	Ala	Pro
				35					40					45
Thr	Pro	Gly	Pro	Gly	Thr	Pro	Ala	Glu	Arg	His	Ala	Asp	Gly	Leu
				50					55					60
Ala	Leu	Ala	Leu	Glu	Pro	Ala	Leu	Ala	Ser	Pro	Ala	Gly	Ala	Ala
				65					70					75
Asn	Phe	Leu	Ala	Met	Val	Asp	Asn	Leu	Gln	Gly	Asp	Ser	Gly	Arg
				80					85					90
Gly	Tyr	Tyr	Leu	Glu	Met	Leu	Ile	Gly	Thr	Pro	Pro	Gln	Lys	Leu
				95					100					105

Gln Ile Leu Val	Asp Thr Gly Ser Ser	Asn Phe Ala Val Ala	Gly
	110	115	120
Thr Pro His Ser	Tyr Ile Asp Thr Tyr	Phe Asp Thr Glu Arg	Ser
	125	130	135
Ser Thr Tyr Arg	Ser Lys Gly Phe Asp	Val Thr Val Lys Tyr	Thr
	140	145	150
Gln Gly Ser Trp	Thr Gly Phe Val Gly	Glu Asp Leu Val Thr	Ile
	155	160	165
Pro Lys Gly Phe	Asn Thr Ser Phe Leu	Val Asn Ile Ala Thr	Ile
	170	175	180
Phe Glu Ser Glu	Asn Phe Phe Leu Pro	Gly Ile Lys Trp Asn	Gly
	185	190	195
Ile Leu Gly Leu	Ala Tyr Ala Thr Leu	Ala Lys Pro Ser Ser	Ser
	200	205	210
Leu Glu Thr Phe	Phe Asp Ser Leu Val	Thr Gln Ala Asn Ile	Pro
	215	220	225
Asn Val Phe Ser	Met Gln Met Cys Gly	Ala Gly Leu Pro Val	Ala
	230	235	240
Gly Ser Gly Thr	Asn Gly Gly Ser Leu	Val Leu Gly Gly Ile	Glu
	245	250	255
Pro Ser Leu Tyr	Lys Gly Asp Ile Trp	Tyr Thr Pro Ile Lys	Glu
	260	265	270
Glu Trp Tyr Tyr	Gln Ile Glu Ile Leu	Lys Leu Glu Ile Gly	Gly
	275	280	285
Gln Ser Leu Asn	Leu Asp Cys Arg Glu	Tyr Asn Ala Asp Lys	Ala
	290	295	300
Ile Val Asp Ser	Gly Thr Thr Leu Leu	Arg Leu Pro Gln Lys	Val
	305	310	315
Phe Asp Ala Val	Val Glu Ala Val Ala	Arg Ala Ser Leu Ile	Pro
	320	325	330
Glu Phe Ser Asp	Gly Phe Trp Thr Gly	Ser Gln Leu Ala Cys	Trp
	335	340	345
Thr Asn Ser Glu	Thr Pro Trp Ser Tyr	Phe Pro Lys Ile Ser	Ile
	350	355	360
Tyr Leu Arg Asp	Glu Asn Ser Ser Arg	Ser Phe Arg Ile Thr	Ile
	365	370	375
Leu Pro Gln Leu	Tyr Ile Gln Pro Met	Met Gly Ala Gly Leu	Asn
	380	385	390
Tyr Glu Cys Tyr	Arg Phe Gly Ile Ser	Pro Ser Thr Asn Ala	Leu

	395		400		405
Val Ile Gly Ala	Thr Val Met Glu Gly	Phe Tyr Val Ile Phe	Asp		
	410		415		420
Arg Ala Gln Lys	Arg Val Gly Phe Ala	Ala Ser Pro Cys Ala	Glu		
	425		430		435
Ile Ala Gly Ala	Ala Val Ser Glu Ile	Ser Gly Pro Phe Ser	Thr		
	440		445		450
Glu Asp Val Ala	Ser Asn Cys Val Pro	Ala Gln Ser Leu Ser	Glu		
	455		460		465
Pro Ile Leu Trp	Ile Val Ser Tyr Ala	Leu Met Ser Val Cys	Gly		
	470		475		480
Ala Ile Leu Leu	Val Leu Ile Val Leu	Leu Leu Leu Pro Phe	Arg		
	485		490		495
Cys Gln Arg Arg	Pro Arg Asp Pro Glu	Val Val Asn Asp Glu	Ser		
	500		505		510
Ser Leu Val Arg	His Arg Trp Lys				
	515				

<210> 197  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 197  
 cgcagaagct acagattctc g 21

<210> 198  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 198  
 ggaaattgga ggccaaagc 19

<210> 199  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 199  
 ggatgtagcc agcaactgtg 20

<210> 200  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 200  
 gccttggtc gttctcttc 19

<210> 201  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 201  
 ggtcctgtgc ctggatgg 18

<210> 202  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 202  
 gacaagacta cctccgttgg tc 22

<210> 203  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 203  
 tgatgcacag ttcagcacct gttg 24

<210> 204  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 204  
 cgctccaagg gctttgacgt cacagtgaag tacacacaag gaagctg 47

<210> 205  
 <211> 1939  
 <212> DNA

<213> Homo sapiens

<400> 205

cgctccgcc ttccggaggct gacgcgcccg ggccgcttc caggcctgtg 50  
cagggcggat cggcagccgc ctggcggcga tccagggcgg tgcggggcct 100  
ggcggggagc cgggaggcgc ggccggcatg gaggcgctgc tgctgggcgc 150  
ggggttgctg ctgggcgctt acgtgcttgt ctactacaac ctggtgaagg 200  
ccccgccgtg cggcggcatg ggcaacctgc ggggccgcac ggccgtggtc 250  
acgggcgcca acagcggcat cggaaagatg acggcgctgg agctggcgcg 300  
ccggggagcg cgcgtgggtg tggcctgccg cagccaggag cgcggggagg 350  
cggctgcctt cgacctccgc caggagagtg ggaacaatga ggtcatcttc 400  
atggccttgg acttggccag tctggcctcg gtgcgggcct ttgccactgc 450  
ctttctgagc tctgagccac ggttggacat cctcatccac aatgccggta 500  
tcagttcctg tggccggacc cgtgaggcgt ttaacctgct gcttcgggtg 550  
aaccatatcg gtccctttct gctgacacat ctgctgctgc cttgcctgaa 600  
ggcatgtgcc cctagccgcg tgggtggtgt agcctcagct gccactgtc 650  
ggggacgtct tgacttcaaa cgcctggacc gccagtggt gggctggcgg 700  
caggagctgc gggcatatgc tgacactaag ctggctaata tactgtttgc 750  
ccgggagctc gccaaaccagc ttgaggccac tggcgtcacc tgctatgcag 800  
cccaccagc gcctgtgaac tcggagctgt tcctgcgcca tgttcctgga 850  
tggctgcgcc cacttttgcg ccattggct tggctgggtc tccgggcacc 900  
aagagggggg gccagacac ccctgtattg tgctctacaa gagggcatcg 950  
agcccctcag tgggagatat ttgccaact gccatgtgga agaggtgcct 1000  
ccagctgccc gagacgaccg ggcagcccat cggctatggg aggccagcaa 1050  
gaggctggca gggcttgggc ctggggagga tgctgaaccc gatgaagacc 1100  
cccagttctga ggactcagag gccccatctt ctctaagcac cccccaccct 1150  
gaggagccca cagttttctc accttaccac agccctcaga gctcaccaga 1200  
tttgtctaag atgacgcacc gaattcaggc taaagttgag cctgagatcc 1250  
agctctccta accctcaggc caggatgctt gccatggcac ttcatggtcc 1300  
ttgaaaacct cggatgtgtg tgaggccatg ccctggacac tgacgggttt 1350  
gtgatcttga cctccgtggg tactttctgg ggccccaagc tgtgccctgg 1400

acatctcttt tcttggttga aggaataatg ggtgattatt tcttctgag 1450  
 agtgacagta accccagatg gagagatagg ggtatgctag aactgtgct 1500  
 tctcggaat ttgatgtag ttttttcagg cccaccctt attgattctg 1550  
 atcagctctg gagcagaggc agggagtttg caatgtgatg cactgccaac 1600  
 attgagaatt agtgaactga tccctttgca accgtctagc taggtagtta 1650  
 aattaccccc atgttaatga agcggaatta ggctcccgag ctaagggact 1700  
 cgcctagggg ctcacagtga gtaggaggag ggctgggat ctgaacccaa 1750  
 gggctcgagg ccagggccga ctgccgtaag atgggtgctg agaagtgagt 1800  
 cagggcaggg cagctggtat cgaggtgcc catgggagta aggggacgcc 1850  
 ttccgggcgg atgcagggtt ggggtcatct gtatctgaag cccctcgaa 1900  
 taaagcgcgt tgaccgcaa aaaaaaaaaa aaaaaaaaaa 1939

<210> 206  
 <211> 377  
 <212> PRT  
 <213> Homo sapiens

<400> 206  
 Met Glu Ala Leu Leu Leu Gly Ala Gly Leu Leu Leu Gly Ala Tyr  
     1                    5                    10                    15  
 Val Leu Val Tyr Tyr Asn Leu Val Lys Ala Pro Pro Cys Gly Gly  
                     20                    25                    30  
 Met Gly Asn Leu Arg Gly Arg Thr Ala Val Val Thr Gly Ala Asn  
                     35                    40                    45  
 Ser Gly Ile Gly Lys Met Thr Ala Leu Glu Leu Ala Arg Arg Gly  
                     50                    55                    60  
 Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg Gly Glu Ala  
                     65                    70                    75  
 Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu Val Ile  
                     80                    85                    90  
 Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala Phe  
                     95                    100                    105  
 Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile  
                     110                    115                    120  
 His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe  
                     125                    130                    135  
 Asn Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr  
                     140                    145                    150



His	Leu	Leu	Leu	Pro	Cys	Leu	Lys	Ala	Cys	Ala	Pro	Ser	Arg	Val	155	160	165
Val	Val	Val	Ala	Ser	Ala	Ala	His	Cys	Arg	Gly	Arg	Leu	Asp	Phe	170	175	180
Lys	Arg	Leu	Asp	Arg	Pro	Val	Val	Gly	Trp	Arg	Gln	Glu	Leu	Arg	185	190	195
Ala	Tyr	Ala	Asp	Thr	Lys	Leu	Ala	Asn	Val	Leu	Phe	Ala	Arg	Glu	200	205	210
Leu	Ala	Asn	Gln	Leu	Glu	Ala	Thr	Gly	Val	Thr	Cys	Tyr	Ala	Ala	215	220	225
His	Pro	Gly	Pro	Val	Asn	Ser	Glu	Leu	Phe	Leu	Arg	His	Val	Pro	230	235	240
Gly	Trp	Leu	Arg	Pro	Leu	Leu	Arg	Pro	Leu	Ala	Trp	Leu	Val	Leu	245	250	255
Arg	Ala	Pro	Arg	Gly	Gly	Ala	Gln	Thr	Pro	Leu	Tyr	Cys	Ala	Leu	260	265	270
Gln	Glu	Gly	Ile	Glu	Pro	Leu	Ser	Gly	Arg	Tyr	Phe	Ala	Asn	Cys	275	280	285
His	Val	Glu	Glu	Val	Pro	Pro	Ala	Ala	Arg	Asp	Asp	Arg	Ala	Ala	290	295	300
His	Arg	Leu	Trp	Glu	Ala	Ser	Lys	Arg	Leu	Ala	Gly	Leu	Gly	Pro	305	310	315
Gly	Glu	Asp	Ala	Glu	Pro	Asp	Glu	Asp	Pro	Gln	Ser	Glu	Asp	Ser	320	325	330
Glu	Ala	Pro	Ser	Ser	Leu	Ser	Thr	Pro	His	Pro	Glu	Glu	Pro	Thr	335	340	345
Val	Ser	Gln	Pro	Tyr	Pro	Ser	Pro	Gln	Ser	Ser	Pro	Asp	Leu	Ser	350	355	360
Lys	Met	Thr	His	Arg	Ile	Gln	Ala	Lys	Val	Glu	Pro	Glu	Ile	Gln	365	370	375

Leu Ser

<210> 207

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 207

cttcatggcc ttggacttgg ccag 24

<210> 208  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 208  
 acgccagtgg cctcaagctg gttg 24

<210> 209  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 209  
 ctttctgagc tctgagccac gggtggacat cctcatccac aatgc 45

<210> 210  
 <211> 3716  
 <212> DNA  
 <213> Homo sapiens

<400> 210  
 ggaggagaca gcctcctggg gggcaggggt tccctgcctc tgctgctcct 50  
 gctcatcatg ggaggcatgg ctcaggactc cccgccccag atcctagtcc 100  
 acccccagga ccagctgttc cagggccctg gccctgccag gatgagctgc 150  
 caagcctcag gccagccacc tcccaccatc cgctgggtgc tgaatgggca 200  
 gccctgagc atggtgcccc cagaccaca ccacctcctg cctgatggga 250  
 cccttctgct gctacagccc cctgcccggg gacatgccca cgatggccag 300  
 gccctgtcca cagacctggg tgtctacaca tgtgaggcca gcaaccggct 350  
 tggcacggca gtcagcagag gcgctcggct gtctgtggct gtcctccggg 400  
 aggatttcca gatccagcct cgggacatgg tggctgtggt gggtagcag 450  
 ttactctgg aatgtgggcc gccctggggc caccagagc ccacagtctc 500  
 atggtggaaa gatgggaaac ccctggccct ccagcccga aggcacacag 550  
 tgtccggggg gtccctgctg atggcaagag cagagaagag tgacgaagg 600  
 acctacatgt gtgtggccac caacagcgca ggacataggg agagccgcgc 650  
 agcccgggtt tccatccagg agcccagga ctacacggag cctgtggagc 700  
 ttctggctgt gcgaattcag ctggaaaatg tgacactgct gaaccgggat 750

cctgcagagg gccccaagcc tagaccggcg gtgtggctca gctggaaggt 800  
cagtggccct gctgcgcctg cccaatctta cacggccttg ttcaggaccc 850  
agactgcccc gggaggccag ggagctccgt gggcagagga gctgctggcc 900  
ggctggcaga gcgcagagct tggaggcctc cactggggcc aagactacga 950  
gttcaaagtg agaccatcct ctggccgggc tcgaggccct gacagcaacg 1000  
tgctgctcct gaggctgccg gaaaaagtgc ccagtgcccc acctcaggaa 1050  
gtgactctaa agcctggcaa tggcactgtc tttgtgagct gggccccacc 1100  
acctgctgaa aaccacaatg gcatcatccg tggtaccag gtctggagcc 1150  
tgggcaacac atcactgcca ccagccaact ggactgtagt tggtagagcag 1200  
accagctgg aaatcgccac ccatatgcca ggctcctact gcgtgcaagt 1250  
ggctgcagtc actggtgctg gagctgggga gccagtaga cctgtctgcc 1300  
tccttttaga gcaggccatg gagcgagcca cccaagaacc cagtgagcat 1350  
ggcccttga ccctggagca gctgagggt accttgaagc ggcctgaggt 1400  
cattgccacc tgcggtgtt cactctgggt gctgcttctg ggcaccgccg 1450  
tgtgtatcca ccgccggcg cgagctaggg tgcacctggg ccaggtctg 1500  
tacagatata ccagtgagga tgccatccta aaacacagga tggatcacag 1550  
tgactcccag tggttggcag acacttggcg ttccacctct ggctctcggg 1600  
acctgagcag cagcagcagc ctccagcagtc ggctgggggc ggatgcccgg 1650  
gacccactag actgtcgtcg ctcccttgtc tcctgggact cccgaagccc 1700  
cggcgtgccc ctgcttccag acaccagcac tttttatggc tccctcatcg 1750  
ctgagctgcc ctccagtacc ccagccaggc caagtcccca ggtcccagct 1800  
gtcaggcgcc tcccaccca gctggcccag ctctccagcc cctgttccag 1850  
ctcagacagc ctctgcagcc gcaggggact ctcttctccc cgcttgtctc 1900  
tggccccctgc agaggcttgg aaggccaaaa agaagcagga gctgcagcat 1950  
gccaacagtt cccactgct ccggggcagc cactccttgg agctccgggc 2000  
ctgtgagtta ggaaatagag gtccaagaa cctttcccaa agcccaggag 2050  
ctgtgcccc agetctggtt gcctggcggg ccctgggacc gaaactcctc 2100  
agctcctcaa atgagctggt tactcgtcat ctccctccag caccctctt 2150  
tcctcatgaa actccccaa ctcagagtca acagaccag cctccggtgg 2200

caccacaggc tccctcctcc atcctgctgc cagcagcccc catccccatc 2250  
cttagccccct gcagtcccc tagccccag gcctcttccc tctctggccc 2300  
cagcccagct tccagtcgcc tgtccagctc ctcaactgtca tccctggggg 2350  
aggatcaaga cagcgtgctg acccctgagg aggtagccct gtgcttgga 2400  
ctcagtgagg gtgaggagac tcccaggaac agcgtctctc ccatgccaa 2450  
ggctccttca cccccacca cctatgggta catcagcgtc ccaacagcct 2500  
cagagttcac ggacatgggc aggactggag gaggggtggg gccaagggg 2550  
ggagtcttgc tgtgcccacc tcggccctgc ctacccccca ccccagcga 2600  
gggctcctta gccaatgggt ggggctcagc ctctgaggac aatgccgcca 2650  
gcgccagagc cagccttctc agctcctccg atggctcctt cctcgtgat 2700  
gctcactttg cccgggccct ggcagtggct gtggatagct ttggtttcgg 2750  
tctagagccc agggaggcag actgcgtctt catagatgcc tcatcacctc 2800  
cctccccacg ggatgagatc ttctgaccc ccaacctctc cctgcccctg 2850  
tgggagtgga ggccagactg gttggaagac atggaggtca gccacacca 2900  
gcggctggga agggggatgc ctccctggcc ccctgactct cagatctctt 2950  
cccagagaag tcagctccac tgctgtatgc ccaaggctgg tgcttctct 3000  
gtagattact cctgaaccgt gtccctgaga cttcccagac gggaatcaga 3050  
accacttctc ctgtccaccc acaagacctg ggctgtggtg tgtgggtctt 3100  
ggcctgtgtt tctctgcagc tgggggtccac cttcccagc ctccagagag 3150  
ttctccctcc acgattgtga aaacaaatga aaacaaaatt agagcaaagc 3200  
tgacctggag ccctcaggga gcaaaacatc atctccacct gactcctagc 3250  
caactgtttc tcctctgtgc catccactcc caccaccagg ttgttttggc 3300  
ctgaggagca gccctgcctg ctgctcttcc cccaccattt ggatcacagg 3350  
aagtggagga gccagagggt cctttgtgga ggacagcagt ggctgctggg 3400  
agagggtgt ggaggaagga gcttctcgga gccccctctc agccttacct 3450  
gggcccctcc tctagagaag agctcaactc tctcccaccc tcaccatgga 3500  
aagaaaataa ttatgaatgc cactgaggca ctgaggccct acctcatgcc 3550  
aaacaaaggg ttcaaggctg ggtctagcga ggatgctgaa ggaaggagg 3600  
tatgagaccg taggtcaaaa gcaccatcct cgtactgttg tcaactatgag 3650

cttaagaaat ttgataccat aaaatggtaa aaaaaaaaaa aaaaaaaaaa 3700

aaaaaaaaaa aaaaaa 3716

<210> 211

<211> 985

<212> PRT

<213> Homo sapiens

<400> 211

Met	Gly	Gly	Met	Ala	Gln	Asp	Ser	Pro	Pro	Gln	Ile	Leu	Val	His
1				5					10					15

Pro	Gln	Asp	Gln	Leu	Phe	Gln	Gly	Pro	Gly	Pro	Ala	Arg	Met	Ser
			20						25					30

Cys	Gln	Ala	Ser	Gly	Gln	Pro	Pro	Pro	Thr	Ile	Arg	Trp	Leu	Leu
				35					40					45

Asn	Gly	Gln	Pro	Leu	Ser	Met	Val	Pro	Pro	Asp	Pro	His	His	Leu
				50					55					60

Leu	Pro	Asp	Gly	Thr	Leu	Leu	Leu	Leu	Gln	Pro	Pro	Ala	Arg	Gly
				65					70					75

His	Ala	His	Asp	Gly	Gln	Ala	Leu	Ser	Thr	Asp	Leu	Gly	Val	Tyr
				80					85					90

Thr	Cys	Glu	Ala	Ser	Asn	Arg	Leu	Gly	Thr	Ala	Val	Ser	Arg	Gly
				95					100					105

Ala	Arg	Leu	Ser	Val	Ala	Val	Leu	Arg	Glu	Asp	Phe	Gln	Ile	Gln
				110					115					120

Pro	Arg	Asp	Met	Val	Ala	Val	Val	Gly	Glu	Gln	Phe	Thr	Leu	Glu
				125					130					135

Cys	Gly	Pro	Pro	Trp	Gly	His	Pro	Glu	Pro	Thr	Val	Ser	Trp	Trp
				140					145					150

Lys	Asp	Gly	Lys	Pro	Leu	Ala	Leu	Gln	Pro	Gly	Arg	His	Thr	Val
				155					160					165

Ser	Gly	Gly	Ser	Leu	Leu	Met	Ala	Arg	Ala	Glu	Lys	Ser	Asp	Glu
				170					175					180

Gly	Thr	Tyr	Met	Cys	Val	Ala	Thr	Asn	Ser	Ala	Gly	His	Arg	Glu
				185					190					195

Ser	Arg	Ala	Ala	Arg	Val	Ser	Ile	Gln	Glu	Pro	Gln	Asp	Tyr	Thr
				200					205					210

Glu	Pro	Val	Glu	Leu	Leu	Ala	Val	Arg	Ile	Gln	Leu	Glu	Asn	Val
				215					220					225

Thr	Leu	Leu	Asn	Pro	Asp	Pro	Ala	Glu	Gly	Pro	Lys	Pro	Arg	Pro
				230					235					240

Ala Val Trp Leu	Ser 245	Trp Lys Val Ser	Gly 250	Pro Ala Ala Pro	Ala 255
Gln Ser Tyr Thr	Ala 260	Leu Phe Arg Thr	Gln 265	Thr Ala Pro Gly	Gly 270
Gln Gly Ala Pro	Trp 275	Ala Glu Glu Leu	Leu 280	Ala Gly Trp Gln	Ser 285
Ala Glu Leu Gly	Gly 290	Leu His Trp Gly	Gln 295	Asp Tyr Glu Phe	Lys 300
Val Arg Pro Ser	Ser 305	Gly Arg Ala Arg	Gly 310	Pro Asp Ser Asn	Val 315
Leu Leu Leu Arg	Leu 320	Pro Glu Lys Val	Pro 325	Ser Ala Pro Pro	Gln 330
Glu Val Thr Leu	Lys 335	Pro Gly Asn Gly	Thr 340	Val Phe Val Ser	Trp 345
Val Pro Pro Pro	Ala 350	Glu Asn His Asn	Gly 355	Ile Ile Arg Gly	Tyr 360
Gln Val Trp Ser	Leu 365	Gly Asn Thr Ser	Leu 370	Pro Pro Ala Asn	Trp 375
Thr Val Val Gly	Glu 380	Gln Thr Gln Leu	Glu 385	Ile Ala Thr His	Met 390
Pro Gly Ser Tyr	Cys 395	Val Gln Val Ala	Ala 400	Val Thr Gly Ala	Gly 405
Ala Gly Glu Pro	Ser 410	Arg Pro Val Cys	Leu 415	Leu Leu Glu Gln	Ala 420
Met Glu Arg Ala	Thr 425	Gln Glu Pro Ser	Glu 430	His Gly Pro Trp	Thr 435
Leu Glu Gln Leu	Arg 440	Ala Thr Leu Lys	Arg 445	Pro Glu Val Ile	Ala 450
Thr Cys Gly Val	Ala 455	Leu Trp Leu Leu	Leu 460	Leu Gly Thr Ala	Val 465
Cys Ile His Arg	Arg 470	Arg Arg Ala Arg	Val 475	His Leu Gly Pro	Gly 480
Leu Tyr Arg Tyr	Thr 485	Ser Glu Asp Ala	Ile 490	Leu Lys His Arg	Met 495
Asp His Ser Asp	Ser 500	Gln Trp Leu Ala	Asp 505	Thr Trp Arg Ser	Thr 510
Ser Gly Ser Arg	Asp 515	Leu Ser Ser Ser	Ser 520	Ser Leu Ser Ser	Arg 525
Leu Gly Ala Asp	Ala Arg Asp Pro	Leu Asp Cys Arg	Arg Ser Leu		

	530		535		540
Leu Ser Trp Asp	Ser Arg Ser Pro Gly	Val Pro Leu Leu Pro	Asp		
	545		550		555
Thr Ser Thr Phe	Tyr Gly Ser Leu Ile	Ala Glu Leu Pro Ser	Ser		
	560		565		570
Thr Pro Ala Arg	Pro Ser Pro Gln Val	Pro Ala Val Arg Arg	Leu		
	575		580		585
Pro Pro Gln Leu	Ala Gln Leu Ser Ser	Pro Cys Ser Ser Ser	Asp		
	590		595		600
Ser Leu Cys Ser	Arg Arg Gly Leu Ser	Ser Pro Arg Leu Ser	Leu		
	605		610		615
Ala Pro Ala Glu	Ala Trp Lys Ala Lys	Lys Lys Gln Glu Leu	Gln		
	620		625		630
His Ala Asn Ser	Ser Pro Leu Leu Arg	Gly Ser His Ser Leu	Glu		
	635		640		645
Leu Arg Ala Cys	Glu Leu Gly Asn Arg	Gly Ser Lys Asn Leu	Ser		
	650		655		660
Gln Ser Pro Gly	Ala Val Pro Gln Ala	Leu Val Ala Trp Arg	Ala		
	665		670		675
Leu Gly Pro Lys	Leu Leu Ser Ser Ser	Asn Glu Leu Val Thr	Arg		
	680		685		690
His Leu Pro Pro	Ala Pro Leu Phe Pro	His Glu Thr Pro Pro	Thr		
	695		700		705
Gln Ser Gln Gln	Thr Gln Pro Pro Val	Ala Pro Gln Ala Pro	Ser		
	710		715		720
Ser Ile Leu Leu	Pro Ala Ala Pro Ile	Pro Ile Leu Ser Pro	Cys		
	725		730		735
Ser Pro Pro Ser	Pro Gln Ala Ser Ser	Leu Ser Gly Pro Ser	Pro		
	740		745		750
Ala Ser Ser Arg	Leu Ser Ser Ser Ser	Leu Ser Ser Leu Gly	Glu		
	755		760		765
Asp Gln Asp Ser	Val Leu Thr Pro Glu	Glu Val Ala Leu Cys	Leu		
	770		775		780
Glu Leu Ser Glu	Gly Glu Glu Thr Pro	Arg Asn Ser Val Ser	Pro		
	785		790		795
Met Pro Arg Ala	Pro Ser Pro Pro Thr	Thr Tyr Gly Tyr Ile	Ser		
	800		805		810
Val Pro Thr Ala	Ser Glu Phe Thr Asp	Met Gly Arg Thr Gly	Gly		
	815		820		825

Gly Val Gly Pro	Lys Gly Gly Val Leu	Leu Cys Pro Pro Arg Pro
830		835 840
Cys Leu Thr Pro	Thr Pro Ser Glu Gly	Ser Leu Ala Asn Gly Trp
845		850 855
Gly Ser Ala Ser	Glu Asp Asn Ala Ala	Ser Ala Arg Ala Ser Leu
860		865 870
Val Ser Ser Ser	Asp Gly Ser Phe Leu	Ala Asp Ala His Phe Ala
875		880 885
Arg Ala Leu Ala	Val Ala Val Asp Ser	Phe Gly Phe Gly Leu Glu
890		895 900
Pro Arg Glu Ala	Asp Cys Val Phe Ile	Asp Ala Ser Ser Pro Pro
905		910 915
Ser Pro Arg Asp	Glu Ile Phe Leu Thr	Pro Asn Leu Ser Leu Pro
920		925 930
Leu Trp Glu Trp	Arg Pro Asp Trp Leu	Glu Asp Met Glu Val Ser
935		940 945
His Thr Gln Arg	Leu Gly Arg Gly Met	Pro Pro Trp Pro Pro Asp
950		955 960
Ser Gln Ile Ser	Ser Gln Arg Ser Gln	Leu His Cys Arg Met Pro
965		970 975
Lys Ala Gly Ala	Ser Pro Val Asp Tyr	Ser
980		985

<210> 212  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 212  
 gaagggacct acatgtgtgt ggcc 24

<210> 213  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 213  
 actgaccttc cagctgagcc acac 24

<210> 214  
 <211> 50  
 <212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 214

aggactacac ggagcctgtg gagcttctgg ctgtgcgaat tcagctggaa 50

<210> 215

<211> 2749

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 1869, 1887

<223> unknown base

<400> 215

ctcccacggt gtccagcgcc cagaatgcgg cttctgggtcc tgctatgggg 50

ttgcctgctg ctcccaggtt atgaagccct ggagggccca gaggaatca 100

gcgggttcga aggggacact gtgtccctgc agtgcaccta caggaagag 150

ctgagggacc accggaagta ctggtgcagg aagggtggga tcctcttctc 200

tcgctgctct ggcaccatct atgcagaaga agaaggccag gagacaatga 250

agggcaggggt gtccatccgt gacagccgcc aggagctctc gtcattgtg 300

acctgtgga acctcaccct gcaagacgct ggggagtact ggtgtgggg 350

cgaaaaacgg ggccccgatg agtctttact gatctctctg ttctgtcttc 400

caggaccctg ctgtcctccc tccccttctc ccaccttcca gcctctggct 450

acaacacgcc tgcagcccaa ggcaaaagct cagcaaacc agccccag 500

attgacttct cctgggtctt acccggcagc caccacagcc aagcagggga 550

agacaggggc tgaggccct ccattgccag ggacttcca gtacgggcac 600

gaaaggactt ctcatcac aggaacctt cctcaccag cgacctctcc 650

tcctgcaggg agtcccgc ccccatgca gctggactcc acctcagcag 700

aggacaccag tccagctctc agcagtggca gctctaagcc cagggtgtcc 750

atcccgatgg tccgcatact ggccccagtc ctggtgctgc tgagccttct 800

gtcagccgca ggctgatcg cttctgcag ccacctgtc ctgtggagaa 850

aggaagctca acaggccacg gagacacaga ggaacgagaa gttctggctc 900

tcacgcttga ctgcggagga aaaggaagcc ccttcccagg cccctgaggg 950

ggacgtgatc tcgatgcctc ccctccacac atctgaggag gagctgggct 1000

09978199-101501

tctcgaagtt tgtctcagcg tagggcagga ggccctcctg gccaggccag 1050  
cagtgaagca gtatggctgg ctggatcagc accgattccc gaaagctttc 1100  
cacctcagcc tcagagtcca gctgcccgga ctccagggtc ctccccaccc 1150  
tccccaggct ctctcttgc atgttccagc ctgacctaga agcgtttgtc 1200  
agccctggag ccagagcgg tggccttgct ctcccggtc gagactggga 1250  
catccctgat aggttcacat ccctgggcag agtaccaggc tgctgaccct 1300  
cagcagggcc agacaaggct cagtggatct ggtctgagtt tcaatctgcc 1350  
aggaactcct gggcctcatg ccagtgctg gacctgcct tcctccact 1400  
ccagacccca ccttgtcttc cctccctggc gtctcagac ttagtccac 1450  
ggtctcctgc atcagctggg gatgaagagg agcatgctgg ggtgagactg 1500  
ggattctggc ttctcttga accacctgca tccagccctt caggaagcct 1550  
gtgaaaaacg tgattcctgg cccaccaag acccaccaa accatctctg 1600  
ggcttgggtgc aggactctga attctaaca tgcccagtga ctgtgcact 1650  
tgagtttgag ggccagtggg cctgatgaac gctcacacc ctccagctta 1700  
gagtctgcat ttgggctgtg acgtctccac ctgccccaat agatctgctc 1750  
tgtctgcgac accagatcca cgtggggact cccctgaggc ctgctaagtc 1800  
caggccttgg tcaggtcagg tgcacattgc aggataagcc caggaccggc 1850  
acagaagtgg ttgcctttnc catttgccct ccctggacca tgccttcttg 1900  
cctttggaaa aaatgatgaa gaaaacctg gctccttct tgtctggaaa 1950  
gggttacttg cctatgggtt ctggtggcta gagagaaaag tagaaaacca 2000  
gagtgcacgt aggtgtctaa cacagaggag agtaggaaca gggcggatac 2050  
ctgaaggtga ctccgagtc agccccctgg agaaggggtc gggggtggtg 2100  
gtaaagtagc acaactacta tttttttct ttttccatta ttattgtttt 2150  
ttaagacaga atctcgtgct gctgccagg ctggagtga gtggcacgat 2200  
ctgcaaactc cgcctcctgg gttcaagtga ttcttctgcc tcagcctccc 2250  
gagtagctgg gattacaggc acgcaccacc acacctggt aatttttgta 2300  
cttttagtag agatggggtt tcaccatggt ggccaggctg gtcttgaact 2350  
cctgacctca aatgagcctc ctgcttcagt ctcccaaatt gcgggatta 2400  
caggcatgag ccactgtgtc tggccctatt tcctttaaaa agtgaaatta 2450

agagttgttc agtatgcaaa acttggaag atggaggaga aaaagaaaag 2500  
gaagaaaaaa atgtcaccca tagtctcacc agagactatc attatttcgt 2550  
tttgtgttac ttccttcac tcttttcttc ttcacataat ttgccggtgt 2600  
tctttttaca gagcaattat cttgtatata caactttgta tcctgccttt 2650  
tccaccttat cgttccatca ctttattcca gcacttctct gtgttttaca 2700  
gaccttttta taaataaaat gttcatcagc tgcataaaaa aaaaaaaaaa 2749

<210> 216  
<211> 332  
<212> PRT  
<213> Homo sapiens

<400> 216

Met	Arg	Leu	Leu	Val	Leu	Leu	Trp	Gly	Cys	Leu	Leu	Leu	Pro	Gly		1		5		10		15
Tyr	Glu	Ala	Leu	Glu	Gly	Pro	Glu	Glu	Ile	Ser	Gly	Phe	Glu	Gly			20		25		30	
Asp	Thr	Val	Ser	Leu	Gln	Cys	Thr	Tyr	Arg	Glu	Glu	Leu	Arg	Asp			35		40		45	
His	Arg	Lys	Tyr	Trp	Cys	Arg	Lys	Gly	Gly	Ile	Leu	Phe	Ser	Arg			50		55		60	
Cys	Ser	Gly	Thr	Ile	Tyr	Ala	Glu	Glu	Glu	Gly	Gln	Glu	Thr	Met			65		70		75	
Lys	Gly	Arg	Val	Ser	Ile	Arg	Asp	Ser	Arg	Gln	Glu	Leu	Ser	Leu			80		85		90	
Ile	Val	Thr	Leu	Trp	Asn	Leu	Thr	Leu	Gln	Asp	Ala	Gly	Glu	Tyr			95		100		105	
Trp	Cys	Gly	Val	Glu	Lys	Arg	Gly	Pro	Asp	Glu	Ser	Leu	Leu	Ile			110		115		120	
Ser	Leu	Phe	Val	Phe	Pro	Gly	Pro	Cys	Cys	Pro	Pro	Ser	Pro	Ser			125		130		135	
Pro	Thr	Phe	Gln	Pro	Leu	Ala	Thr	Thr	Arg	Leu	Gln	Pro	Lys	Ala			140		145		150	
Lys	Ala	Gln	Gln	Thr	Gln	Pro	Pro	Gly	Leu	Thr	Ser	Pro	Gly	Leu			155		160		165	
Tyr	Pro	Ala	Ala	Thr	Thr	Ala	Lys	Gln	Gly	Lys	Thr	Gly	Ala	Glu			170		175		180	
Ala	Pro	Pro	Leu	Pro	Gly	Thr	Ser	Gln	Tyr	Gly	His	Glu	Arg	Thr			185		190		195	
Ser	Gln	Tyr	Thr	Gly	Thr	Ser	Pro	His	Pro	Ala	Thr	Ser	Pro	Pro								

	200	205	210
Ala Gly Ser Ser	Arg Pro Pro Met Gln	Leu Asp Ser Thr Ser	Ala
	215	220	225
Glu Asp Thr Ser	Pro Ala Leu Ser Ser	Gly Ser Ser Lys Pro	Arg
	230	235	240
Val Ser Ile Pro	Met Val Arg Ile Leu	Ala Pro Val Leu Val	Leu
	245	250	255
Leu Ser Leu Leu	Ser Ala Ala Gly Leu	Ile Ala Phe Cys Ser	His
	260	265	270
Leu Leu Leu Trp	Arg Lys Glu Ala Gln	Gln Ala Thr Glu Thr	Gln
	275	280	285
Arg Asn Glu Lys	Phe Trp Leu Ser Arg	Leu Thr Ala Glu Glu	Lys
	290	295	300
Glu Ala Pro Ser	Gln Ala Pro Glu Gly	Asp Val Ile Ser Met	Pro
	305	310	315
Pro Leu His Thr	Ser Glu Glu Glu Leu	Gly Phe Ser Lys Phe	Val
	320	325	330
Ser Ala			

<210> 217  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 217  
 ccctgcagtg cacctacagg gaag 24

<210> 218  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 218  
 ctgtcttccc ctgcttggt gtgg 24

<210> 219  
 <211> 47  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 219  
 ggtgcaggaa ggggtgggatc ctcttctctc gctgctctgg ccacatc 47

<210> 220  
 <211> 950  
 <212> DNA  
 <213> Homo sapiens

<400> 220  
 ttgtgactaa aagctggcct agcaggccag ggagtgcagc tgcaggcgtg 50  
 ggggtggcag gagccgcaga gccagagcag acagccgaga aacagggtga 100  
 cagtgtgaaa gaaccagtgg tctcgctctg ttgccaggc tagagtgtac 150  
 tggcgtgatc atagctcact gcagcctcag actcctggac ttgagaaatc 200  
 ctctgcctt agcctcctgc atatctggga ctccaggggt gcactcaagc 250  
 cctgtttctt ctcttctgt gagtggacca cggaggctgg tgagctgcct 300  
 gtcattccaa agctcagctc tgagccagag tgggtgtggc tccacctctg 350  
 ccgccggcat agaagccagg agcagggtc tcagaaggcg gtggtgcca 400  
 gctgggatca tgttgttggc cctggtctgt ctgctcagct gcctgctacc 450  
 ctccagttag gccaaagctc acggctggtg tgaactggcc agagtgtac 500  
 atgacttcgg gctggacgga taccggggat acagcctggc tgactgggtc 550  
 tgccttgctt atttcacaag cggtttcaac gcagctgctt tggactacga 600  
 ggctgatggg agcaccaaca acgggatctt ccagatcaac agccggaggt 650  
 ggtgcagcaa cctcaccocg aacgtcccca acgtgtgccg gatgtactgc 700  
 tcagatttgt tgaatcctaa tctcaaggat accgttatct gtgccatgaa 750  
 gataacccaa gagcctcagg gtctgggtta ctgggaggcc tggaggcatc 800  
 actgccaggg aaaagacctc actgaatggg tggatggctg tgacttctag 850  
 gatggacgga accatgcaca gcaggctggg aaatgtggtt tggttcctga 900  
 cctaggcttg ggaagacaag ccagcgaata aaggatggtt gaacgtgaaa 950

<210> 221  
 <211> 146  
 <212> PRT  
 <213> Homo sapiens

<400> 221  
 Met Leu Leu Ala Leu Val Cys Leu Leu Ser Cys Leu Leu Pro Ser  
 1 5 10 15  
 Ser Glu Ala Lys Leu Tyr Gly Arg Cys Glu Leu Ala Arg Val Leu  
 20 25 30

His Asp Phe Gly Leu Asp Gly Tyr Arg Gly Tyr Ser Leu Ala Asp  
                   35                                  40                                  45  
 Trp Val Cys Leu Ala Tyr Phe Thr Ser Gly Phe Asn Ala Ala Ala  
                   50                                  55                                  60  
 Leu Asp Tyr Glu Ala Asp Gly Ser Thr Asn Asn Gly Ile Phe Gln  
                   65                                  70                                  75  
 Ile Asn Ser Arg Arg Trp Cys Ser Asn Leu Thr Pro Asn Val Pro  
                   80                                  85                                  90  
 Asn Val Cys Arg Met Tyr Cys Ser Asp Leu Leu Asn Pro Asn Leu  
                   95                                  100                                 105  
 Lys Asp Thr Val Ile Cys Ala Met Lys Ile Thr Gln Glu Pro Gln  
                  110                                 115                                 120  
 Gly Leu Gly Tyr Trp Glu Ala Trp Arg His His Cys Gln Gly Lys  
                  125                                 130                                 135  
 Asp Leu Thr Glu Trp Val Asp Gly Cys Asp Phe  
                  140                                 145

<210> 222  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 222  
 gggatcatgt tgttggccct ggtc 24

<210> 223  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 223  
 gcaaggcaga cccagtcagc cag 23

<210> 224  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 224  
 ctgcctgcta ccctccaagt gaggccaagc tctacggtcg ttgtg 45

<210> 225

<211> 2049  
<212> DNA  
<213> Homo sapiens

<400> 225  
agccgctgcc ccgggccggg cgcccgcggc ggcaccatga gtccccgctc 50  
gtgcctgcgt tcgctgcgcc tcctcgtctt cgccgtcttc tcagccgccg 100  
cgagcaactg gctgtacctg gccaaagtgt cgtcgggtggg gagcatctca 150  
gaggaggaga cgtgcgagaa actcaagggc ctgatccaga ggcagggtgca 200  
gatgtgcaag cggaacctgg aagtcattga ctcgggtgcgc gcgggtgccc 250  
agctggccat tgaggagtgc cagtaccagt tccggaaccg gcgctggaac 300  
tgctccacac tcgactcctt gcccgcttcc ggcaagggtg tgacgcaagg 350  
gactcgggag gcggccttcg tgtacgccat ctcttcggca ggtgtggcct 400  
ttgcagtgc gcgggcgtgc agcagtgggg agctggagaa gtgcggctgt 450  
gacaggacag tgcattgggt cagcccacag ggcttccagt ggtcaggatg 500  
ctctgacaac atcgccctac gtgtggcctt ctcacagtcg tttgtggatg 550  
tgccgggagag aagcaagggg gcctcgtcca gcagagccct catgaacctc 600  
cacaacaatg aggccggcag gaaggccatc ctgacacaca tgcgggtgga 650  
atgcaagtgc cacggggtgt caggctcctg tgaggtaaag acgtgctggc 700  
gagccgtgcc gcccttccgc cagggtgggtc acgcactgaa ggagaagttt 750  
gatggtgcca ctgagggtga gccacgccgc gtgggctcct ccagggcact 800  
ggtaccacgc aacgcacagt tcaagccgca cacagatgag gacctggtgt 850  
acttgagacc tagccccgac ttctgtgagc aggacatgcg cagcggcgtg 900  
ctgggcacga ggggccgcac atgcaacaag acgtccaagg ccatcgacgg 950  
ctgtgagctg ctgtgctgtg gccgcggcct ccacacggcg cagggtggagc 1000  
tggctgaacg ctgcagctgc aaattccact ggtgctgctt cgtcaagtgc 1050  
cggcagtgcc agcggctcgt ggagttgcac acgtgccgat gaccgcctgc 1100  
ctagccctgc gccggcaacc acctagtggc ccagggaagg ccgataattt 1150  
aaacagtctc ccaccaccta cccaagaga tactggttgt attttttgtt 1200  
ctggttttgt ttttgggtcc tcatgttatt tattgccgaa accaggcagg 1250  
caaccccaag ggcaccaacc agggcctccc caaagcctgg gcctttgtgg 1300  
ctgccactga ccaaaggac cttgctcgtg ccgctggctg cccgcatgtg 1350

gctgccactg accactcagt tggtatctgt gtccgttttt ctacttgcag 1400  
acctaagggtg gagtaacaag gagtattacc accacatggc tactgaccgt 1450  
gtcatcgggg aagagggggc cttatggcag ggaaaatagg taccgacttg 1500  
atggaagtca caccctctgg aaaaaagaac tcttaactct ccagcacaca 1550  
tacacatgga ctctctggcag cttgagccta gaagccatgt ctctcaaagt 1600  
ccctgagaaa gggaacaagc agataccagg tcaagggcac caggttcatt 1650  
tcagccctta catggacagc tagaggttcg atatctgtgg gtccttccag 1700  
gcaagaagag ggagatgaga gcaagagacg actgaagtcc caccctagaa 1750  
cccagcctgc cccagcctgc ccctgggaag aggaaaactta accactcccc 1800  
agaccacct aggcaggcat ataggctgcc atcctggacc agggatcccc 1850  
gctgtgcctt tgcagtcatg cccgagtcac ctttcacagc gctgttcctc 1900  
catgaaactg aaaaacacac acacacacac acacacacac acacacacac 1950  
acacacacac ggacacacac acacacctgc gagagagagg gaggaaagg 2000  
ctgtgccttt gcagtcatgc ccgagtcacc tttcacagca ctgttcctc 2049

<210> 226  
<211> 351  
<212> PRT  
<213> Homo sapiens

<400> 226  
Met Ser Pro Arg Ser Cys Leu Arg Ser Leu Arg Leu Leu Val Phe  
1 5 10 15  
Ala Val Phe Ser Ala Ala Ala Ser Asn Trp Leu Tyr Leu Ala Lys  
20 25 30  
Leu Ser Ser Val Gly Ser Ile Ser Glu Glu Glu Thr Cys Glu Lys  
35 40 45  
Leu Lys Gly Leu Ile Gln Arg Gln Val Gln Met Cys Lys Arg Asn  
50 55 60  
Leu Glu Val Met Asp Ser Val Arg Arg Gly Ala Gln Leu Ala Ile  
65 70 75  
Glu Glu Cys Gln Tyr Gln Phe Arg Asn Arg Arg Trp Asn Cys Ser  
80 85 90  
Thr Leu Asp Ser Leu Pro Val Phe Gly Lys Val Val Thr Gln Gly  
95 100 105  
Thr Arg Glu Ala Ala Phe Val Tyr Ala Ile Ser Ser Ala Gly Val  
110 115 120



Ala Phe Ala Val Thr Arg Ala Cys Ser Ser Gly Glu Leu Glu Lys	125	130	135
Cys Gly Cys Asp Arg Thr Val His Gly Val Ser Pro Gln Gly Phe	140	145	150
Gln Trp Ser Gly Cys Ser Asp Asn Ile Ala Tyr Gly Val Ala Phe	155	160	165
Ser Gln Ser Phe Val Asp Val Arg Glu Arg Ser Lys Gly Ala Ser	170	175	180
Ser Ser Arg Ala Leu Met Asn Leu His Asn Asn Glu Ala Gly Arg	185	190	195
Lys Ala Ile Leu Thr His Met Arg Val Glu Cys Lys Cys His Gly	200	205	210
Val Ser Gly Ser Cys Glu Val Lys Thr Cys Trp Arg Ala Val Pro	215	220	225
Pro Phe Arg Gln Val Gly His Ala Leu Lys Glu Lys Phe Asp Gly	230	235	240
Ala Thr Glu Val Glu Pro Arg Arg Val Gly Ser Ser Arg Ala Leu	245	250	255
Val Pro Arg Asn Ala Gln Phe Lys Pro His Thr Asp Glu Asp Leu	260	265	270
Val Tyr Leu Glu Pro Ser Pro Asp Phe Cys Glu Gln Asp Met Arg	275	280	285
Ser Gly Val Leu Gly Thr Arg Gly Arg Thr Cys Asn Lys Thr Ser	290	295	300
Lys Ala Ile Asp Gly Cys Glu Leu Leu Cys Cys Gly Arg Gly Phe	305	310	315
His Thr Ala Gln Val Glu Leu Ala Glu Arg Cys Ser Cys Lys Phe	320	325	330
His Trp Cys Cys Phe Val Lys Cys Arg Gln Cys Gln Arg Leu Val	335	340	345
Glu Leu His Thr Cys Arg	350		

<210> 227

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 227

gctgcagctg caaattccac tgg 23

<210> 228  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 228  
tggtgggaga ctgtttaaat tatcggcc 28

<210> 229  
<211> 41  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 229  
tgcttcgtca agtgccggca gtgccagcgg ctogtggagt t 41

<210> 230  
<211> 1355  
<212> DNA  
<213> Homo sapiens

<400> 230  
cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50  
gggtgcctgc atgccatgg acaccaccag gtacagcaag tggggcggca 100  
gctccgagga ggtccccgga gggccctggg gacgctgggt gcaactggagc 150  
aggagacccc tcttcttggc cctggctgtc ctggtcacca cagtcccttg 200  
ggctgtgatt ctgagtatcc tattgtccaa ggccctccacg gagcgcgcgg 250  
cgctgcttga cggccacgac ctgctgagga caaacgcctc gaagcagaag 300  
gcggcgctgg gtgccctgaa ggaggaggtc ggagactgcc acagctgctg 350  
ctcggggacg caggcgcagc tgcagaccac gcgcgcggag cttggggagg 400  
cgcaggcgaa gctgatggag caggagagcg ccctgcggga actgcgtgag 450  
cgcgtgaccc agggcttggc tgaagccggc aggggcgctg aggacgtccg 500  
cactgagctg ttccgggcgc tggaggccgt gaggctccag aacaactcct 550  
gcgagccgtg cccacgctg tggctgtcct tcgagggctc ctgctacttt 600  
ttctctgtgc caaagacgac gtgggcggcg gcgcaggatc actgcgcaga 650  
tgccagcgcg cacctgggtga tcgttggggg cctggatgag cagggttcc 700  
tcaactggaa cagcgtggc cgtggttact ggctgggcct gagggtgtg 750

cgccatctgg gcaaggttca gggctaccag tgggtggacg gagtctctct 800  
 cagcttcagc cactggaacc agggagagcc caatgacgct tgggggcgcg 850  
 agaactgtgt catgatgctg cacacggggc tgtggaacga cgcaccgtgt 900  
 gacagcgaga aggacggctg gatctgtgag aaaaggcaca actgctgacc 950  
 ccgcccagtg ccctggagcc gcgcccattg cagcatgtcg tatcctgggg 1000  
 gctgctcacc tccctggctc ctggagctga ttgcaaaga gtttttttct 1050  
 tctcatcca ccgctgctga gtctcagaaa cacttggtccc aacatagccc 1100  
 tgtccagccc agtgcctggg ctctgggacc tccatgccga cctcatccta 1150  
 actccactca cgcagaccca acctaacctc cactagctcc aaaatccctg 1200  
 ctctgcgctc ccogtgatat gcctccactt ctctccctaa ccaaggttag 1250  
 gtgactgagg actggagctg tttggttttc tcgcattttc caccaaactg 1300  
 gaagctgttt ttgcagcctg aggaagcatc aataaatatt tgagaaatga 1350  
 aaaaa 1355

<210> 231  
 <211> 293  
 <212> PRT  
 <213> Homo sapiens

<400> 231  
 Met Asp Thr Thr Arg Tyr Ser Lys Trp Gly Gly Ser Ser Glu Glu  
 1 5 10 15  
 Val Pro Gly Gly Pro Trp Gly Arg Trp Val His Trp Ser Arg Arg  
 20 25 30  
 Pro Leu Phe Leu Ala Leu Ala Val Leu Val Thr Thr Val Leu Trp  
 35 40 45  
 Ala Val Ile Leu Ser Ile Leu Leu Ser Lys Ala Ser Thr Glu Arg  
 50 55 60  
 Ala Ala Leu Leu Asp Gly His Asp Leu Leu Arg Thr Asn Ala Ser  
 65 70 75  
 Lys Gln Thr Ala Ala Leu Gly Ala Leu Lys Glu Glu Val Gly Asp  
 80 85 90  
 Cys His Ser Cys Cys Ser Gly Thr Gln Ala Gln Leu Gln Thr Thr  
 95 100 105  
 Arg Ala Glu Leu Gly Glu Ala Gln Ala Lys Leu Met Glu Gln Glu  
 110 115 120  
 Ser Ala Leu Arg Glu Leu Arg Glu Arg Val Thr Gln Gly Leu Ala  
 125 130 135

Glu	Ala	Gly	Arg	Gly	Arg	Glu	Asp	Val	Arg	Thr	Glu	Leu	Phe	Arg	140	145	150
Ala	Leu	Glu	Ala	Val	Arg	Leu	Gln	Asn	Asn	Ser	Cys	Glu	Pro	Cys	155	160	165
Pro	Thr	Ser	Trp	Leu	Ser	Phe	Glu	Gly	Ser	Cys	Tyr	Phe	Phe	Ser	170	175	180
Val	Pro	Lys	Thr	Thr	Trp	Ala	Ala	Ala	Gln	Asp	His	Cys	Ala	Asp	185	190	195
Ala	Ser	Ala	His	Leu	Val	Ile	Val	Gly	Gly	Leu	Asp	Glu	Gln	Gly	200	205	210
Phe	Leu	Thr	Arg	Asn	Thr	Arg	Gly	Arg	Gly	Tyr	Trp	Leu	Gly	Leu	215	220	225
Arg	Ala	Val	Arg	His	Leu	Gly	Lys	Val	Gln	Gly	Tyr	Gln	Trp	Val	230	235	240
Asp	Gly	Val	Ser	Leu	Ser	Phe	Ser	His	Trp	Asn	Gln	Gly	Glu	Pro	245	250	255
Asn	Asp	Ala	Trp	Gly	Arg	Glu	Asn	Cys	Val	Met	Met	Leu	His	Thr	260	265	270
Gly	Leu	Trp	Asn	Asp	Ala	Pro	Cys	Asp	Ser	Glu	Lys	Asp	Gly	Trp	275	280	285
Ile	Cys	Glu	Lys	Arg	His	Asn	Cys								290		

<210> 232  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 232  
 gcgagaactg tgtcatgatg ctgc 24  
  
 <210> 233  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 233  
 gtttctgaga ctcagcagcg gtgg 24  
  
 <210> 234  
 <211> 50  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 234

caccgtgtga cagcgagaag gacggctgga tctgtgagaa aaggcacaac 50

<210> 235

<211> 1847

<212> DNA

<213> Homo sapiens

<400> 235

gccaggggaa gagggatgatc cgacccgggg aaggtcgctg ggcagggcga 50  
gttgggaaag cggcagcccc cgccgcccc gcagcccctt ctctccttt 100  
ctccacgtc ctatctgcct ctcgctggag gccaggccgt gcagcatcga 150  
agacaggagg aactggagcc tcattggccg gcccgggcg ccggcctcgg 200  
gcttaaataag gagctccggg ctctggctgg gacccgaccg ctgccggccg 250  
cgctcccgt gtcctgccg ggtgatggaa aacccagcc cggccgccgc 300  
cctgggcaag gccctctgcg ctctcctcct ggccactctc ggcgccgccg 350  
gccagcctct tgggggagag tccatctgtt ccgccagagc cccggccaaa 400  
tacagcatca cttcacggg caagtggagc cagacggcct tcccaagca 450  
gtaccccctg ttccgcccc ctgcgcagtg gtcttcgctg ctgggggccg 500  
cgcatagctc cgactacagc atgtggagga agaaccagta cgtcagtaac 550  
gggctgcgcg actttgcgga gcgcggcgag gcctgggcgc tgatgaagga 600  
gatcgaggcg gcgggggagg cgctgcagag cgtgcacgag gtgttttcgg 650  
cgcccgccgt cccagcggc accgggcaga cgtcggcgga gctggaggtg 700  
cagcgcaggc actcgttgtt ctcgtttgtg gtgcgcatcg tgcccagccc 750  
cgactggttc gtgggcgtgg acagcctgga cctgtgcgac ggggaccgtt 800  
ggcgggaaca ggcggcgtg gacctgtacc cctacgacgc cgggacggac 850  
agcggcttca ccttctcctc ccccaacttc gccaccatcc cgcaggacac 900  
ggtgaccgag ataacgtcct cctctcccag ccacccggcc aactccttct 950  
actaccgcg gctgaaggcc ctgcctccca tcgccagggt gacactgctg 1000  
cggctgcgac agagccccag ggccttcac cctcccgcc cagtcctgcc 1050  
cagcagggac aatgagattg tagacagcgc ctcaattcca gaaacgccgc 1100

09978192.101501

tggactgcga ggtctccctg tggctcgtcct ggggactgtg cggaggccac 1150  
 tgtgggaggc tcgggaccaa gagcaggact cgctacgtcc ggggccagcc 1200  
 cgccaacaac gggagcccct gccccgagct cgaagaagag gctgagtgcg 1250  
 tccctgataa ctgctgtctaa gaccagagcc ccgcagcccc tggggccccc 1300  
 cggagccatg ggggtgtcggg ggctcctgtg caggctcatg ctgcaggcgg 1350  
 ccgagggcac aggggggtttc gcgctgtctc tgaccgcggt gaggccgcgc 1400  
 cgaccatctc tgcactgaag ggccctctgg tggccggcac gggcattggg 1450  
 aaacagcctc ctcttttccc aaccttgctt cttaggggcc cccgtgtccc 1500  
 gtctgtctctc agcctcctcc tcctgcagga taaagtcac cccaaggctc 1550  
 cagctactct aaattatgtc tccttataag ttattgctgc tccaggagat 1600  
 tgtccttcat cgtccagggg cctggctccc acgtggttgc agatacctca 1650  
 gacctggtgc tctaggctgt gctgagccca ctctcccgag ggcgcattcca 1700  
 agcggggggcc acttgagaag tgaataaatg gggcggtttc ggaagcgtca 1750  
 gtgtttccat gttatggatc tctctgcgtt tgaataaaga ctatctctgt 1800  
 tgctcacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1847

<210> 236

<211> 331

<212> PRT

<213> Homo sapiens

<400> 236

Met	Glu	Asn	Pro	Ser	Pro	Ala	Ala	Ala	Leu	Gly	Lys	Ala	Leu	Cys
1				5					10					15
Ala	Leu	Leu	Leu	Ala	Thr	Leu	Gly	Ala	Ala	Gly	Gln	Pro	Leu	Gly
				20					25					30
Gly	Glu	Ser	Ile	Cys	Ser	Ala	Arg	Ala	Pro	Ala	Lys	Tyr	Ser	Ile
				35					40					45
Thr	Phe	Thr	Gly	Lys	Trp	Ser	Gln	Thr	Ala	Phe	Pro	Lys	Gln	Tyr
				50					55					60
Pro	Leu	Phe	Arg	Pro	Pro	Ala	Gln	Trp	Ser	Ser	Leu	Leu	Gly	Ala
				65					70					75
Ala	His	Ser	Ser	Asp	Tyr	Ser	Met	Trp	Arg	Lys	Asn	Gln	Tyr	Val
				80					85					90
Ser	Asn	Gly	Leu	Arg	Asp	Phe	Ala	Glu	Arg	Gly	Glu	Ala	Trp	Ala
				95					100					105
Leu	Met	Lys	Glu	Ile	Glu	Ala	Ala	Gly	Glu	Ala	Leu	Gln	Ser	Val

	110		115		120
His Glu Val Phe	Ser Ala Pro Ala Val	Pro Ser Gly Thr Gly Gln			
	125	130			135
Thr Ser Ala Glu	Leu Glu Val Gln Arg	Arg His Ser Leu Val Ser			
	140	145			150
Phe Val Val Arg	Ile Val Pro Ser Pro	Asp Trp Phe Val Gly Val			
	155	160			165
Asp Ser Leu Asp	Leu Cys Asp Gly Asp	Arg Trp Arg Glu Gln Ala			
	170	175			180
Ala Leu Asp Leu	Tyr Pro Tyr Asp Ala	Gly Thr Asp Ser Gly Phe			
	185	190			195
Thr Phe Ser Ser	Pro Asn Phe Ala Thr	Ile Pro Gln Asp Thr Val			
	200	205			210
Thr Glu Ile Thr	Ser Ser Ser Pro Ser	His Pro Ala Asn Ser Phe			
	215	220			225
Tyr Tyr Pro Arg	Leu Lys Ala Leu Pro	Pro Ile Ala Arg Val Thr			
	230	235			240
Leu Leu Arg Leu	Arg Gln Ser Pro Arg	Ala Phe Ile Pro Pro Ala			
	245	250			255
Pro Val Leu Pro	Ser Arg Asp Asn Glu	Ile Val Asp Ser Ala Ser			
	260	265			270
Val Pro Glu Thr	Pro Leu Asp Cys Glu	Val Ser Leu Trp Ser Ser			
	275	280			285
Trp Gly Leu Cys	Gly Gly His Cys Gly	Arg Leu Gly Thr Lys Ser			
	290	295			300
Arg Thr Arg Tyr	Val Arg Val Gln Pro	Ala Asn Asn Gly Ser Pro			
	305	310			315
Cys Pro Glu Leu	Glu Glu Glu Ala Glu	Cys Val Pro Asp Asn Cys			
	320	325			330

Val

<210> 237

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 237

cagcactgcc aggggaagag gg 22

<210> 238  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 238  
 caggactcgc tacgtccg 18  
  
 <210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 239  
 cagccccttc tcctcctttc tccc 24  
  
 <210> 240  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 240  
 gcagttatca gggacgcact cagcc 25  
  
 <210> 241  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 241  
 ccagcgagag gcagatag 18  
  
 <210> 242  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 242  
 cggtcaccgt gtccctgcggg atg 23  
  
 <210> 243  
 <211> 42  
 <212> DNA



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 243

cagccccttc tcctcctttc tcccacgtcc tatctgcctc tc 42

<210> 244

<211> 1894

<212> DNA

<213> Homo sapiens

<400> 244

ggcggcgctcc gtgaggggct cctttgggca ggggtagtgt ttggtgtccc 50  
tgtcttgctg gatattgaca aactgaagct ttcctgcacc actggactta 100  
aggaagagtg tactcgtagg cggacagctt tagtggccgg ccggccgctc 150  
tcatcccccg taaggagcag agtcctttgt actgaccaag atgagcaaca 200  
tctacatcca ggagcctccc acgaatggga aggttttatt gaaaactaca 250  
gctggagata ttgacataga gttgtggtcc aaagaagctc ctaaagcttg 300  
cagaaatfff atccaactff gtttggaagc ttattatgac aataccatff 350  
ttcatagagt tgtgcctggt ttcatagtcc aaggcggaga tcctactggc 400  
acaggggagt gtggagagtc tatctatgga gcgccattca aagatgaatt 450  
tcattcacgg ttgcgtffta atcggagagg actggttgcc atggcaaattg 500  
ctgggttctca tgataatggc agccagttff tcttcacact gggtcgagca 550  
gatgaactta acaataagca taccatctff ggaaaggffa caggggatac 600  
agtatataac atgttgcgac tgtcagaagt agacattgat gatgacgaaa 650  
gaccacataa tccacacaaa ataaaaagct gtgaggttff gtttaatcct 700  
tttgatgaca tcattccaag ggaaattaaa aggctgaaaa aagagaaacc 750  
agaggaggaa gtaaagaaat tgaaacccaa aggcacaaaa aatffftagtt 800  
tactfftcatt tggagaggaa gctgagggaag aaggaggagga agtaaatcga 850  
gttagtcaga gcatgaaggg caaaagcaaa agtagtcatg acttgcttaa 900  
ggatgatcca catctcagtt ctgttccagt thtagaaagt gaaaaagggtg 950  
atgcaccaga tfftagttgat gatggagaag atgaaagtgc agagcatgat 1000  
gaatatattg atggtgatga aaagaacctg atgagagaaa gaattgccaa 1050  
aaaattaaaa aaggacacaa gtgcgaatgt taaatcagct ggagaaggag 1100

09978192.101504

aagtggagaa gaaatcagtc agccgcagtg aagagctcag aaaagaagca 1150  
agacaattaa aacgggaact cttagcagca aaacaaaaaa aagtagaaaa 1200  
tgcagcaaaa caagcagaaa aaagaagtga agaggaagaa gcccctccag 1250  
atggtgctgt tgccgaatac agaagagaaa agcaaaagta tgaagctttg 1300  
aggaagcaac agtcaaagaa gggaaacttcc cgggaagatc agacccttgc 1350  
actgctgaac cagttttaaact cttaaactcac tcaagcaatt gctgaaacac 1400  
ctgaaaatga cattcctgaa acagaagtag aagatgatga aggatggatg 1450  
tcacatgtac ttcagtttga ggataaaagc agaaaagtga aagatgcaag 1500  
catgcaagac tcagatacat ttgaaatcta tgatcctcgg aatccagtga 1550  
ataaaagaag gagggaagaa agcaaaaagc tgatgagaga gaaaaaagaa 1600  
agaagataaa atgagaataa tgataaccag aacttgctgg aaatgtgcct 1650  
acaatggcct tgtaacagcc attgttccca acagcatcac ttaggggtgt 1700  
gaaaagaagt atttttgaac ctgttgcttg gttttgaaaa acaattatct 1750  
tgttttgcaa attgtggaat gatgtaagca aatgcttttg gttactggta 1800  
catgtgtttt ttcctagctg accttttata ttgctaaatc tgaaataaaa 1850  
taactttcct tccacaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1894

<210> 245  
<211> 472  
<212> PRT  
<213> Homo sapiens

<400> 245  
Met Ser Asn Ile Tyr Ile Gln Glu Pro Pro Thr Asn Gly Lys Val  
1 5 10 15  
Leu Leu Lys Thr Thr Ala Gly Asp Ile Asp Ile Glu Leu Trp Ser  
20 25 30  
Lys Glu Ala Pro Lys Ala Cys Arg Asn Phe Ile Gln Leu Cys Leu  
35 40 45  
Glu Ala Tyr Tyr Asp Asn Thr Ile Phe His Arg Val Val Pro Gly  
50 55 60  
Phe Ile Val Gln Gly Gly Asp Pro Thr Gly Thr Gly Ser Gly Gly  
65 70 75  
Glu Ser Ile Tyr Gly Ala Pro Phe Lys Asp Glu Phe His Ser Arg  
80 85 90  
Leu Arg Phe Asn Arg Arg Gly Leu Val Ala Met Ala Asn Ala Gly  
95 100 105

Ser	His	Asp	Asn	Gly	Ser	Gln	Phe	Phe	Phe	Thr	Leu	Gly	Arg	Ala	110	115	120
Asp	Glu	Leu	Asn	Asn	Lys	His	Thr	Ile	Phe	Gly	Lys	Val	Thr	Gly	125	130	135
Asp	Thr	Val	Tyr	Asn	Met	Leu	Arg	Leu	Ser	Glu	Val	Asp	Ile	Asp	140	145	150
Asp	Asp	Glu	Arg	Pro	His	Asn	Pro	His	Lys	Ile	Lys	Ser	Cys	Glu	155	160	165
Val	Leu	Phe	Asn	Pro	Phe	Asp	Asp	Ile	Ile	Pro	Arg	Glu	Ile	Lys	170	175	180
Arg	Leu	Lys	Lys	Glu	Lys	Pro	Glu	Glu	Glu	Val	Lys	Lys	Leu	Lys	185	190	195
Pro	Lys	Gly	Thr	Lys	Asn	Phe	Ser	Leu	Leu	Ser	Phe	Gly	Glu	Glu	200	205	210
Ala	Glu	Glu	Glu	Glu	Glu	Glu	Val	Asn	Arg	Val	Ser	Gln	Ser	Met	215	220	225
Lys	Gly	Lys	Ser	Lys	Ser	Ser	His	Asp	Leu	Leu	Lys	Asp	Asp	Pro	230	235	240
His	Leu	Ser	Ser	Val	Pro	Val	Val	Glu	Ser	Glu	Lys	Gly	Asp	Ala	245	250	255
Pro	Asp	Leu	Val	Asp	Asp	Gly	Glu	Asp	Glu	Ser	Ala	Glu	His	Asp	260	265	270
Glu	Tyr	Ile	Asp	Gly	Asp	Glu	Lys	Asn	Leu	Met	Arg	Glu	Arg	Ile	275	280	285
Ala	Lys	Lys	Leu	Lys	Lys	Asp	Thr	Ser	Ala	Asn	Val	Lys	Ser	Ala	290	295	300
Gly	Glu	Gly	Glu	Val	Glu	Lys	Lys	Ser	Val	Ser	Arg	Ser	Glu	Glu	305	310	315
Leu	Arg	Lys	Glu	Ala	Arg	Gln	Leu	Lys	Arg	Glu	Leu	Leu	Ala	Ala	320	325	330
Lys	Gln	Lys	Lys	Val	Glu	Asn	Ala	Ala	Lys	Gln	Ala	Glu	Lys	Arg	335	340	345
Ser	Glu	Glu	Glu	Glu	Ala	Pro	Pro	Asp	Gly	Ala	Val	Ala	Glu	Tyr	350	355	360
Arg	Arg	Glu	Lys	Gln	Lys	Tyr	Glu	Ala	Leu	Arg	Lys	Gln	Gln	Ser	365	370	375
Lys	Lys	Gly	Thr	Ser	Arg	Glu	Asp	Gln	Thr	Leu	Ala	Leu	Leu	Asn	380	385	390
Gln	Phe	Lys	Ser	Lys	Leu	Thr	Gln	Ala	Ile	Ala	Glu	Thr	Pro	Glu			

	395		400		405
Asn Asp Ile Pro Glu Thr Glu Val Glu Asp Asp Glu Gly Trp Met					
	410		415		420
Ser His Val Leu Gln Phe Glu Asp Lys Ser Arg Lys Val Lys Asp					
	425		430		435
Ala Ser Met Gln Asp Ser Asp Thr Phe Glu Ile Tyr Asp Pro Arg					
	440		445		450
Asn Pro Val Asn Lys Arg Arg Arg Glu Glu Ser Lys Lys Leu Met					
	455		460		465
Arg Glu Lys Lys Glu Arg Arg					
	470				

<210> 246

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 246

tgcggagatc ctactggcac aggg 24

<210> 247

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 247

cgagtttagtc agagcatg 18

<210> 248

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 248

cagatggtgc tgttgccg 18

<210> 249

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 249  
caactggaac aggaactgag atgtggatc 29

<210> 250  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 250  
ctggttcagc agtgcaaggg tctg 24

<210> 251  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 251  
cctctccgat taaaacgc 18

<210> 252  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 252  
gagaggactg gttgccatgg caaatgctgg ttctcatgat aatgg 45

<210> 253  
<211> 2456  
<212> DNA  
<213> Homo sapiens

<400> 253  
cgccgcccgtt ggggctggaa gttcccgcca ggtccgtgcc gggcgagaga 50  
gatgctgcc ggcccgctc ggctttgagg cgagagaagt gtcccagacc 100  
catttcgcct tgctgacggc gtcgagccct ggccagacat gtccacaggg 150  
ttctccttcg ggtccgggac tctgggctcc accaccgtgg ccgccggcgg 200  
gaccagcaca ggcggcggtt tctccttcgg aacgggaacg tctagcaacc 250  
cttctgtggg gctcaatttt ggaaatcttg gaagtacttc aactccagca 300  
actacatctg ctcccttcaag tggttttgga accgggctct ttggatctaa 350  
acctgccact ggggttcactc taggaggaac aaatacaggt gccttgacaca 400

ccaagaggcc tcaagtggc accaaatatg gaaccctgca aggaaaacag 450  
atgcatgtgg ggaagacacc catccaagtc tttttaggag tccccctctc 500  
cagacctcct ctaggtatcc tcaggtttgc acctccagaa cccccggagc 550  
cctggaaagg aatcagagat gctaccacct acccgctgg atggagtctc 600  
gctctgtcgc caggctggag tgcagtggca cgatctcggc tcaactgcaac 650  
ctccgcctcc cgggttcaag cgagtctcct gcctcagcct ctgagtgtct 700  
ggggctacag gtgcctgcag gagtctggg gccagctggc ctcgatgtac 750  
gtcagcacgc ggaacggta caagtggctg cgcttcagcg aggactgtct 800  
gtacctgaac gtgtacgcgc cggcgcgcgc gcccggggat cccagctgc 850  
cagtgatggc ctggttcccg ggaggcgctc tcactgtggg cgctgcttct 900  
tcgtacgagg gctctgactt ggccgcccgc gagaaagtgg tgctggtgtt 950  
tctgcagcac aggtctggca tcttcggctt cctgagcacg gacgacagcc 1000  
acgcgcgcgc gaactggggg ctgctggacc agatggcggc tctgcgctgg 1050  
gtgcaggaga acatcgagc cttcggggga gaccaggaa atgtgacct 1100  
gttcggccag tcggcggggg ccatgagcat ctcaggactg atgatgtcac 1150  
ccctagcctc ggggtctctc catcggggca tttcccagag tggcaccgcg 1200  
ttattcagac ttttcatcac tagtaacca ctgaaagtgg ccaagaaggt 1250  
tgcccacctg gctggatgca accacaacag cacacagatc ctggtaaact 1300  
gcctgagggc actatcaggg accaaggtga tgcgtgtgtc caacaagatg 1350  
agattcctcc aactgaactt ccagagagac ccggaagaga ttatctggtc 1400  
catgagccct gtggtggatg gtgtggtgat cccagatgac cctttggtgc 1450  
tcctgaccca ggggaaggtt tcactctgtc cctaccttct aggtgtcaac 1500  
aacctggaat tcaattggct cttgccttat aatatacca aggagcaggt 1550  
accacttgtg gtggaggagt acctggacaa tgtcaatgag catgactgga 1600  
agatgctacg aaaccgtatg atggacatag ttcaagatgc cactttcgtg 1650  
tatgccacac tgcagactgc tcactaccac cgagaaaccc caatgatggg 1700  
aatctgccct gctggccacg ctacaacaag gatgaaaagt acctgcagct 1750  
ggattttacc acaagagtgg gcatgaagct caaggagaag aagatggctt 1800  
tttgatgag tctgtaccag tctcaaagac ctgagaagca gaggcaattc 1850

09978192.101501

taagggtggc tatgcaggaa ggagccaaag aggggtttgc cccaccatc 1900  
caggccctgg ggagactagc catggacata cctggggaca agagttctac 1950  
ccaccccagt ttagaactgc aggagctccc tgctgcctcc aggccaaagc 2000  
tagagctttt gcctgttgtg tgggacctgc actgcccttt ccagcctgac 2050  
atcccatgat gcccctctac ttcactgttg acatccagtt aggccaggcc 2100  
ctgtcaacac cacactgtgc tcagctctcc agcctcagga caacctcttt 2150  
ttttcccttc ttcaaatoct cccacccttc aatgtctcct tgtgactcct 2200  
tcttatggga ggtcgacca gactgccact gccctgtca ctgcaccag 2250  
cttggcattt accatccatc ctgctcaacc ttgttcctgt ctgttcacat 2300  
tggcctggag gcctagggca ggttgtgaca tggagcaaac ttttggtagt 2350  
ttgggatctt ctctcccacc cacacttata tccccagggg ccactccaaa 2400  
gtctatacac aggggtggtc tcttcaataa agaagtgttg attagaaaaa 2450  
aaaaaa 2456

<210> 254  
<211> 545  
<212> PRT  
<213> Homo sapiens

<400> 254  
Met Ser Thr Gly Phe Ser Phe Gly Ser Gly Thr Leu Gly Ser Thr  
1 5 10 15  
Thr Val Ala Ala Gly Gly Thr Ser Thr Gly Gly Val Phe Ser Phe  
20 25 30  
Gly Thr Gly Thr Ser Ser Asn Pro Ser Val Gly Leu Asn Phe Gly  
35 40 45  
Asn Leu Gly Ser Thr Ser Thr Pro Ala Thr Thr Ser Ala Pro Ser  
50 55 60  
Ser Gly Phe Gly Thr Gly Leu Phe Gly Ser Lys Pro Ala Thr Gly  
65 70 75  
Phe Thr Leu Gly Gly Thr Asn Thr Gly Ala Leu His Thr Lys Arg  
80 85 90  
Pro Gln Val Val Thr Lys Tyr Gly Thr Leu Gln Gly Lys Gln Met  
95 100 105  
His Val Gly Lys Thr Pro Ile Gln Val Phe Leu Gly Val Pro Phe  
110 115 120  
Ser Arg Pro Pro Leu Gly Ile Leu Arg Phe Ala Pro Pro Glu Pro  
125 130 135

Pro	Glu	Pro	Trp	Lys	Gly	Ile	Arg	Asp	Ala	Thr	Thr	Tyr	Pro	Pro	140	145	150
Gly	Trp	Ser	Leu	Ala	Leu	Ser	Pro	Gly	Trp	Ser	Ala	Val	Ala	Arg	155	160	165
Ser	Arg	Leu	Thr	Ala	Thr	Ser	Ala	Ser	Arg	Val	Gln	Ala	Ser	Leu	170	175	180
Leu	Pro	Gln	Pro	Leu	Ser	Val	Trp	Gly	Tyr	Arg	Cys	Leu	Gln	Glu	185	190	195
Ser	Trp	Gly	Gln	Leu	Ala	Ser	Met	Tyr	Val	Ser	Thr	Arg	Glu	Arg	200	205	210
Tyr	Lys	Trp	Leu	Arg	Phe	Ser	Glu	Asp	Cys	Leu	Tyr	Leu	Asn	Val	215	220	225
Tyr	Ala	Pro	Ala	Arg	Ala	Pro	Gly	Asp	Pro	Gln	Leu	Pro	Val	Met	230	235	240
Val	Trp	Phe	Pro	Gly	Gly	Ala	Phe	Ile	Val	Gly	Ala	Ala	Ser	Ser	245	250	255
Tyr	Glu	Gly	Ser	Asp	Leu	Ala	Ala	Arg	Glu	Lys	Val	Val	Leu	Val	260	265	270
Phe	Leu	Gln	His	Arg	Leu	Gly	Ile	Phe	Gly	Phe	Leu	Ser	Thr	Asp	275	280	285
Asp	Ser	His	Ala	Arg	Gly	Asn	Trp	Gly	Leu	Leu	Asp	Gln	Met	Ala	290	295	300
Ala	Leu	Arg	Trp	Val	Gln	Glu	Asn	Ile	Ala	Ala	Phe	Gly	Gly	Asp	305	310	315
Pro	Gly	Asn	Val	Thr	Leu	Phe	Gly	Gln	Ser	Ala	Gly	Ala	Met	Ser	320	325	330
Ile	Ser	Gly	Leu	Met	Met	Ser	Pro	Leu	Ala	Ser	Gly	Leu	Phe	His	335	340	345
Arg	Ala	Ile	Ser	Gln	Ser	Gly	Thr	Ala	Leu	Phe	Arg	Leu	Phe	Ile	350	355	360
Thr	Ser	Asn	Pro	Leu	Lys	Val	Ala	Lys	Lys	Val	Ala	His	Leu	Ala	365	370	375
Gly	Cys	Asn	His	Asn	Ser	Thr	Gln	Ile	Leu	Val	Asn	Cys	Leu	Arg	380	385	390
Ala	Leu	Ser	Gly	Thr	Lys	Val	Met	Arg	Val	Ser	Asn	Lys	Met	Arg	395	400	405
Phe	Leu	Gln	Leu	Asn	Phe	Gln	Arg	Asp	Pro	Glu	Glu	Ile	Ile	Trp	410	415	420
Ser	Met	Ser	Pro	Val	Val	Asp	Gly	Val	Val	Ile	Pro	Asp	Asp	Pro			



425

430

435

Leu Val Leu Leu Thr Gln Gly Lys Val Ser Ser Val Pro Tyr Leu  
440 445 450

Leu Gly Val Asn Asn Leu Glu Phe Asn Trp Leu Leu Pro Tyr Asn  
455 460 465

Ile Thr Lys Glu Gln Val Pro Leu Val Val Glu Glu Tyr Leu Asp  
470 475 480

Asn Val Asn Glu His Asp Trp Lys Met Leu Arg Asn Arg Met Met  
485 490 495

Asp Ile Val Gln Asp Ala Thr Phe Val Tyr Ala Thr Leu Gln Thr  
500 505 510

Ala His Tyr His Arg Glu Thr Pro Met Met Gly Ile Cys Pro Ala  
515 520 525

Gly His Ala Thr Thr Arg Met Lys Ser Thr Cys Ser Trp Ile Leu  
530 535 540

Pro Gln Glu Trp Ala  
545

<210> 255

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 255

aggtgcctgc aggtgcctg ggg 23

<210> 256

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 256

ccacctcagg aagccgaaga tgcc 24

<210> 257

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 257

gaacggtaca agtggctgag cttcagcgag gactgtctgt acctg 45

<210> 258  
 <211> 2764  
 <212> DNA  
 <213> Homo sapiens

<400> 258  
 gagaacaggc ctgtctcagg caggccctgc gcctcctatg cggagatgct 50  
 actgccactg ctgtctgcct cgctgctggg cgggtcccag gctatggatg 100  
 ggagattctg gatacagtg caggagtcag tgatggtgcc ggagggcctg 150  
 tgcattcttg tgccctgctc ttctcctac ccccgacaag actggacagg 200  
 gtctacccca gcttatggct actggttcaa agcagtgact gagacaacca 250  
 aggggtgctcc tgtggccaca aaccaccaga gtcgagaggt ggaaatgagc 300  
 acccgggggc gattccagct cactggggat cccgccagg ggaactgctc 350  
 cttggtgatc agagacgcgc agatgcagga tgagtcacag tacttctttc 400  
 ggggtggagag aggaagctat gtgacatata atttcatgaa cgatgggttc 450  
 tttctaaaag taacagtgct cagcttcacg cccagacccc aggaccacaa 500  
 caccgacctc acctgccatg tggacttctc cagaaagggt gtgagcgcac 550  
 agaggaccgt ccgactccgt gtggcctatg ccccagaga cttgtttatc 600  
 agcatttcac gtgacaacac gccagccctg gagccccagc cccagggaaa 650  
 tgtcccatc ctggaagccc aaaaaggcca gttcctgcgg ctctctctgtg 700  
 ctgctgacag ccagccccct gccacactga gctgggtcct gcagaacaga 750  
 gtcctctcct cgtcccatcc ctggggccct agacccttg ggctggagct 800  
 gcccggggtg aaggctgggg attcagggcg ctacacctgc cgagcggaga 850  
 acaggcttgg ctcccagcag cgagccctgg acctctctgt gcagtatcct 900  
 ccagagaacc tgagagtgat ggtttcccaa gcaaacagga cagtccctgga 950  
 aaaccttggg aacggcacgt ctctccagct actggagggc caaagcctgt 1000  
 gcctggtctg tgtcacacac agcagcccc cagccaggct gagctggacc 1050  
 cagaggggac aggttctgag cccctcccag cctcagacc ccggggtcct 1100  
 ggagctgcct cgggttcaag tggagcacga aggagagttc acctgccacg 1150  
 ctcggcaccc actgggctcc cagcacgtct ctctcagcct ctccgtgcac 1200  
 tataagaagg gactcatctc aacggcattc tccaacggag cgtttctggg 1250  
 aatcggcac cgggtcttc tttctctctg cctggccctg atcatcatga 1300

09978192.101501

agattctacc gaagagacgg actcagacag aaaccccgag gccaggttc 1350  
 tcccggcaca gcacgatcct ggattacatc aatgtggtcc cgacggctgg 1400  
 ccccttggtc cagaagcgga atcagaaagc cacaccaaac agtcctcgga 1450  
 cccctcctcc accaggtgct ccctccccag aatcaaagaa gaaccagaaa 1500  
 aagcagtatc agttgcccag tttcccagaa cccaaatcat ccaactcaagc 1550  
 cccagaatcc caggagagcc aagaggagct ccattatgcc acgctcaact 1600  
 tcccaggcgt cagacccagg cctgaggccc ggatgcccac gggcaccag 1650  
 gcggattatg cagaagtcaa gttccaatga ggtctcttta ggcttttagga 1700  
 ctgggacttc ggctagggag gaaggtagag taagagggtg aagataacag 1750  
 agtgcaaagt ttccttctct ccctctctct ctctcttct ctctctctct 1800  
 ctcttctct ctcttttaaa aaaacatctg gccagggcac agtggctcac 1850  
 gcctgtaatc ccagcacttt gggagggtga ggtgggcaga tcgcctgagg 1900  
 tcgggagttc gagaccagcc tggccaactt ggtgaaacc cgtctctact 1950  
 aaaaatacaa aaattagctg ggcatggtgg caggcgctg taatcctacc 2000  
 tacttgggaa gctgaggcag gagaatcact tgaacctggg agacggagggt 2050  
 tgcagtgagc caagatcaca ccattgcacg ccagcctggg caacaaagcg 2100  
 agactccatc tcaaaaaaaaa aatcctccaa atgggttggg tgtctgtaat 2150  
 cccagcactt tgggaggcta aggtgggtgg attgcttgag cccaggagtt 2200  
 cgagaccagc ctgggcaaca tggtgaaacc ccctctctac aaaaaataca 2250  
 aaacatagct gggcttggtg gtgtgtgcct gtagtcccag ctgtcagaca 2300  
 tttaaaccag agcaactcca tctggaatag gagctgaata aaatgaggct 2350  
 gagacctact gggctgcatt ctgagacagt ggaggcattc taagtcacag 2400  
 gatgagacag gaggtccgta caagatacag gtcataaaga ctttgctgat 2450  
 aaaacagatt gcagtaaaga agccaaccaa atcccaccaa aaccaagttg 2500  
 gccacgagag tgacctctgg tcgtcctcac tgctacactc ctgacagcac 2550  
 catgacagtt tacaaatgcc atggcaacat caggaagtta cccgatatgt 2600  
 cccaaaaggg ggaggaatga ataatccacc ccttgtttag caaataagca 2650  
 agaaataacc ataaaagtgg gcaaccagca gctctaggcg ctgctcttgt 2700  
 ctatggagta gccattcttt tgttccttta ctttcttaat aaacttgctt 2750

tcaccttaaa aaaa 2764

<210> 259

<211> 544

<212> PRT

<213> Homo sapiens

<400> 259

Met Leu Leu Pro Leu Leu Leu Ser Ser Leu Leu Gly Gly Ser Gln  
1 5 10 15

Ala Met Asp Gly Arg Phe Trp Ile Arg Val Gln Glu Ser Val Met  
20 25 30

Val Pro Glu Gly Leu Cys Ile Ser Val Pro Cys Ser Phe Ser Tyr  
35 40 45

Pro Arg Gln Asp Trp Thr Gly Ser Thr Pro Ala Tyr Gly Tyr Trp  
50 55 60

Phe Lys Ala Val Thr Glu Thr Thr Lys Gly Ala Pro Val Ala Thr  
65 70 75

Asn His Gln Ser Arg Glu Val Glu Met Ser Thr Arg Gly Arg Phe  
80 85 90

Gln Leu Thr Gly Asp Pro Ala Lys Gly Asn Cys Ser Leu Val Ile  
95 100 105

Arg Asp Ala Gln Met Gln Asp Glu Ser Gln Tyr Phe Phe Arg Val  
110 115 120

Glu Arg Gly Ser Tyr Val Thr Tyr Asn Phe Met Asn Asp Gly Phe  
125 130 135

Phe Leu Lys Val Thr Val Leu Ser Phe Thr Pro Arg Pro Gln Asp  
140 145 150

His Asn Thr Asp Leu Thr Cys His Val Asp Phe Ser Arg Lys Gly  
155 160 165

Val Ser Ala Gln Arg Thr Val Arg Leu Arg Val Ala Tyr Ala Pro  
170 175 180

Arg Asp Leu Val Ile Ser Ile Ser Arg Asp Asn Thr Pro Ala Leu  
185 190 195

Glu Pro Gln Pro Gln Gly Asn Val Pro Tyr Leu Glu Ala Gln Lys  
200 205 210

Gly Gln Phe Leu Arg Leu Leu Cys Ala Ala Asp Ser Gln Pro Pro  
215 220 225

Ala Thr Leu Ser Trp Val Leu Gln Asn Arg Val Leu Ser Ser Ser  
230 235 240

His Pro Trp Gly Pro Arg Pro Leu Gly Leu Glu Leu Pro Gly Val  
245 250 255

09978192-101501

Lys Ala Gly Asp	Ser Gly Arg Tyr Thr	Cys Arg Ala Glu Asn Arg	260	265	270
Leu Gly Ser Gln	Gln Arg Ala Leu Asp	Leu Ser Val Gln Tyr Pro	275	280	285
Pro Glu Asn Leu	Arg Val Met Val Ser	Gln Ala Asn Arg Thr Val	290	295	300
Leu Glu Asn Leu	Gly Asn Gly Thr Ser	Leu Pro Val Leu Glu Gly	305	310	315
Gln Ser Leu Cys	Leu Val Cys Val Thr	His Ser Ser Pro Pro Ala	320	325	330
Arg Leu Ser Trp	Thr Gln Arg Gly Gln	Val Leu Ser Pro Ser Gln	335	340	345
Pro Ser Asp Pro	Gly Val Leu Glu Leu	Pro Arg Val Gln Val Glu	350	355	360
His Glu Gly Glu	Phe Thr Cys His Ala	Arg His Pro Leu Gly Ser	365	370	375
Gln His Val Ser	Leu Ser Leu Ser Val	His Tyr Lys Lys Gly Leu	380	385	390
Ile Ser Thr Ala	Phe Ser Asn Gly Ala	Phe Leu Gly Ile Gly Ile	395	400	405
Thr Ala Leu Leu	Phe Leu Cys Leu Ala	Leu Ile Ile Met Lys Ile	410	415	420
Leu Pro Lys Arg	Arg Thr Gln Thr Glu	Thr Pro Arg Pro Arg Phe	425	430	435
Ser Arg His Ser	Thr Ile Leu Asp Tyr	Ile Asn Val Val Pro Thr	440	445	450
Ala Gly Pro Leu	Ala Gln Lys Arg Asn	Gln Lys Ala Thr Pro Asn	455	460	465
Ser Pro Arg Thr	Pro Pro Pro Pro Gly	Ala Pro Ser Pro Glu Ser	470	475	480
Lys Lys Asn Gln	Lys Lys Gln Tyr Gln	Leu Pro Ser Phe Pro Glu	485	490	495
Pro Lys Ser Ser	Thr Gln Ala Pro Glu	Ser Gln Glu Ser Gln Glu	500	505	510
Glu Leu His Tyr	Ala Thr Leu Asn Phe	Pro Gly Val Arg Pro Arg	515	520	525
Pro Glu Ala Arg	Met Pro Lys Gly Thr	Gln Ala Asp Tyr Ala Glu	530	535	540
Val Lys Phe Gln					

<210> 260  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 260  
 caaagcctgc gcctggtctg tg 22

<210> 261  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 261  
 ttctggagcc cagaggggtgc tgag 24

<210> 262  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 262  
 ggagctgcca cccattcaaa tggagcacga aggagagttc acctg 45

<210> 263  
 <211> 2857  
 <212> DNA  
 <213> Homo sapiens

<400> 263  
 tgaagagtaa tagttggaat caaaagagtc aacgcaatga actggtatatt 50  
 actgctgcgt tttatgttgg gaattcctct cctatggcct tgtcttggag 100  
 caacagaaaa ctctcaaaca aagaaagtca agcagccagt gcgatctcat 150  
 ttgagagtga agcgtggctg ggtgtggaac caattttttg taccagagga 200  
 aatgaatacg actagtcatc acatcggcca gctaagatct gatttagaca 250  
 atggaaacaa ttctttccag tacaagcttt tgggagctgg agctggaagt 300  
 acttttatca ttgatgaaag aacaggtgac atatatgcca tacagaagct 350  
 tgatagagag gagcgatccc tctacatctt aagagcccag gtaatagaca 400  
 tcgctactgg aagggctgtg gaacctgagt ctgagtttgt catcaaagtt 450

tcggatatca atgacaatga accaaaattc ctagatgaac cttatgaggc 500  
cattgtacca gagatgtctc cagaaggaac attagttatc caggtgacag 550  
caagtgatgc tgacgatccc tcaagtggta ataatgctcg tctcctctac 600  
agcttacttc aaggccagcc atatttttct gttgaaccaa caacaggagt 650  
cataagaata tcttctaaaa tggatagaga actgcaagat gagtattggg 700  
taatcattca agccaaggac atgattggtc agccaggagc gttgtctgga 750  
acaacaagtg tattaattaa actttcagat gttaatgaca ataagcctat 800  
atttaaagaa agtttatacc gcttgactgt ctctgaatct gcacccactg 850  
ggacttctat aggaacaatc atggcatatg ataatgacat aggagagaat 900  
gcagaaatgg attacagcat tgaagaggat gattcgcaaa catttgacat 950  
tattactaat catgaaactc aagaaggaat agttatatta aaaaagaaag 1000  
tggattttga gcaccagaac cactacggta ttagagcaaa agttaaaaac 1050  
catcatgttc ctgagcagct catgaagtac cacactgagg cttccaccac 1100  
tttcattaag atccaggtgg aagatgttga tgagcctcct cttttcctcc 1150  
ttccatatta tgtatttgaa gtttttgaag aaacccaca gggatcattt 1200  
gtaggcgtgg tgtctgccac agaccagac aataggaaat ctctatcag 1250  
gtattctatt actaggagca aagtgttcaa tatcaatgat aatggtacaa 1300  
tcactacaag taactcactg gatcgtgaaa tcagtgttg gtacaacct 1350  
agtattacag ccacagaaaa atacaatata gaacagatct cttcgatccc 1400  
actgtatgtg caagttctta acatcaatga tcatgtcct gagttctctc 1450  
aatactatga gacttatgtt tgtgaaaatg caggctctgg tcaggtaatt 1500  
cagactatca gtgcagtgg tagagatgaa tccatagaag agcaccattt 1550  
ttactttaat ctatctgtag aagacactaa caattcaagt tttaaatca 1600  
tagataatca agataacaca gctgtcattt tgactaatag aactggtttt 1650  
aaccttcaag aagaacctgt cttctacatc tccatcttaa ttgccgacaa 1700  
tggaatcccg tcacttaca gtacaaacac ccttaccatc catgtctgtg 1750  
actgtgggtga cagtgggagc acacagacct gccagtacca ggagcttgtg 1800  
ctttccatgg gattcaagac agaagttatc attgctattc tcatttgcac 1850  
tatgatcata tttgggttta tttttttgac tttgggttta aaacaacgga 1900

gaaaacagat tctatttctt gagaaaagtg aagatttcag agagaatata 1950  
 ttccaatatg atgatgaagg ggggtggagaa gaagatacag aggcctttga 2000  
 tatagcagag ctgaggagta gtaccataat gcgggaacgc aagactcgga 2050  
 aaaccacaag cgctgagatc aggagcctat acaggcagtc tttgcaagtt 2100  
 ggccccgaca gtgccatatt caggaaattc attctggaaa agctcgaaga 2150  
 agctaatact gatccgtgtg cccctccttt tgattccctc cagacctacg 2200  
 cttttgaggg aacaggggtca ttagctggat cctgagctc cttagaatca 2250  
 gcagtctctg atcaggatga aagctatgat taccttaatg agttgggacc 2300  
 tcgcttttaa agattagcat gcatgtttgg ttctgcagtg cagtcaaata 2350  
 attagggctt ttaccatca aaatttttaa aagtgctaatt gtgtattcga 2400  
 acccaatggt agtcttaaag agttttgtgc cctggctcta tggcggggaa 2450  
 agccctagtc tatggagttt tctgatttcc ctggagtaaa tactccatgg 2500  
 ttatttttaag ctacctacat gctgtcattg aacagagatg tggggagaaa 2550  
 tgtaaacaat cagctcacag gcatcaatac aaccagattt gaagtaaaat 2600  
 aatgtaggaa gatattaaaa gtagatgaga ggacacaaga ttagtgcgat 2650  
 ccttatgcga ttatatcatt atttacttag gaaagagtaa aaataccaaa 2700  
 cgagaaaatt taaaggagca aaaatttgca agtcaaataa aaatgtacaa 2750  
 atcgagataa catttacatt tctatcatat tgacatgaaa attgaaaatg 2800  
 tatagtcaga gaaattttca tgaattattc catgaagtat tgtttccttt 2850  
 atttaaa 2857

<210> 264  
 <211> 772  
 <212> PRT  
 <213> Homo sapiens

<400> 264  
 Met Asn Cys Tyr Leu Leu Leu Arg Phe Met Leu Gly Ile Pro Leu  
 1 5 10 15  
 Leu Trp Pro Cys Leu Gly Ala Thr Glu Asn Ser Gln Thr Lys Lys  
 20 25 30  
 Val Lys Gln Pro Val Arg Ser His Leu Arg Val Lys Arg Gly Trp  
 35 40 45  
 Val Trp Asn Gln Phe Phe Val Pro Glu Glu Met Asn Thr Thr Ser  
 50 55 60



His	His	Ile	Gly	Gln	Leu	Arg	Ser	Asp	Leu	Asp	Asn	Gly	Asn	Asn		65	70	75
Ser	Phe	Gln	Tyr	Lys	Leu	Leu	Gly	Ala	Gly	Ala	Gly	Ser	Thr	Phe		80	85	90
Ile	Ile	Asp	Glu	Arg	Thr	Gly	Asp	Ile	Tyr	Ala	Ile	Gln	Lys	Leu		95	100	105
Asp	Arg	Glu	Glu	Arg	Ser	Leu	Tyr	Ile	Leu	Arg	Ala	Gln	Val	Ile		110	115	120
Asp	Ile	Ala	Thr	Gly	Arg	Ala	Val	Glu	Pro	Glu	Ser	Glu	Phe	Val		125	130	135
Ile	Lys	Val	Ser	Asp	Ile	Asn	Asp	Asn	Glu	Pro	Lys	Phe	Leu	Asp		140	145	150
Glu	Pro	Tyr	Glu	Ala	Ile	Val	Pro	Glu	Met	Ser	Pro	Glu	Gly	Thr		155	160	165
Leu	Val	Ile	Gln	Val	Thr	Ala	Ser	Asp	Ala	Asp	Asp	Pro	Ser	Ser		170	175	180
Gly	Asn	Asn	Ala	Arg	Leu	Leu	Tyr	Ser	Leu	Leu	Gln	Gly	Gln	Pro		185	190	195
Tyr	Phe	Ser	Val	Glu	Pro	Thr	Thr	Gly	Val	Ile	Arg	Ile	Ser	Ser		200	205	210
Lys	Met	Asp	Arg	Glu	Leu	Gln	Asp	Glu	Tyr	Trp	Val	Ile	Ile	Gln		215	220	225
Ala	Lys	Asp	Met	Ile	Gly	Gln	Pro	Gly	Ala	Leu	Ser	Gly	Thr	Thr		230	235	240
Ser	Val	Leu	Ile	Lys	Leu	Ser	Asp	Val	Asn	Asp	Asn	Lys	Pro	Ile		245	250	255
Phe	Lys	Glu	Ser	Leu	Tyr	Arg	Leu	Thr	Val	Ser	Glu	Ser	Ala	Pro		260	265	270
Thr	Gly	Thr	Ser	Ile	Gly	Thr	Ile	Met	Ala	Tyr	Asp	Asn	Asp	Ile		275	280	285
Gly	Glu	Asn	Ala	Glu	Met	Asp	Tyr	Ser	Ile	Glu	Glu	Asp	Asp	Ser		290	295	300
Gln	Thr	Phe	Asp	Ile	Ile	Thr	Asn	His	Glu	Thr	Gln	Glu	Gly	Ile		305	310	315
Val	Ile	Leu	Lys	Lys	Lys	Val	Asp	Phe	Glu	His	Gln	Asn	His	Tyr		320	325	330
Gly	Ile	Arg	Ala	Lys	Val	Lys	Asn	His	His	Val	Pro	Glu	Gln	Leu		335	340	345
Met	Lys	Tyr	His	Thr	Glu	Ala	Ser	Thr	Thr	Phe	Ile	Lys	Ile	Gln				

	350		355		360
Val Glu Asp Val	Asp Glu Pro Pro Leu	Phe Leu Leu Pro Tyr	Tyr		
	365		370		375
Val Phe Glu Val	Phe Glu Glu Thr Pro	Gln Gly Ser Phe Val	Gly		
	380		385		390
Val Val Ser Ala	Thr Asp Pro Asp Asn	Arg Lys Ser Pro Ile	Arg		
	395		400		405
Tyr Ser Ile Thr	Arg Ser Lys Val Phe	Asn Ile Asn Asp Asn	Gly		
	410		415		420
Thr Ile Thr Thr	Ser Asn Ser Leu Asp	Arg Glu Ile Ser Ala	Trp		
	425		430		435
Tyr Asn Leu Ser	Ile Thr Ala Thr Glu	Lys Tyr Asn Ile Glu	Gln		
	440		445		450
Ile Ser Ser Ile	Pro Leu Tyr Val Gln	Val Leu Asn Ile Asn	Asp		
	455		460		465
His Ala Pro Glu	Phe Ser Gln Tyr Tyr	Glu Thr Tyr Val Cys	Glu		
	470		475		480
Asn Ala Gly Ser	Gly Gln Val Ile Gln	Thr Ile Ser Ala Val	Asp		
	485		490		495
Arg Asp Glu Ser	Ile Glu Glu His His	Phe Tyr Phe Asn Leu	Ser		
	500		505		510
Val Glu Asp Thr	Asn Asn Ser Ser Phe	Thr Ile Ile Asp Asn	Gln		
	515		520		525
Asp Asn Thr Ala	Val Ile Leu Thr Asn	Arg Thr Gly Phe Asn	Leu		
	530		535		540
Gln Glu Glu Pro	Val Phe Tyr Ile Ser	Ile Leu Ile Ala Asp	Asn		
	545		550		555
Gly Ile Pro Ser	Leu Thr Ser Thr Asn	Thr Leu Thr Ile His	Val		
	560		565		570
Cys Asp Cys Gly	Asp Ser Gly Ser Thr	Gln Thr Cys Gln Tyr	Gln		
	575		580		585
Glu Leu Val Leu	Ser Met Gly Phe Lys	Thr Glu Val Ile Ile	Ala		
	590		595		600
Ile Leu Ile Cys	Ile Met Ile Ile Phe	Gly Phe Ile Phe Leu	Thr		
	605		610		615
Leu Gly Leu Lys	Gln Arg Arg Lys Gln	Ile Leu Phe Pro Glu	Lys		
	620		625		630
Ser Glu Asp Phe	Arg Glu Asn Ile Phe	Gln Tyr Asp Asp Glu	Gly		
	635		640		645

Gly Gly Glu Glu Asp Thr Glu Ala Phe Asp Ile Ala Glu Leu Arg	650	655	660
Ser Ser Thr Ile Met Arg Glu Arg Lys Thr Arg Lys Thr Thr Ser	665	670	675
Ala Glu Ile Arg Ser Leu Tyr Arg Gln Ser Leu Gln Val Gly Pro	680	685	690
Asp Ser Ala Ile Phe Arg Lys Phe Ile Leu Glu Lys Leu Glu Glu	695	700	705
Ala Asn Thr Asp Pro Cys Ala Pro Pro Phe Asp Ser Leu Gln Thr	710	715	720
Tyr Ala Phe Glu Gly Thr Gly Ser Leu Ala Gly Ser Leu Ser Ser	725	730	735
Leu Glu Ser Ala Val Ser Asp Gln Asp Glu Ser Tyr Asp Tyr Leu	740	745	750
Asn Glu Leu Gly Pro Arg Phe Lys Arg Leu Ala Cys Met Phe Gly	755	760	765
Ser Ala Val Gln Ser Asn Asn	770		

<210> 265  
 <211> 349  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 24, 60, 141, 226, 228, 249, 252  
 <223> unknown base

<400> 265  
 atttcaaggc cagccatatt tttntgttga accaacaaca ggagtcataa 50  
 gaatatttttn taaaatggat agagaactgc aagatgagta ttgggtaatc 100  
 attcaagcca aggacatgat tggtcagcca ggagcgttgt ntggaacaac 150  
 aagtgtatta attaaacttt cagatgttaa tgacaataag cctatattta 200  
 aagaaagttt ataccgcttg actgtntntg aatctgcacc cactgggant 250  
 tntataggaa caatcatggc atatgataat gacataggag agaatgcaga 300  
 aatggattac agcattgaag aggatgattc gcaaacattt gacattatt 349

<210> 266  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
 <220>

<223> Synthetic oligonucleotide probe

<400> 266

cttgactgtc tctgaatctg caccc 25

<210> 267

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 267

aagtgggtgga agcctccagt gtgg 24

<210> 268

<211> 52

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 268

ccactacggt attagagcaa aagttaaaaa ccatcatggt tcctggagca 50

gc 52

<210> 269

<211> 2747

<212> DNA

<213> Homo sapiens

<400> 269

gcaacctcag cttctagat ccagaactcca gcgcgcgcgc gggcgcgagc 50

cccaaccccg acccagagct tctccagcgg cggcgcagcgc agcagggctc 100

cccgccttaa cttcctccgc ggggcccagc caccttcggg agtccgggtt 150

gcccacctgc aaactctccg ctttctgcac ctgccacccc tgagccagcg 200

cgggcccccg agcgagtcag ggccaacgcg gggctgcagc tgttgggctt 250

cattctcgcc ttctgggat ggatcggcgc catcgtcagc actgccctgc 300

cccagtgag gatttactcc tatgccggcg acaacatcgt gaccgcccag 350

gccatgtacg aggggctgtg gatgtcctgc gtgtcgcaga gcaccgggca 400

gatccagtgc aaagtctttg actccttgct gaatctgagc agcacattgc 450

aagcaacccg tgccttgatg gtggttgga tcctcctggg agtgatagca 500

atctttgtgg ccaccgttg catgaagtgt atgaagtgt tggaagacga 550

tgaggtgcag aagatgagga tggctgtcat tgggggtgcg atatttcttc 600

ttgcaggctct ggctatittta gttgccacag catggtatgg caatagaatc 650  
 gttcaagaat tctatgaccc tatgacccca gtcaatgccca ggtacgaatt 700  
 tggtcaggct ctcttcaactg gctgggctgc tgcttctctc tgccttctgg 750  
 gaggtgccct actttgctgt tctgtcccc gaaaaacaac ctcttaccca 800  
 acaccaaggc cctatccaaa acctgcacct tccagcggga aagactacgt 850  
 gtgacacaga ggcaaaagga gaaaatcatg ttgaaacaaa ccgaaaatgg 900  
 acattgagat actatcatta acattaggac cttagaattt tgggtattgt 950  
 aatctgaagt atggtattac aaaacaaaca aacaaacaaa aaacccatgt 1000  
 gttaaaatac tcagtgcata acatggctta atcttatttt atcttctttc 1050  
 ctcaatatag gaggggaagat ttttccattt gtattactgc ttcccattga 1100  
 gtaatcatatc tcaaatgggg gaaggggtgc tccttaaata tatatagata 1150  
 tgtatatata catgtttttc tattaataat agacagtaaa atactattct 1200  
 cattatgttg atactagcat acttaaaata tctctaaaat aggtaaatgt 1250  
 atttaattcc atattgatga agatgtttat tgggtatattt tctttttcgt 1300  
 ccttatatac atatgtaaca gtcaaataatc atttactctt cttcattagc 1350  
 tttgggtgcc tttgccacaa gacctagcct aatttaccaa ggatgaattc 1400  
 tttcaattct tcatgogtgc ccttttcata tacttatttt attttttacc 1450  
 ataatcttat agcacttgca tcgttattaa gcccttattt gttttgtgtt 1500  
 tcattggtct ctatctcctg aatctaacac atttcatagc ctacatttta 1550  
 gtttctaaag ccaagaagaa tttattacaa atcagaactt tggaggcaaa 1600  
 tctttctgca tgaccaaagt gataaattcc tgttgacctt cccacacaat 1650  
 cctgtactc tgacccatag cactcttggt tgccttgaaa atatttgtcc 1700  
 aattgagtag ctgcatgctg ttccccaggt tgttgtaaca caactttatt 1750  
 gattgaattt ttaagctact tattcatagt tttatattccc cctaaactac 1800  
 ctttttgttc cccattcctt aattgtattg ttttccaag tgtaattatc 1850  
 atgogtttta tatcttcta ataagggtgtg gtctgtttgt ctgaacaaag 1900  
 tgctagactt tctggagtga taatctggtg acaaattatc tctctgtagc 1950  
 tgtaagcaag tcaacttaatc tttctacctc tttttctat ctgccaaatt 2000  
 gagataatga tacttaacca gttagaagag gtagtgtgaa tattaattag 2050

tttatattac tcttattcct tgaacatgaa ctatgcctat gtagtgtcct 2100  
tatttgctca gctggctgag aactgaaga agtcactgaa caaacctac 2150  
acacgtacct tcatgtgatt cactgccttc ctctctctac cagtctatct 2200  
ccactgaaca aaacctacac acataccttc atgtgggttca gtgccttcct 2250  
ctctctacca gtctatttcc actgaacaaa acctacgcac ataccttcat 2300  
gtggctcagt gccttcctct ctctaccagt ctatttccat tctttcagct 2350  
gtgtctgaca tgtttggtgt ctgttccatt ttaacaactg ctcttacttt 2400  
tccagtctgt acagaatgct atttacttg agcaagatga tgtaatggaa 2450  
agggtgttgg cactgggtgtc tggagacctg gatttgagtc ttggtgctat 2500  
caatcaccgt ctgtgtttga gcaaggcatt tggctgctgt aagcttattg 2550  
cttcatctgt aagcgggtgg ttgtaattcc tgatcttccc acctcacagt 2600  
gatgttggtg ggatccagtg agatagaata catgtaagtg tggttttgta 2650  
atttaaaaag tgctatacta agggaaagaa ttgaggaatt aactgcatac 2700  
gttttggtgt tgcttttcaa atgtttgaaa ataaaaaaaa tgtttaag 2747

<210> 270  
<211> 211  
<212> PRT  
<213> Homo sapiens

<400> 270  
Met Ala Asn Ala Gly Leu Gln Leu Leu Gly Phe Ile Leu Ala Phe  
1 5 10 15  
Leu Gly Trp Ile Gly Ala Ile Val Ser Thr Ala Leu Pro Gln Trp  
20 25 30  
Arg Ile Tyr Ser Tyr Ala Gly Asp Asn Ile Val Thr Ala Gln Ala  
35 40 45  
Met Tyr Glu Gly Leu Trp Met Ser Cys Val Ser Gln Ser Thr Gly  
50 55 60  
Gln Ile Gln Cys Lys Val Phe Asp Ser Leu Leu Asn Leu Ser Ser  
65 70 75  
Thr Leu Gln Ala Thr Arg Ala Leu Met Val Val Gly Ile Leu Leu  
80 85 90  
Gly Val Ile Ala Ile Phe Val Ala Thr Val Gly Met Lys Cys Met  
95 100 105  
Lys Cys Leu Glu Asp Asp Glu Val Gln Lys Met Arg Met Ala Val  
110 115 120

Ile Gly Gly Ala	Ile Phe Leu Leu Ala	Gly Leu Ala Ile Leu Val
125	130	135
Ala Thr Ala Trp Tyr	Gly Asn Arg Ile Val	Gln Glu Phe Tyr Asp
140	145	150
Pro Met Thr Pro Val	Asn Ala Arg Tyr Glu	Phe Gly Gln Ala Leu
155	160	165
Phe Thr Gly Trp Ala	Ala Ala Ser Leu Cys	Leu Leu Gly Gly Ala
170	175	180
Leu Leu Cys Cys Ser	Cys Pro Arg Lys Thr	Thr Ser Tyr Pro Thr
185	190	195
Pro Arg Pro Tyr Pro	Lys Pro Ala Pro Ser	Ser Gly Lys Asp Tyr
200	205	210

Val

<210> 271  
 <211> 564  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 21, 69, 163, 434, 436, 444  
 <223> unknown base

<400> 271  
 ttctggccaa acccggggct ncagctgttg ggcttcatct cgccttctctg 50  
 ggatggatcg ggcacatnt cacactgccc ttcccagtg gaggatttta 100  
 ctccctatgc tggcgacaac atcgtgaccg cccagcccat gtacgagggg 150  
 ctgtggatgt ccongctgtc gcagagcacc gggcagatcc agtgcaaagt 200  
 ctttgactcc ttgctgaatc tgagcagcac attgcaagca acccgtgcct 250  
 tgatggtggt tggcatcctc ctgggagtga tagcaatctt tgtggccacc 300  
 gttggcatga agtgtatgaa gtgcttggaa gacgatgagg tgcagaagat 350  
 gaggatggct gtcattgggg gcgcgatatt tcttcttgca ggtctggcta 400  
 ttttagttgc cacagcatgg tatggcaata gaancnttca acantttctat 450  
 gaccctatga cccagtcaa tgccaggtac gaatttggtc aggctctctt 500  
 cactggctgg gctgctgctt ctctctgcct tctgggaggt gccctacttt 550  
 gctgttctctg tccc 564

<210> 272  
 <211> 498

<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 30, 49, 102, 141, 147, 171, 324-325, 339-341  
<223> unknown base

<400> 272  
acccttgacc caacgcggcc ccccgaccgn ttcattggcca aacgcgggnc 50  
tccagctgtt gggcttcatt ctccccttcc tgggatggac cggcgcccat 100  
cntcagcact gccctgcccc agtggaggat ttactcctat nccggenaca 150  
acatcgtgac cggccaggcc ntgtacgagg ggctgtggat gtcctgcgtg 200  
tcgcagagca ccgggcagat ccagtgc aaa gtctttgact cccttgctga 250  
atctgagcag cacattgcaa gcaaccctg ccttgatggg ggttgccatc 300  
ctcctgggag tgatagcaat cttnttggcc accgttgtnn ntgaagtgt 350  
tgaagtgtt ggaagacgat gaggtgcaga agatgaggat ggctgtcatt 400  
gggggcgcga tatttcttct tgcaggctctg gctatttttag ttgccacagc 450  
atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccga 498

<210> 273  
<211> 552  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 25, 57, 67, 94-95, 116, 152, 165, 212, 233, 392-394  
<223> unknown base

<400> 273  
gggcccgacc attatccaac cgggntcact gttggctcat ctcccctctg 50  
gatgaancgc gccatntca gactccctgc cccatggaga tttnnccat 100  
gctggcgaca acatontgac ccccgaccat gtacgagggg ctttgaacgt 150  
cngcgtgtcg caganaccg ggcagatcca gtgcaaagtc tttgactcct 200  
tgctgaatct gngcagcaca ttgcagcaac cntgcccctg atggtgggtg 250  
gcatcctcct gggagtgata gcaatctttg tggccaccgt tggcatgaag 300  
tgtatgaagt gcttgaaga cgatgaggtg cagaagatga ggatggctgt 350  
cattgggggc gcgatatttc ttcttgacagg tctggctatt tnnngttgcc 400  
acagcatggg atggcaatag aatcgttcaa gaattctatg accctatgac 450



cccagtcaat gccaggtagc aatttgggtca ggctctcttc actggctggg 500  
 ctgctgcttc tctctgcctt ctgggaggtg ccctactttg ctgttcctgc 550  
 ga 552

<210> 274  
 <211> 526  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 25, 50, 60, 123, 127, 370, 395, 397-398, 402-403, 405-407  
 <223> unknown base

<400> 274  
 attctccctt cctggatgga tcgcncacc gtcacattgc cttccccan 50  
 tggaggattn actcctatgc tggcgacaac atcgtgaccc cccaggccat 100  
 ttaccgaggg gctttggatg tcntgcntgt cgcagagcac cgggcagatc 150  
 ccagtgcaaa gtctttgact ccttgctgaa tctgagcagc acattgcaag 200  
 caaccctgtc cttgatgggg ttggcatcct cctgggagtg atagcaacct 250  
 ttgtggccac cgttggcatg aagtgtatga agtgcttga agacgatgag 300  
 gtgccagaag atgaggatgg ctgtcattgg gggcgcgata tttcttggtg 350  
 caggtctggc tatttttagtn gccacagcat ggtatggcaa tagantnntt 400  
 cnnnnntct atgaccctat gacccagtc aatgccaggt acgaatttgg 450  
 tcaggctctc ttacttggtt gggctgctgc ttctctctgc cttctgggag 500  
 gtgccctact ttgctgttcc tgtccc 526

<210> 275  
 <211> 398  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 22, 61, 91, 144, 238-239, 262, 265-266, 271, 274  
 <223> unknown base

<400> 275  
 agagcaccgg cagatcccag tncaaagtct ttgacccttg ctgaatctga 50  
 gcagcacatt ncaagcaacc ccttgccctg aagggtggtg ncatcccccc 100  
 tgggagtgaa tagcaatctt tgtggccacc gttggcatga agtntatgaa 150  
 gtgcttgga gacgatgagg tgcagaagat gaggatggct gtcattgggg 200

09978192.10501

gcgcgatatt tcttcttgca ggtctggcta ttttagtnnc cacagcatgg 250  
 tatggcaata gnatnnttcg nggnttctat gaccctatga cccagtcaa 300  
 tgccaggtag gaatttggtc aggctctctt cactggctgg gctgctgctt 350  
 ctctctgcct tctgggaggt gccctacttt gctgttcctg tccccgaa 398

<210> 276  
 <211> 495  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 39, 58, 130, 234, 314, 364, 427, 450, 461, 476  
 <223> unknown base

<400> 276  
 agcaatgccc tgccccaggt ggaggattaa ttcctatgnt ggggacaaca 50  
 ttgtgacngc ccaggccatg tacggggggc tgtggatgtc ctgctgtctg 100  
 cagagcaccg ggcagatcca gtgcaaagtn tttgactcct tgctgaattt 150  
 gagcagcaca ttgcaagcaa cccgtgcctt gatggtggtt ggcatcttcc 200  
 tgggagtgat agcaatcttt gtggccaccg tggnaatgaa gtgtatgaag 250  
 tgcttggaag acgatgaggt gcagaagatg aggatggctg tcattggggg 300  
 gcgcgatattt cttnttgtag gtctggctat tttagtggc acagcatggg 350  
 atggcaatag aatngttcaa gaattttatg accctatgac cccagtcaat 400  
 gccaggtagc aatttggtca ggctttnttc actggctggg ctgctgcttn 450  
 tttctgcctt ntgggaggtg ccctantttg ctgttcctgc gaacc 495

<210> 277  
 <211> 200  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 34, 87, 138, 147, 163, 165-166, 172  
 <223> unknown base

<400> 277  
 tcataggggg gcgcgatatt ttttcttgca ggtntgggta ttttagttgc 50  
 cacagcatgg tatggcaata gaatcgttca agaattntat gaccctatga 100  
 cccagtcaa tgccaggtag gaatttggtc aggctctntt cactggntgg 150  
 gctgctgctt ctntnngcct tntgggaggt gccctacttt gctgttcctg 200

<210> 278  
<211> 542  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 26, 43, 55, 77, 198, 361-362, 391-392, 396  
<223> unknown base

<400> 278  
ttcctgggat ggatccgccc ccatctcac atgccctgcc cnttgagat 50  
ttacnccat gctggcgaac aacatctga ccgccaggc catgtacgag 100  
gggctgtgga atgtcctgcg tgtcccagag caccgggcag atccagtgc 150  
aagtctttga ctccttgctg aatctgagca gcacattgca agcaacctg 200  
ccttgatggt ggttggcatc ctctgggag tgatagcaat ctttgtggcc 250  
accgttggca tgaaagtgt tgaagtgctt ggaagacgat gaggtgcaga 300  
agatgaggat ggctgtcatt gggggcgcga tattctctt tgcaggctctg 350  
gctattttag nngccacagc atggtatggc aatcagacc nntcanaaac 400  
tctatgacc tatgaccca gtcaatgcc ggtacgaatt tggtcaggct 450  
ctcttcactg gctgggctgc tgcttctctc tgcttctgg gaggtgccct 500  
actttgctgt tctgtcccc gaaaaacaac ctcttacca cg 542

<210> 279  
<211> 548  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 90, 115, 147, 228, 387  
<223> unknown base

<400> 279  
cggggctgca gctgttgggc ttcactctgc ttcctgggat ggaatcggcg 50  
ccatcgtcag cactgccctg ccccatggag gatttactn tatgctggcg 100  
acaacatcgt gaccnccag gccatgtacg aggggctgtg gatgtcngcg 150  
tgtcgcagag caccgggcag atccagtgc aagtctttga ctccttgctg 200  
aatctgagca gcacattgca agcaacctg ccttgatggt ggttggcatc 250  
ctcctgggag tgatagcaat ctttgtggcc accgttggca tgaagtgtat 300  
gaagtgcttg gaagacgatg aggtgcagaa gatgaggatg gctgtcattg 350

ggggcgcgat atttcttctt gcaggtctgg ctatttntag ttgccacagc 400  
 atggtatggc aatagaatcg ttcaagaatt ctatgaccct atgaccccag 450  
 tcaatgccag gtacgaattt ggtcaggctc tcttcactgg ctgggctgct 500  
 gcttctctct gccttctggg aggtgcccta ctttgctggt cctgcgaa 548

<210> 280  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 280  
 cgagcgagtc atggccaacg c 21

<210> 281  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 281  
 gtgtcacacg tagtctttcc cgctgg 26

<210> 282  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 282  
 ctgcagctgt tgggcttcat tctcgccctc ctgggatgga tcg 43

<210> 283  
 <211> 2285  
 <212> DNA  
 <213> Homo sapiens

<400> 283  
 gcgtgccgtc agctcgccgg gcaccgcggc ctgcacctcg cctccgccc 50  
 ctgcgcctgc accgcgtaga ccgaccccc cctccagcgc gccacccgg 100  
 tagaggaccc ccgcccgtgc ccgacccggt ccccgccctt ttgtaaaact 150  
 taaagcgggc gcagcattaa cgcttccgc cccggtgacc tctcaggggt 200  
 ctccccgcca aaggtgctcc gccgctaagg aacatggcga aggtggagca 250  
 ggtcctgagc ctgcagccgc agcacgagct caaattccga ggtcccttca 300

ccgatgttgt caccaccaac ctaaagcttg gcaacccgac agaccgaaat 350  
gtgtgtttta aggtgaagac tacagcacca cgtaggtact gtgtgaggcc 400  
caacagcgga atcatcgatg caggggcctc aattaatgta tctgtgatgt 450  
tacagccttt cgattatgat cccaatgaga aaagtaaaca caagtttatg 500  
gttcagtcta tgtttgctcc aactgacact tcagatatgg aagcagtatg 550  
gaaggaggca aaaccggaag accttatgga ttcaaaactt agatgtgtgt 600  
ttgaattgcc agcagagaat gataaaccac atgatgtaga aataaataaa 650  
attatatcca caactgcac aaagacagaa acaccaatag tgtctaagtc 700  
tctgagttct tctttggatg acaccgaagt taagaagggt atggaagaat 750  
gtaagaggct gcaaggtgaa gttcagaggc tacgggagga gaacaagcag 800  
ttcaaggaag aagatggact gcggatgagg aagacagtgc agagcaacag 850  
ccccatttca gcattagccc caactgggaa ggaagaaggc cttagcacc 900  
ggctcttggc tctggtggtt ttgttcttta tcgttggtgt aattattggg 950  
aagattgcct tgtagaggta gcatgcacag gatggtaa at tggattggtg 1000  
gatccaccat atcatgggat ttaaatttat cataaccatg tgtaaaaaga 1050  
aattaatgta tgatgacac tcacaggtct tgcctttaa ttaccctcc 1100  
ctgcacacac atacacagat acacacacac aaatataatg taacgatctt 1150  
ttagaaagt aa aaatgtat agtaactgat tgagggggaa aaagaatgat 1200  
ctttattaat gacaagggaa accatgagta atgccacaat ggcattattgt 1250  
aaatgtcatt ttaaacattg gtaggccttg gtacatgatg ctggattacc 1300  
tctcttaaaa tgacaccctt cctgcctgt tgggtgctggc ccttggggag 1350  
ctggagccca gcatgctggg gagtgcggtc agctccacac agtagtcccc 1400  
acgtggccca ctcccgccc aggtgcttt cegtgtcttc agttctgtcc 1450  
aagccatcag ctcttgga ctgatgaaca gagtcagaag cccaaaggaa 1500  
ttgcaactgtg gcagcatcag acgtactcgt cataagtgag aggcgtgtgt 1550  
tgactgattg acccagcgct ttggaaataa atggcagtgc tttgttact 1600  
taaagggacc aagctaaatt tgtattggtt catgtagtga agtcaaactg 1650  
ttattcagag atgtttaatg catatttaac ttatttaatg tatttcatct 1700  
catgttttct tattgtcaca agagtacagt taatgctgcg tgctgctgaa 1750

ctctgttggg tgaactggtg ttgctgctgg agggctgtgg gctcctctgt 1800  
ctctggagag tctgggtcatg tggaggtggg gtttattggg atgctggaga 1850  
agagctgcca ggaagtgttt tttctgggtc agtaaataac aactgtcata 1900  
gggagggaaa ttctcagtag tgacagtcaa ctctaggtta ccttttttaa 1950  
tgaagagtag tcagtcttct agattgttct tataccacct ctcaaccatt 2000  
actcacactt ccagcgccca ggtccaagtc tgagcctgac ctccccttgg 2050  
ggacctagcc tggagtcagg acaaatggat cgggctgcag agggttagaa 2100  
gcgagggcac cagcagttgt ggggtggggag caagggaaga gagaaactct 2150  
tcagcgaatc cttctagtag tagttgagag ttgactgtg aattaatttt 2200  
atgccataaa agaccaaccc agttctgttt gactatgtag catcttgaaa 2250  
agaaaaatta taataagcc ccaaaattaa gaaaa 2285

<210> 284

<211> 243

<212> PRT

<213> Homo sapiens

<400> 284

Met	Ala	Lys	Val	Glu	Gln	Val	Leu	Ser	Leu	Glu	Pro	Gln	His	Glu
1				5					10					15
Leu	Lys	Phe	Arg	Gly	Pro	Phe	Thr	Asp	Val	Val	Thr	Thr	Asn	Leu
				20					25					30
Lys	Leu	Gly	Asn	Pro	Thr	Asp	Arg	Asn	Val	Cys	Phe	Lys	Val	Lys
				35					40					45
Thr	Thr	Ala	Pro	Arg	Arg	Tyr	Cys	Val	Arg	Pro	Asn	Ser	Gly	Ile
				50					55					60
Ile	Asp	Ala	Gly	Ala	Ser	Ile	Asn	Val	Ser	Val	Met	Leu	Gln	Pro
				65					70					75
Phe	Asp	Tyr	Asp	Pro	Asn	Glu	Lys	Ser	Lys	His	Lys	Phe	Met	Val
				80					85					90
Gln	Ser	Met	Phe	Ala	Pro	Thr	Asp	Thr	Ser	Asp	Met	Glu	Ala	Val
				95					100					105
Trp	Lys	Glu	Ala	Lys	Pro	Glu	Asp	Leu	Met	Asp	Ser	Lys	Leu	Arg
				110					115					120
Cys	Val	Phe	Glu	Leu	Pro	Ala	Glu	Asn	Asp	Lys	Pro	His	Asp	Val
				125					130					135
Glu	Ile	Asn	Lys	Ile	Ile	Ser	Thr	Thr	Ala	Ser	Lys	Thr	Glu	Thr
				140					145					150

Pro	Ile	Val	Ser	Lys	Ser	Leu	Ser	Ser	Ser	Leu	Asp	Asp	Thr	Glu
				155					160					165
Val	Lys	Lys	Val	Met	Glu	Glu	Cys	Lys	Arg	Leu	Gln	Gly	Glu	Val
				170					175					180
Gln	Arg	Leu	Arg	Glu	Glu	Asn	Lys	Gln	Phe	Lys	Glu	Glu	Asp	Gly
				185					190					195
Leu	Arg	Met	Arg	Lys	Thr	Val	Gln	Ser	Asn	Ser	Pro	Ile	Ser	Ala
				200					205					210
Leu	Ala	Pro	Thr	Gly	Lys	Glu	Glu	Gly	Leu	Ser	Thr	Arg	Leu	Leu
				215					220					225
Ala	Leu	Val	Val	Leu	Phe	Phe	Ile	Val	Gly	Val	Ile	Ile	Gly	Lys
				230					235					240

Ile Ala Leu

<210> 285  
 <211> 418  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 40, 53, 68, 119, 134, 177-178, 255  
 <223> unknown base

<400> 285  
 gtcagtcttc tagattgtcc ttatcccacc ttccaaccan tactcacatt 50  
 tcnagcgccc aggtccangt ctgagcctga cttccccttg gggacctagc 100  
 ctggagtcag gacaatggnt cgggctgcag aggnntagaa gcgagggcac 150  
 cagcagtttt ggggtggggag caagggngga gagaaactct tcagcgaatc 200  
 cttctagtac tagttgagag ttgactgtg aattaatttt atgccataaa 250  
 agacnaaccc agttctgttt gactatgtag catcttgaaa agaaaaatta 300  
 taataaagcc ccaaaaattaa gaattctttt gtcattttgt cacatttgct 350  
 ctatgggggg aattattatt ttatcatttt tattattttg ccattggaag 400  
 gttaacttta aaatgagc 418

<210> 286  
 <211> 543  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 73, 97

<223> unknown base

<400> 286

tattgtaaaag gccatttttaa accattggta ggccttggtg catgatgctg 50  
gattacctcc ttaaattgaca ccnttcctcg cctgttggtg ctggccnttg 100  
gggagctgga gcccagcat gctggggagt gcggtcagct ccacacagta 150  
gtccccacgt ggcccactcc cggcccaggc tgctttccgt gtcttcagtt 200  
ctgtccaagc catcagctcc ttgggactga tgaacagagt cagaagccca 250  
aaggaattgc cactgtggca gcatcagacg tactcgatcat aagtgagagg 300  
cgtgtgttga ctgattgacc cagcgctttg gaaataaatg gcagtgcctt 350  
gttcacttaa agggaccaag ctaaattgta ttggttcatg tagtgaagtc 400  
aaactgttat tcagagatgt ttaatgcata ttaacttat ttaatgtatt 450  
tcattctcatg ttttcttatt gtcacaagag tacagttaat gctgcgtgct 500  
gctgaactct gttgggtgaa ctggtattgc tgctggaggg ctg 543

<210> 287

<211> 270

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 38, 64, 72, 164, 198, 200, 220, 222, 229, 242

<223> unknown base

<400> 287

ccctggtggt tttgttcttt aattcgttgg tgtaattntt gggaagattg 50  
cttgtagagg tagnatgcac cnggctggta aattggattg gtggatccac 100  
catatccatg ggattttaaatt ttatcataac catgtgtaaa aagaaattaa 150  
tgtatgatga catntcacag gtattgcctt taaattaccc atccctgnan 200  
acacatacac agatacacan anacaaatnt aatgtaacga tnttttagaa 250  
agttaaaaat gtatagtaac 270

<210> 288

<211> 428

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 35, 116, 129, 197, 278, 294, 297, 349, 351

<223> unknown base



<400> 288

ggtggcccat tcccggccca ggctgctttc cggtnttcag ttctgtccaa 50  
gccatcagct ccttgggact gatgaacaga gtcagaagcc caaaggaatt 100  
gcactgtggc agcatnagac gtacttgtna taagtgagag gcgtgtgttg 150  
actgattgac ccagcgcttt ggaaataaat ggcagtgcct tgttcantta 200  
aagggaccaa gctaaatttg tatttggttca tgtagtgaag tcaaactgtt 250  
attcagagat gtttaatgca tatttaantt atttaatgta tttnatntca 300  
tgttttctta ttgtcacaag agtacagtta atgctgcgtg ctgctgaant 350  
ntgttgggtg aactggtatt gctgctggag ggctgtgggc tcctctgtct 400  
ttggagagtc tggatcatgtg gaggtggg 428

<210> 289

<211> 320

<212> DNA

<213> Homo sapiens

<400> 289

tgctttccgt gtcttcagtt ctgtccaagc catcagctcc ttgggacttg 50  
atgaacagag tcagaagccc aaaggaattg cactgtggca gcatcagacg 100  
tactcgtcat aagtgagagg cgtgtgttga ctgattgacc cagcgctttg 150  
gaaataaatg gcagtgcctt gttcacttaa agggaccaag ctaaatttgt 200  
attggttcat gtagtgaagt caaactgtta ttcagagatg tttaatgcat 250  
atttaactta tttaatgtat ttcattctcat gttttcttat tgtcacaaga 300  
gtacagttaa tgctgcgtgc 320

<210> 290

<211> 609

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> 57, 60, 186, 235, 244, 304, 339, 355, 359, 361, 387, 432, 441,  
447, 481, 513, 532, 584, 598

<223> unknown base

<400> 290

aaacctttaa aagttgaggg gaaaagaatg atcctttatt aatgacaagg 50  
gaaacntgn gtaatgccac aatggcatat tgtaaattgc attttaaaca 100  
ttggtaggcc ttggtacatg atgctggatt acctctotta aaatgacacc 150  
cttctctgcc tgttgggtgct ggcccttggg gagctngagc ccagcatgct 200

ggggagtgcg gtctgctcca cacagtagtc cccangtggc ccantcccgg 250  
 cccaggctgc tttccgtgtc ttcagttctg tccaagccat cagctccttg 300  
 ggantgatga acagagtcag aagcccaaag gaattgcant gtggcagcat 350  
 cagangtant ngtcataagt gagaggcgtg tgttgantga ttgaccacgc 400  
 gctttggaaa taaatggcag tgctttgttc anttaaaggg nccaagntaa 450  
 atttgtattg gttcatgtag tgaagtcaaa ntgttattca gagatgttta 500  
 atgcatattt aanttattta atgtatttca tntcatgttt tcttattgtc 550  
 acaagggtag agttaatgct gcgtgctgct gaantctggt gggatgaantg 600  
 gtattgctg 609

<210> 291  
 <211> 493  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
 ggcccttggg gagctggagc ccagcatgct ggggagtgcg gtcagctcca 50  
 cacagtagtc cccacgtggc ccaactcccgg cccaggctgc tttccgtgtc 100  
 ttcagttctg tccaagccat cagctccttg ggactgatga acagagtcag 150  
 aagcccaaag gaattgcact gtggcagcat cagacgtact cgtcataagt 200  
 gagaggcgtg tgttgactga ttgaccacgc gctttggaaa taaatggcag 250  
 tgctttgttc acttaaaggg accaagctaa atttgtattg gttcatgtag 300  
 tgaagtcaaa ctgttattca gagatgttta atgcatattt aacttattta 350  
 atgtatttca tctcatgttt tcttattgtc acaagagtag agttaatgct 400  
 gcgtgctgct gaactctggt gggatgaactg gtattgctgc tggagggctg 450  
 tgggctcctc tgtctctgga gagtctgggc atgtggaggt ggg 493

<210> 292  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 292  
 gcaccaccgt aggtacttgt gtgaggc 27

<210> 293  
 <211> 23  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 293

aaccaccaga gccaaagagcc ggg 23

<210> 294

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 294

cagcgggaatc atcgatgcag gggcctcaat taatgtatct gtgatgttac 50

<210> 295

<211> 2530

<212> DNA

<213> Homo sapiens

<400> 295

gcgagctccg ggtgctgtgg cccggccttg gcggggcggc ctccggctca 50

ggctggctga gaggctccca gctgcagcgt ccccgccgc ctctcgga 100

gctctgatct cagctgacag tgccctggg gaccaaaca gcctggcagg 150

gtctcacttt gttgccagg ctggagttca gtgcatgat catggtttac 200

tgcagccttg acctcctggg ttcaagcag cctgctgagt agctgggact 250

acaggacaaa attagaagat caaaatggaa aatatgctgc tttggttgat 300

atttttcacc cctgggtgga ccctcattga tggatctgaa atggaatggg 350

attttatgtg gcacttgaga aaggtacccc ggattgtcag tgaaaggact 400

ttccatctca ccagccccgc atttgaggca gatgctaaga tgatggtaaa 450

tacagtgtgt ggcacgaat gccagaaaga actcccaact cccagccttt 500

ctgaattgga ggattatctt tcctatgaga ctgtctttga gaatggcacc 550

cgaaccttaa ccagggtgaa agttcaagat ttggttcttg agccgactca 600

aaatatcacc acaaaggag tatctgttag gagaaagaga cagggtgtatg 650

gcaccgacag caggttcagc atcttgaca aaaggttctt aaccaatttc 700

cctttcagca cagctgtgaa gctttccacg ggctgtagtg gcattctcat 750

ttcccctcag catgttctaa ctgctgccca ctgtgttcat gatggaaagg 800

actatgtcaa agggagtaaa aagctaagg tagggttgtt gaagatgagg 850

aataaaagtg gaggcaagaa acgtcgaggt tctaagagga gcaggagaga 900  
agctagtggg ggtgaccaa gagaggggtac cagagagcat ctgcaggaga 950  
gagcgaaggg tgggagaaga agaaaaaat ctggccgggg tcagaggatt 1000  
gccgaagggg ggccttcctt tcagtggacc cgggtcaaga ataccacat 1050  
tccgaagggc tgggcacgag gaggcattgg ggacgctacc ttggactatg 1100  
actatgctct tctggagctg aagcgtgctc acaaaaagaa atacatggaa 1150  
cttggaatca gcccaacgat caagaaaatg cctgggtggaa tgatccactt 1200  
ctcaggattt gataacgata gggctgatca gttgggtctat cggttttgca 1250  
gtgtgtccga cgaatccaat gatctccttt accaatactg cgatgctgag 1300  
tcgggctcca ccggttcggg ggtctatctg cgtctgaaag atccagacaa 1350  
aaagaattgg aagcgcaaaa tcattgcggt ctactcaggg caccagtggg 1400  
tggatgtcca cgggggttcag aaggactaca acgttgctgt tcgcatcact 1450  
cccctaaaat acgccagat ttgcctctgg attcacggga acgatgccaa 1500  
ttgtgcttac ggctaacaga gacctgaaac agggcgggtg atcatctaaa 1550  
tcacagagaa aaccagctct gcttacgta gtgagatcac ttcatagggt 1600  
atgcctggac ttgaactctg tcaatagcat ttcaacattt ttcaaatca 1650  
ggagattttc gtccatttaa aaaatgtata ggtgcagata ttgaaactag 1700  
gtgggcactt caatgccaa tatatactct tctttacatg gtgatgagtt 1750  
tcattttagt aaaaattttg ttgccttctt aaaaattaga cacactttaa 1800  
accttcaaac aggtattata aataacatgt gactccttaa tggacttatt 1850  
ctcagggtcc tactctaaga agaatcta ataggatgctgg ttgtgtatta 1900  
aatgtgaaat tgcatagata aaggtagatg gtaaagcaat tagtatcaga 1950  
atagagacag aaagttacaa cacagtttgt actactctga gatggatcca 2000  
ttcagctcat gccctcaatg tttatattgt gttatctgtt gggctctggga 2050  
catttagttt agtttttttg aagaattaca aatcagaaga aaaagcaagc 2100  
attataaaca aaactaataa ctgttttact gctttaagaa ataacaatta 2150  
caatgtgtat ttttaaaaa tgggagaaat agtttgttct atgaaataaa 2200  
cctagtttag aaataggga gctgagacat tttaagatct caagttttta 2250  
tttaactaat actcaaaata tggacttttc atgtatgcat agggaagaca 2300

cttcacaaat tatgaatgat catgtgttga aagccacatt attttatgct 2350  
 atacattcta tgtatgaggt gctacatttt taggacaaag aattctgtaa 2400  
 tctttttcaa gaaagagtct ttttctcctt gacaaaatcc agcttttgta 2450  
 tgaggactat aggggtgaatt ctctgattag taattttaga tatgtccttt 2500  
 cctaaaaatg aataaaattt atgaatatga 2530

<210> 296  
 <211> 413  
 <212> PRT  
 <213> Homo sapiens

<400> 296  
 Met Glu Asn Met Leu Leu Trp Leu Ile Phe Phe Thr Pro Gly Trp  
 1 5 10 15  
 Thr Leu Ile Asp Gly Ser Glu Met Glu Trp Asp Phe Met Trp His  
 20 25 30  
 Leu Arg Lys Val Pro Arg Ile Val Ser Glu Arg Thr Phe His Leu  
 35 40 45  
 Thr Ser Pro Ala Phe Glu Ala Asp Ala Lys Met Met Val Asn Thr  
 50 55 60  
 Val Cys Gly Ile Glu Cys Gln Lys Glu Leu Pro Thr Pro Ser Leu  
 65 70 75  
 Ser Glu Leu Glu Asp Tyr Leu Ser Tyr Glu Thr Val Phe Glu Asn  
 80 85 90  
 Gly Thr Arg Thr Leu Thr Arg Val Lys Val Gln Asp Leu Val Leu  
 95 100 105  
 Glu Pro Thr Gln Asn Ile Thr Thr Lys Gly Val Ser Val Arg Arg  
 110 115 120  
 Lys Arg Gln Val Tyr Gly Thr Asp Ser Arg Phe Ser Ile Leu Asp  
 125 130 135  
 Lys Arg Phe Leu Thr Asn Phe Pro Phe Ser Thr Ala Val Lys Leu  
 140 145 150  
 Ser Thr Gly Cys Ser Gly Ile Leu Ile Ser Pro Gln His Val Leu  
 155 160 165  
 Thr Ala Ala His Cys Val His Asp Gly Lys Asp Tyr Val Lys Gly  
 170 175 180  
 Ser Lys Lys Leu Arg Val Gly Leu Leu Lys Met Arg Asn Lys Ser  
 185 190 195  
 Gly Gly Lys Lys Arg Arg Gly Ser Lys Arg Ser Arg Arg Glu Ala  
 200 205 210

09978192.10501

Ser Gly Gly Asp Gln Arg Glu Gly Thr Arg Glu His Leu Gln Glu  
215 220 225

Arg Ala Lys Gly Gly Arg Arg Arg Lys Lys Ser Gly Arg Gly Gln  
230 235 240

Arg Ile Ala Glu Gly Arg Pro Ser Phe Gln Trp Thr Arg Val Lys  
245 250 255

Asn Thr His Ile Pro Lys Gly Trp Ala Arg Gly Gly Met Gly Asp  
260 265 270

Ala Thr Leu Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Arg Ala  
275 280 285

His Lys Lys Lys Tyr Met Glu Leu Gly Ile Ser Pro Thr Ile Lys  
290 295 300

Lys Met Pro Gly Gly Met Ile His Phe Ser Gly Phe Asp Asn Asp  
305 310 315

Arg Ala Asp Gln Leu Val Tyr Arg Phe Cys Ser Val Ser Asp Glu  
320 325 330

Ser Asn Asp Leu Leu Tyr Gln Tyr Cys Asp Ala Glu Ser Gly Ser  
335 340 345

Thr Gly Ser Gly Val Tyr Leu Arg Leu Lys Asp Pro Asp Lys Lys  
350 355 360

Asn Trp Lys Arg Lys Ile Ile Ala Val Tyr Ser Gly His Gln Trp  
365 370 375

Val Asp Val His Gly Val Gln Lys Asp Tyr Asn Val Ala Val Arg  
380 385 390

Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Leu Trp Ile His Gly  
395 400 405

Asn Asp Ala Asn Cys Ala Tyr Gly  
410

<210> 297

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 297

gcacatgcag gagagagcga aggg 24

<210> 298

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 298  
catcggtccc gtgaatccag aggc 24

<210> 299  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 299  
gaaggaggc cttcctttca gtggaccggt gtcaagaata cccac 45

<210> 300  
<211> 1869  
<212> DNA  
<213> Homo sapiens

<400> 300  
aatgtgagag gggctgatgg aagctgatag gcaggactgg agtggttagca 50  
ccagtactgg atgtgacagc aggcagagga gcacttagca gcttattcag 100  
tgtccgattc tgattccggc aaggatccaa gcatggaatg ctgccgtcgg 150  
gcaactcctg gcacactgct cctctttctg gctttcctgc tcctgagttc 200  
caggaccgca cgctccgagg aggaccggga cggcctatgg gatgcctggg 250  
gcccattggag tgaatgctca cgcacctgag ggggaggggc ctctactct 300  
ctgaggcgct gcctgagcag caagagctgt gaaggaagaa atatccgata 350  
cagaacatgc agtaatgtgg actgcccacc agaagcagggt gatttccgag 400  
ctcagcaatg ctcagctcat aatgatgtca agcaccatgg ccagttttat 450  
gaatggcttc ctgtgtctaa tgaccctgac aacctatgtt cactcaagtg 500  
ccaagccaaa ggaacaacct tgggtgttga actagcacct aaggtcttag 550  
atggtacgag ttgctataca gaatctttgg atatgtgcat cagtgggtta 600  
tgccaaattg ttggctgaga tcaccagctg ggaagcaccg tcaaggaaga 650  
taactgtggg gtctgcaacg gagatgggtc cacctgccgg ctgggtccgag 700  
ggcagtataa atcccagctc tccgcaacca aatcggtatga tactgtgggt 750  
gcacttccct atggaagtag acatattcgc cttgtcttaa aaggtcctga 800  
tcacttatat ctggaaacca aaacctcca ggggactaaa ggtgaaaaca 850  
gtctcagctc cacaggaact ttccttgggg acaattctag tgtggacttc 900

cagaaatttc cagacaaaga gatactgaga atggctggac cactcacagc 950  
 agatttcatt gtcaagattc gtaactcggg ctccgctgac agtacagtcc 1000  
 agttcatctt ctatcaaccc atcatccacc gatggaggga gacggatttc 1050  
 ttctcttgct cagcaacctg tggaggaggt tatcagctga catcggctga 1100  
 gtgctacgat ctgaggagca accgtgtggt tgctgaccaa tactgtcact 1150  
 attaccaga gaacatcaaa cccaaaccca agcttcagga gtgcaacttg 1200  
 gatccttgtc cagccagtga cggatacaag cagatcatgc cttatgacct 1250  
 ctaccatccc ctctctcggg gggaggccac cccatggacc gcgtgctcct 1300  
 cctcgtgtgg ggggggcac cagagccggg cagtttcctg tgtggaggag 1350  
 gacatccagg ggcattgtac ttcagtggaa gaggggaaat gcatgtacac 1400  
 ccctaagatg cccatcgcgc agccctgcaa catTTTTgac tgccctaaat 1450  
 ggctggcaca ggagtgggtc ccgtgcacag tgacatgtgg ccagggcctc 1500  
 agataccgtg tggctcctctg catcgaccat cgaggaaatgc acacaggagg 1550  
 ctgtagccca aaaacaaagc cccacataaa agaggaaatgc atcgtaccca 1600  
 ctccctgcta taaacccaaa gagaaacttc cagtcgaggc caagttgcca 1650  
 tggttcaaac aagctcaaga gctagaagaa ggagctgctg tgtcagagga 1700  
 gccctcgtaa gttgtaaaag cacagactgt tctatatttg aaactgtttt 1750  
 gtttaaagaa agcagtgtct cactggttgt agctttcatg ggttctgaac 1800  
 taagtgtaat catctacca aagctttttg gctctcaaat taaagattga 1850  
 ttagtttcaa aaaaaaaaa 1869

<210> 301  
 <211> 525  
 <212> PRT  
 <213> Homo sapiens

<400> 301  
 Met Glu Cys Cys Arg Arg Ala Thr Pro Gly Thr Leu Leu Leu Phe  
     1                    5                    10                    15  
 Leu Ala Phe Leu Leu Leu Ser Ser Arg Thr Ala Arg Ser Glu Glu  
                     20                    25                    30  
 Asp Arg Asp Gly Leu Trp Asp Ala Trp Gly Pro Trp Ser Glu Cys  
                     35                    40                    45  
 Ser Arg Thr Cys Gly Gly Gly Ala Ser Tyr Ser Leu Arg Arg Cys  
                     50                    55                    60



Leu	Ser	Ser	Lys	Ser	Cys	Glu	Gly	Arg	Asn	Ile	Arg	Tyr	Arg	Thr		65	70	75
Cys	Ser	Asn	Val	Asp	Cys	Pro	Pro	Glu	Ala	Gly	Asp	Phe	Arg	Ala		80	85	90
Gln	Gln	Cys	Ser	Ala	His	Asn	Asp	Val	Lys	His	His	Gly	Gln	Phe		95	100	105
Tyr	Glu	Trp	Leu	Pro	Val	Ser	Asn	Asp	Pro	Asp	Asn	Pro	Cys	Ser		110	115	120
Leu	Lys	Cys	Gln	Ala	Lys	Gly	Thr	Thr	Leu	Val	Val	Glu	Leu	Ala		125	130	135
Pro	Lys	Val	Leu	Asp	Gly	Thr	Arg	Cys	Tyr	Thr	Glu	Ser	Leu	Asp		140	145	150
Met	Cys	Ile	Ser	Gly	Leu	Cys	Gln	Ile	Val	Gly	Cys	Asp	His	Gln		155	160	165
Leu	Gly	Ser	Thr	Val	Lys	Glu	Asp	Asn	Cys	Gly	Val	Cys	Asn	Gly		170	175	180
Asp	Gly	Ser	Thr	Cys	Arg	Leu	Val	Arg	Gly	Gln	Tyr	Lys	Ser	Gln		185	190	195
Leu	Ser	Ala	Thr	Lys	Ser	Asp	Asp	Thr	Val	Val	Ala	Leu	Pro	Tyr		200	205	210
Gly	Ser	Arg	His	Ile	Arg	Leu	Val	Leu	Lys	Gly	Pro	Asp	His	Leu		215	220	225
Tyr	Leu	Glu	Thr	Lys	Thr	Leu	Gln	Gly	Thr	Lys	Gly	Glu	Asn	Ser		230	235	240
Leu	Ser	Ser	Thr	Gly	Thr	Phe	Leu	Val	Asp	Asn	Ser	Ser	Val	Asp		245	250	255
Phe	Gln	Lys	Phe	Pro	Asp	Lys	Glu	Ile	Leu	Arg	Met	Ala	Gly	Pro		260	265	270
Leu	Thr	Ala	Asp	Phe	Ile	Val	Lys	Ile	Arg	Asn	Ser	Gly	Ser	Ala		275	280	285
Asp	Ser	Thr	Val	Gln	Phe	Ile	Phe	Tyr	Gln	Pro	Ile	Ile	His	Arg		290	295	300
Trp	Arg	Glu	Thr	Asp	Phe	Phe	Pro	Cys	Ser	Ala	Thr	Cys	Gly	Gly		305	310	315
Gly	Tyr	Gln	Leu	Thr	Ser	Ala	Glu	Cys	Tyr	Asp	Leu	Arg	Ser	Asn		320	325	330
Arg	Val	Val	Ala	Asp	Gln	Tyr	Cys	His	Tyr	Tyr	Pro	Glu	Asn	Ile		335	340	345
Lys	Pro	Lys	Pro	Lys	Leu	Gln	Glu	Cys	Asn	Leu	Asp	Pro	Cys	Pro				

350	355	360
Ala Ser Asp Gly Tyr Lys Gln Ile Met	Pro Tyr Asp Leu Tyr His	
365	370	375
Pro Leu Pro Arg Trp Glu Ala Thr Pro	Trp Thr Ala Cys Ser Ser	
380	385	390
Ser Cys Gly Gly Gly Ile Gln Ser Arg	Ala Val Ser Cys Val Glu	
395	400	405
Glu Asp Ile Gln Gly His Val Thr Ser	Val Glu Glu Trp Lys Cys	
410	415	420
Met Tyr Thr Pro Lys Met Pro Ile Ala	Gln Pro Cys Asn Ile Phe	
425	430	435
Asp Cys Pro Lys Trp Leu Ala Gln Glu	Trp Ser Pro Cys Thr Val	
440	445	450
Thr Cys Gly Gln Gly Leu Arg Tyr Arg	Val Val Leu Cys Ile Asp	
455	460	465
His Arg Gly Met His Thr Gly Gly Cys	Ser Pro Lys Thr Lys Pro	
470	475	480
His Ile Lys Glu Glu Cys Ile Val Pro	Thr Pro Cys Tyr Lys Pro	
485	490	495
Lys Glu Lys Leu Pro Val Glu Ala Lys	Leu Pro Trp Phe Lys Gln	
500	505	510
Ala Gln Glu Leu Glu Glu Gly Ala Ala	Val Ser Glu Glu Pro Ser	
515	520	525

<210> 302  
 <211> 1533  
 <212> DNA  
 <213> Homo sapiens

<400> 302  
 cggacgcgtg ggcggcggct gcggaactcc cgtggagggg ccggtggggc 50  
 ctcgggcctg acagatggca gtggccactg cggcggcagt actggccgct 100  
 ctggggcggg cgctgtggct ggcggcccgc cggttcgtgg ggcccagggt 150  
 ccagcggctg cgcagaggcg gggaccccg cctcatgcac gggaagactg 200  
 tgctgatcac cggggcgaac agcggcctgg gccgcgccac ggccgcccag 250  
 ctactgcgcc tgggagcgcg ggtgatcatg ggctgccggg accgcgcgcg 300  
 cgccgaggag gcgggcggtc agctccgccg cgagctccgc caggccgcgg 350  
 agtgcgggcc agagcctggc gtcagcgggg tgggcgagct catagtccgg 400  
 gagctggacc tcgcctcgct gcgctcggtg cgcgccttct gccaggaaat 450

gctccaggaa gagcctaggc tggatgtctt gatcaataac gcagggatct 500  
 tccagtgcc ttacatgaag actgaagatg ggtttgagat gcagttcgga 550  
 gtgaaccatc tggggcactt tctactcacc aatcttctcc ttggactcct 600  
 caaaagttca gctcccagca ggattgtggt agtttcttcc aaactttata 650  
 aatacggaga catcaatttt gatgacttga acagtgaaca aagctataat 700  
 aaaagctttt gttatagccg gagcaaactg gctaacattc tttttaccag 750  
 ggaactagcc cgccgcttag aaggcacaaa tgtcacccgc aatgtgttgc 800  
 atcctggtat tgtacggaca aatctgggga ggcacataca cattccactg 850  
 ttggtcaaac cactcttcaa tttggtgtca tgggcttttt tcaaaaactcc 900  
 agtagaaggt gccagactt ccattttattt ggccctcttca cctgaggtag 950  
 aaggagtgtc aggaagatac tttggggatt gtaaagagga agaactgttg 1000  
 cccaaagcta tggatgaatc tgttgcaaga aaactctggg atatcagtga 1050  
 agtgatgggt ggccctgctaa aataggaaca aggagtaaaa gagctgttta 1100  
 taaaactgca tatcagttat atctgtgatc aggaatggtg tggattgaga 1150  
 acttgttact tgaagaaaaa gaattttgat attggaatag cctgctaaga 1200  
 ggtacatgtg ggtattttgg agttactgaa aaattatttt tgggataaga 1250  
 gaatttcagc aaagatgttt taaatatata tagtaagtat aatgaataat 1300  
 aagtacaatg aaaaatacaa ttatatgtta aaattataac tgggcaagca 1350  
 tggatgacat attaataattt gtcagaatta agtgactcaa agtgctatcg 1400  
 agaggttttt caagtatctt tgagtttcat ggccaaagtg ttaactagtt 1450  
 ttactacaat gtttggtggt tgtgtggaaa ttatctgcct ggtgtgtgca 1500  
 cacaagtctt acttggaata aatttactgg tac 1533

<210> 303  
 <211> 336  
 <212> PRT  
 <213> Homo sapiens

<400> 303  
 Met Ala Val Ala Thr Ala Ala Ala Val Leu Ala Ala Leu Gly Gly  
 1 5 10 15  
 Ala Leu Trp Leu Ala Ala Arg Arg Phe Val Gly Pro Arg Val Gln  
 20 25 30  
 Arg Leu Arg Arg Gly Gly Asp Pro Gly Leu Met His Gly Lys Thr  
 35 40 45

Val	Leu	Ile	Thr	Gly	Ala	Asn	Ser	Gly	Leu	Gly	Arg	Ala	Thr	Ala	
				50					55					60	
Ala	Glu	Leu	Leu	Arg	Leu	Gly	Ala	Arg	Val	Ile	Met	Gly	Cys	Arg	
				65					70					75	
Asp	Arg	Ala	Arg	Ala	Glu	Glu	Ala	Ala	Gly	Gln	Leu	Arg	Arg	Glu	
				80					85					90	
Leu	Arg	Gln	Ala	Ala	Glu	Cys	Gly	Pro	Glu	Pro	Gly	Val	Ser	Gly	
				95					100					105	
Val	Gly	Glu	Leu	Ile	Val	Arg	Glu	Leu	Asp	Leu	Ala	Ser	Leu	Arg	
				110					115					120	
Ser	Val	Arg	Ala	Phe	Cys	Gln	Glu	Met	Leu	Gln	Glu	Glu	Pro	Arg	
				125					130					135	
Leu	Asp	Val	Leu	Ile	Asn	Asn	Ala	Gly	Ile	Phe	Gln	Cys	Pro	Tyr	
				140					145					150	
Met	Lys	Thr	Glu	Asp	Gly	Phe	Glu	Met	Gln	Phe	Gly	Val	Asn	His	
				155					160					165	
Leu	Gly	His	Phe	Leu	Leu	Thr	Asn	Leu	Leu	Leu	Gly	Leu	Leu	Lys	
				170					175					180	
Ser	Ser	Ala	Pro	Ser	Arg	Ile	Val	Val	Val	Ser	Ser	Lys	Leu	Tyr	
				185					190					195	
Lys	Tyr	Gly	Asp	Ile	Asn	Phe	Asp	Asp	Leu	Asn	Ser	Glu	Gln	Ser	
				200					205					210	
Tyr	Asn	Lys	Ser	Phe	Cys	Tyr	Ser	Arg	Ser	Lys	Leu	Ala	Asn	Ile	
				215					220					225	
Leu	Phe	Thr	Arg	Glu	Leu	Ala	Arg	Arg	Leu	Glu	Gly	Thr	Asn	Val	
				230					235					240	
Thr	Val	Asn	Val	Leu	His	Pro	Gly	Ile	Val	Arg	Thr	Asn	Leu	Gly	
				245					250					255	
Arg	His	Ile	His	Ile	Pro	Leu	Leu	Val	Lys	Pro	Leu	Phe	Asn	Leu	
				260					265					270	
Val	Ser	Trp	Ala	Phe	Phe	Lys	Thr	Pro	Val	Glu	Gly	Ala	Gln	Thr	
				275					280					285	
Ser	Ile	Tyr	Leu	Ala	Ser	Ser	Pro	Glu	Val	Glu	Gly	Val	Ser	Gly	
				290					295					300	
Arg	Tyr	Phe	Gly	Asp	Cys	Lys	Glu	Glu	Glu	Leu	Leu	Pro	Lys	Ala	
				305					310					315	
Met	Asp	Glu	Ser	Val	Ala	Arg	Lys	Leu	Trp	Asp	Ile	Ser	Glu	Val	
				320					325					330	
Met	Val	Gly	Leu	Leu	Lys										

<210> 304  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 20, 34, 62, 87, 221, 229  
 <223> unknown base

<400> 304  
 ggggattgta aagaggaagn actgtgccca aagntatgga tgaatctgtt 50  
 gcaagaaaat tntgggatat cagtgaagtg atggttngcc tgctaaaata 100  
 ggaacaagga gtaaaagagc tgtttataaa actgcatatc agttatatct 150  
 gtgatcagga atgggtgtgga ttgagaactt gttacttgaa gaaaaagaat 200  
 tttgatattg gaatagcctg ntaagaggna catgtgggta ttttggagtt 250  
 actgaaaaat tatttttggg ataagagaat ttcagcaaag atgttttaaa 300  
 tatatatagt aagtataatg aataataagt acaatgaaaa atacaattat 350  
 attgtaaaat tataactggg caagcatgga tgacatatta atatttgtca 400  
 gaattaagtg actcaaagtg ctatcgagag gtttttcaag tatctttgag 450  
 tttcatggcc aaagtgttaa ctagttttac tacaatgttt ggtgtttgtg 500  
 tggaaattat ctgcctggct t 521

<210> 305  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 305  
 ccaggaaatg ctccaggaag agcc 24

<210> 306  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 306  
 gcccatgaca ccaaattgaa gagtgg 26

<210> 307

09978192.101501

<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 307  
aacgcagggga tcttccagtg cccttacatg aagactgaag atggg 45

<210> 308  
<211> 1523  
<212> DNA  
<213> Homo sapiens

<400> 308  
gagaggacga ggtgccgctg cctggagaat cctccgctgc cgtcggctcc 50  
cggagcccag ccctttccta acccaaccca acctagccca gtcccagccg 100  
ccagcgcctg tccctgtcac ggaccccagc gttaccatgc atcctgccgt 150  
cttcctatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 200  
gggtttttac tctgttaaca actgaaataa caagtcttgc tacagagaat 250  
atagatgaaa ttttaaacaa tgctgatgtt gctttagtaa atttttatgc 300  
tgactggtgt cgtttcagtc agatgttgca tccaattttt gaggaagctt 350  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 400  
agagttgatt gtgatcagca ctctgacata gcccagagat acaggataag 450  
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 500  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggcaa 550  
caaaaaagtg accccattca agaaattcgg gacttagcag aaatcaccac 600  
tcttgatcgc agcaaaagaa atatcattgg atattttgag caaaaggact 650  
cggacaacta tagagttttt gaacgagtag cgaatatttt gcatgatgac 700  
tgtgcctttc tttctgcatt tggggatgtt tcaaaaccgg aaagatatag 750  
tggcgacaac ataatctaca aaccaccagg gcattctgct ccggatatgg 800  
tgtacttggg agctatgaca aattttgatg tgacttaca ttggattcaa 850  
gataaatgtg ttcctcttgt ccgagaaata acatttgaaa atggagagga 900  
attgacagaa gaaggactgc cttttctcat actctttcac atgaaagaag 950  
atacagaaag tttagaaata ttccagaatg aagtagctcg gcaattaata 1000  
agtgaaaaag gtacaataaa ctttttacat gccgattgtg acaaatttag 1050

acatcctctt ctgcacatac agaaaactcc agcagattgt cctgtaatcg 1100  
ctattgacag ctttaggcac atgtatgtgt ttggagactt caaagatgta 1150  
ttaattcctg gaaaactcaa gcaattcgta tttgacttac attctggaaa 1200  
actgcacaga gaattccatc atggacctga cccaactgat acagccccag 1250  
gagagcaagc ccaagatgta gcaagcagtc cacctgagag ctccttcag 1300  
aaactagcac ccagtgaata taggtatact ctattgaggg atcgagatga 1350  
gctttaaaaaa cttgaaaaac agtttgtaag cctttcaaca gcagcatcaa 1400  
cctacgtggt ggaaatagta aacctatatt ttcataattc tatgtgtatt 1450  
tttattttga ataaacagaa agaaatttaa aaaaaaaaaa aaaaaaaaaa 1500  
aaaaaaaaaa aaaaaaaaaa aaa 1523

<210> 309  
<211> 406  
<212> PRT  
<213> Homo sapiens

<400> 309  
Met His Pro Ala Val Phe Leu Ser Leu Pro Asp Leu Arg Cys Ser  
1 5 10 15  
Leu Leu Leu Leu Val Thr Trp Val Phe Thr Pro Val Thr Thr Glu  
20 25 30  
Ile Thr Ser Leu Ala Thr Glu Asn Ile Asp Glu Ile Leu Asn Asn  
35 40 45  
Ala Asp Val Ala Leu Val Asn Phe Tyr Ala Asp Trp Cys Arg Phe  
50 55 60  
Ser Gln Met Leu His Pro Ile Phe Glu Glu Ala Ser Asp Val Ile  
65 70 75  
Lys Glu Glu Phe Pro Asn Glu Asn Gln Val Val Phe Ala Arg Val  
80 85 90  
Asp Cys Asp Gln His Ser Asp Ile Ala Gln Arg Tyr Arg Ile Ser  
95 100 105  
Lys Tyr Pro Thr Leu Lys Leu Phe Arg Asn Gly Met Met Met Lys  
110 115 120  
Arg Glu Tyr Arg Gly Gln Arg Ser Val Lys Ala Leu Ala Asp Tyr  
125 130 135  
Ile Arg Gln Gln Lys Ser Asp Pro Ile Gln Glu Ile Arg Asp Leu  
140 145 150  
Ala Glu Ile Thr Thr Leu Asp Arg Ser Lys Arg Asn Ile Ile Gly  
155 160 165

Tyr	Phe	Glu	Gln	Lys	Asp	Ser	Asp	Asn	Tyr	Arg	Val	Phe	Glu	Arg
				170					175					180
Val	Ala	Asn	Ile	Leu	His	Asp	Asp	Cys	Ala	Phe	Leu	Ser	Ala	Phe
				185					190					195
Gly	Asp	Val	Ser	Lys	Pro	Glu	Arg	Tyr	Ser	Gly	Asp	Asn	Ile	Ile
				200					205					210
Tyr	Lys	Pro	Pro	Gly	His	Ser	Ala	Pro	Asp	Met	Val	Tyr	Leu	Gly
				215					220					225
Ala	Met	Thr	Asn	Phe	Asp	Val	Thr	Tyr	Asn	Trp	Ile	Gln	Asp	Lys
				230					235					240
Cys	Val	Pro	Leu	Val	Arg	Glu	Ile	Thr	Phe	Glu	Asn	Gly	Glu	Glu
				245					250					255
Leu	Thr	Glu	Glu	Gly	Leu	Pro	Phe	Leu	Ile	Leu	Phe	His	Met	Lys
				260					265					270
Glu	Asp	Thr	Glu	Ser	Leu	Glu	Ile	Phe	Gln	Asn	Glu	Val	Ala	Arg
				275					280					285
Gln	Leu	Ile	Ser	Glu	Lys	Gly	Thr	Ile	Asn	Phe	Leu	His	Ala	Asp
				290					295					300
Cys	Asp	Lys	Phe	Arg	His	Pro	Leu	Leu	His	Ile	Gln	Lys	Thr	Pro
				305					310					315
Ala	Asp	Cys	Pro	Val	Ile	Ala	Ile	Asp	Ser	Phe	Arg	His	Met	Tyr
				320					325					330
Val	Phe	Gly	Asp	Phe	Lys	Asp	Val	Leu	Ile	Pro	Gly	Lys	Leu	Lys
				335					340					345
Gln	Phe	Val	Phe	Asp	Leu	His	Ser	Gly	Lys	Leu	His	Arg	Glu	Phe
				350					355					360
His	His	Gly	Pro	Asp	Pro	Thr	Asp	Thr	Ala	Pro	Gly	Glu	Gln	Ala
				365					370					375
Gln	Asp	Val	Ala	Ser	Ser	Pro	Pro	Glu	Ser	Ser	Phe	Gln	Lys	Leu
				380					385					390
Ala	Pro	Ser	Glu	Tyr	Arg	Tyr	Thr	Leu	Leu	Arg	Asp	Arg	Asp	Glu
				395					400					405

Leu

<210> 310  
 <211> 182  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure



<222> 36, 48  
<223> unknown base

<400> 310  
attaaggaag aatttcctaaa tgaaaatcaa gtagtntttg ccagagtnga 50  
ttgtgatcag cactctgaca tagcccagag atacaggata agcaaatacc 100  
caaccctcaa attgtttcgt aatgggatga tgatgaagag agaatacagg 150  
ggtcagcgat cagtgaagc attggcagat ta 182

<210> 311  
<211> 598  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 38, 59, 140, 169, 174, 183, 282-283, 294-295, 319, 396  
<223> unknown base

<400> 311  
agaggcctct ctggaagttg tcccgggtgt tcgccgcngg agcccgggtc 50  
gagaggacna ggtgccgctg cctggagaat cctccgctgc cgtcgggtcc 100  
cggagcccag ccctttccta acccaaccca acctagccn gtcccagccg 150  
ccagcgctctg tccctgtcnc gganccagc gtnaccatgc atcctgccgt 200  
cttccctatcc ttacccgacc tcagatgctc ccttctgctc ctggtaactt 250  
gggtttttac tccctgtaaca actgaaataa cnngtcttga tacnnagaat 300  
atagatgaaa ttttaaacna tgctgatgtg gctttagtca atttttatgc 350  
tgactggtgt cgtttcagtc agatgtggca tccaattttt gaggangctt 400  
ccgatgtcat taaggaagaa tttccaaatg aaaatcaagt agtgtttgcc 450  
agagttgatt gtgatcagca ctctgacata gccagagat acaggataag 500  
caaataccca accctcaaat tgtttcgtaa tgggatgatg atgaagagag 550  
aatacagggg tcagcgatca gtgaaagcat tggcagatta catcaggc 598

<210> 312  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 312  
tgagaggcct ctctggaagt tg 22

<210> 313  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 313  
 gtcagcgatc agtgaaagc 19  
  
 <210> 314  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 314  
 ccagaatgaa gtagctcggc 20  
  
 <210> 315  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 315  
 ccgactcaaa atgcattgtc 20  
  
 <210> 316  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 316  
 catttggcag gaattgtcc 19  
  
 <210> 317  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 317  
 ggtgctatag gccaaagg 18  
  
 <210> 318  
 <211> 24  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 318

ctgtatctct gggctatgtc agag 24

<210> 319

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 319

ctacatataa tggcacatgt cagcc 25

<210> 320

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 320

cgtcttctta tccttaccgc acctcagatg ctcccttctg ctctg 46

<210> 321

<211> 1333

<212> DNA

<213> Homo sapiens

<400> 321

gcccacgcgt ccgatggcgt tcacgttcgc ggccttctgc tacatgctgg 50

cgctgctgct cactgcgcgc ctcatcttct tcgccatttg gcacattata 100

gcatttgatg agctgaagac tgattacaag aatcctatag accagtgtaa 150

tacctgaat ccccttgtag tcccagagta cctcatccac gctttcttct 200

gtgtcatgtt tctttgtgca gcagagtggc ttacactggg tctcaatatg 250

cccctcttgg catatcatat ttggagggtat atgagtagac cagtgatgag 300

tggcccagga ctctatgacc ctacaacat catgaatgca gatattctag 350

catattgtca gaaggaagga tgggtgcaa at tagcttttta tcttctagca 400

tttttttact acctatatgg catgatctat gttttggtga gctcttagaa 450

caacacacag aagaattggc ccagtttaagt gcatgcaaaa agccaccaa 500

tgaagggatt ctatccagca agatcctgtc caagagtagc ctgtggaatc 550

tgatcagtta ctttaaaaaa tgactcctta ttttttaa at gtttccacat 600  
 ttttgcttgt ggaaagactg ttttcatatg ttatactcag ataaagattt 650  
 taaatggtat tacgtataaa ttaatatata atgattacct ctggtgttga 700  
 caggtttgaa cttgcacttc ttaaggaaca gccataatcc tctgaatgat 750  
 gcattaatta ctgactgtcc tagtacattg gaagcttttg tttataggaa 800  
 cttgtagggc tcatttttgg ttcattgaaa cagtatctaa ttataaatta 850  
 gctgtagata tcaggtgctt ctgatgaagt gaaaatgtat atctgactag 900  
 tgggaaactt catgggtttc ctcatctgtc atgtcgatga ttatatatgg 950  
 atacatttac aaaaataaaa agcgggaatt ttcccttcgc ttgaatatta 1000  
 tccctgtata ttgcatgaat gagagatttc ccatatttcc atcagagtaa 1050  
 taaatatact tgctttaatt cttaagcata agtaaacaatg atataaaaat 1100  
 atatgctgaa ttacttgtga agaatgcatt taaagctatt ttaaagtgtg 1150  
 ttttatttgt aagacattac ttattaagaa attggttatt atgcttactg 1200  
 ttctaactcg gtggttaaagg tattcttaag aatttgcagg tactacagat 1250  
 tttcaaaact gaatgagaga aaattgtata accatcctgc tgttccttta 1300  
 gtgcaataca ataaaactct gaaattaaga ctc 1333

<210> 322  
 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 322  
 Met Ala Phe Thr Phe Ala Ala Phe Cys Tyr Met Leu Ala Leu Leu  
 1 5 10 15  
 Leu Thr Ala Ala Leu Ile Phe Phe Ala Ile Trp His Ile Ile Ala  
 20 25 30  
 Phe Asp Glu Leu Lys Thr Asp Tyr Lys Asn Pro Ile Asp Gln Cys  
 35 40 45  
 Asn Thr Leu Asn Pro Leu Val Leu Pro Glu Tyr Leu Ile His Ala  
 50 55 60  
 Phe Phe Cys Val Met Phe Leu Cys Ala Ala Glu Trp Leu Thr Leu  
 65 70 75  
 Gly Leu Asn Met Pro Leu Leu Ala Tyr His Ile Trp Arg Tyr Met  
 80 85 90  
 Ser Arg Pro Val Met Ser Gly Pro Gly Leu Tyr Asp Pro Thr Thr  
 95 100 105

Ile Met Asn Ala Asp Ile Leu Ala Tyr Cys Gln Lys Glu Gly Trp  
 110 115 120

Cys Lys Leu Ala Phe Tyr Leu Leu Ala Phe Phe Tyr Tyr Leu Tyr  
 125 130 135

Gly Met Ile Tyr Val Leu Val Ser Ser  
 140

<210> 323  
 <211> 477  
 <212> DNA  
 <213> Homo sapiens

<400> 323  
 attatagcat ttgatgagct gaagactgat tacaagatcc tatagaccag 50  
 tgtaataccc tgaatccct tgtactcca gactacctca tccacgcttt 100  
 cttctgtgtc atgtttcttt gtgcagcaga gtgggttaca ctgggtctca 150  
 atatgcccct cttggcatat catatttggg ggtatatgag tagaccagt 200  
 atgagtggcc caggactcta tgaccctaca accatcatga atgcagatat 250  
 tctagcatat tgtcagaagg aaggatggtg caaattagct ttttatcttc 300  
 tagcattttt ttactacctata tatggcatga tctatgtttt ggtgagctct 350  
 tagaacaaca cacagaagaa ttgggtccagt taagtgcattg caaaaagcca 400  
 ccaaatgaag ggattctatc cagcaagatc ctgtccaaga gtagcctgtg 450  
 gaatctgac agttacttta aaaaatg 477

<210> 324  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 324  
 tgtaaaacga cggccagtta aatagacctg caattattaa tct 43

<210> 325  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 325  
 caggaaacag ctatgaccac ctgcacacct gcaaattccat t 41

<210> 326

<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 326  
gtgcagcaga gtggcttaca 20

<210> 327  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 327  
actggaccaa ttcttctgtg 20

<210> 328  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 328  
gatattctag catattgtca gaaggaagga tgggtgcaaatt tagct 45

<210> 329  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 329  
cggacgcgtg ggggaaaccc ttccgagaaa acagcaacaa gctgagctgc 50  
tgtgacagag gggaacaaga tggcggcgcc gaaggggagc ctctgggtga 100  
ggacccaact ggggctcccg ccgctgctgc tgctgacctt ggccttggcc 150  
ggagggttcgg ggaccgcttc ggctgaagca ttgactcgg tcttgggtga 200  
tacggcgtct tgccaccggg cctgtcagtt gacctacccc ttgcacacct 250  
accctaagga agaggagttg tacgcatgtc agagagggtg caggctgttt 300  
tcaatttgtc agtttgtgga tgatggaatt gacttaaatt gaactaaatt 350  
ggaatgtgaa tctgcatgta cagaagcata ttcccaattt gatgagcaat 400  
atgcttgcca tcttggttgc cagaatcagc tgccattcgc tgaactgaga 450  
caagaacaac ttatgtccct gatgcaaaaa atgcacctac tctttcctct 500

aactctggtg aggtcattct ggagtgcacat gatggactcc gcacagagct 550  
tcataacctc ttcattggact ttttatcttc aagccgatga cggaaaaata 600  
gttatattcc agtctaagcc agaaatccag tacgcaccac atttgagca 650  
ggagcctaca aatttgagag aatcatctct aagcaaaatg tcctatctgc 700  
aaatgagaaa ttcacaagcg cacaggaatt ttcttgaaga tggagaaagt 750  
gatggctttt taagatgcct ctctcttaac tctgggtgga ttttaactac 800  
aactcttgct ctctoggtga tggatttgct ttggatttgt tgtgcaactg 850  
ttgctacagc tgtggagcag tatgttccct ctgagaagct gagtatctat 900  
ggtgacttgg agtttatgaa tgaacaaaag ctaaacagat atccagcttc 950  
ttctcttggtg gttgttagat ctaaaactga agatcatgaa gaagcagggc 1000  
ctctacctac aaaagtgaat ctgtctcatt ctgaaattta agcatttttc 1050  
ttttaaaaga caagtgtaat agacatctaa aattccactc ctcatagagc 1100  
ttttaaaatg gtttcattgg atataggcct taagaaatca ctataaaatg 1150  
caaataaagt tactcaaatc tgtg 1174

<210> 330

<211> 323

<212> PRT

<213> Homo sapiens

<400> 330

Met	Ala	Ala	Pro	Lys	Gly	Ser	Leu	Trp	Val	Arg	Thr	Gln	Leu	Gly
1				5					10					15
Leu	Pro	Pro	Leu	Leu	Leu	Leu	Thr	Met	Ala	Leu	Ala	Gly	Gly	Ser
			20						25					30
Gly	Thr	Ala	Ser	Ala	Glu	Ala	Phe	Asp	Ser	Val	Leu	Gly	Asp	Thr
			35						40					45
Ala	Ser	Cys	His	Arg	Ala	Cys	Gln	Leu	Thr	Tyr	Pro	Leu	His	Thr
			50						55					60
Tyr	Pro	Lys	Glu	Glu	Glu	Leu	Tyr	Ala	Cys	Gln	Arg	Gly	Cys	Arg
			65						70					75
Leu	Phe	Ser	Ile	Cys	Gln	Phe	Val	Asp	Asp	Gly	Ile	Asp	Leu	Asn
			80						85					90
Arg	Thr	Lys	Leu	Glu	Cys	Glu	Ser	Ala	Cys	Thr	Glu	Ala	Tyr	Ser
			95						100					105
Gln	Ser	Asp	Glu	Gln	Tyr	Ala	Cys	His	Leu	Gly	Cys	Gln	Asn	Gln
			110						115					120

Leu	Pro	Phe	Ala	Glu	Leu	Arg	Gln	Glu	Gln	Leu	Met	Ser	Leu	Met	
				125					130					135	
Pro	Lys	Met	His	Leu	Leu	Phe	Pro	Leu	Thr	Leu	Val	Arg	Ser	Phe	
				140					145					150	
Trp	Ser	Asp	Met	Met	Asp	Ser	Ala	Gln	Ser	Phe	Ile	Thr	Ser	Ser	
				155					160					165	
Trp	Thr	Phe	Tyr	Leu	Gln	Ala	Asp	Asp	Gly	Lys	Ile	Val	Ile	Phe	
				170					175					180	
Gln	Ser	Lys	Pro	Glu	Ile	Gln	Tyr	Ala	Pro	His	Leu	Glu	Gln	Glu	
				185					190					195	
Pro	Thr	Asn	Leu	Arg	Glu	Ser	Ser	Leu	Ser	Lys	Met	Ser	Tyr	Leu	
				200					205					210	
Gln	Met	Arg	Asn	Ser	Gln	Ala	His	Arg	Asn	Phe	Leu	Glu	Asp	Gly	
				215					220					225	
Glu	Ser	Asp	Gly	Phe	Leu	Arg	Cys	Leu	Ser	Leu	Asn	Ser	Gly	Trp	
				230					235					240	
Ile	Leu	Thr	Thr	Thr	Leu	Val	Leu	Ser	Val	Met	Val	Leu	Leu	Trp	
				245					250					255	
Ile	Cys	Cys	Ala	Thr	Val	Ala	Thr	Ala	Val	Glu	Gln	Tyr	Val	Pro	
				260					265					270	
Ser	Glu	Lys	Leu	Ser	Ile	Tyr	Gly	Asp	Leu	Glu	Phe	Met	Asn	Glu	
				275					280					285	
Gln	Lys	Leu	Asn	Arg	Tyr	Pro	Ala	Ser	Ser	Leu	Val	Val	Val	Arg	
				290					295					300	
Ser	Lys	Thr	Glu	Asp	His	Glu	Glu	Ala	Gly	Pro	Leu	Pro	Thr	Lys	
				305					310					315	
Val	Asn	Leu	Ala	His	Ser	Glu	Ile								
				320											

<210> 331  
 <211> 350  
 <212> DNA  
 <213> Homo sapiens

<400> 331  
 ttgggtgata cggcgtcttg ccaccgggcc tgtcagttga cctaccctt 50  
 gcacacctac cctaaggaag aggagttgta cgcattgtcag agagggttgca 100  
 ggctgttttc aatttgtag tttgtggatg atggaattga cttaaattga 150  
 actaaattgg aatgtgaatc tgcattgtaca gaagcatatt cccaattctga 200  
 tgagcaatat gcttgccatc ttggttgcca gaatcagctg ccattcgtg 250



aactgagaca agaacaactt atgtccctga tgccaaaaat gcacctactc 300  
 ttctctctaa ctctgggtgag gtcattctgg agtgacatga tggactccgc 350

<210> 332  
 <211> 562  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 47  
 <223> unknown base

<400> 332  
 cacactggcc ggatctttta gagtcctttg accttgacca agggctcngga 50  
 aaacagcaac aagctgagct gctgtgacag agggaacaag atggcggcgc 100  
 cgaagggagc ctttgggtga ggacccaact ggggctcccg ccgctgctgc 150  
 tgctgaccat ggcccttgcc ggaggttcgg ggaccgcttc ggctgaagca 200  
 ttgactcgg tcttgggtga tacggcgtct tgccaccggg cctgtcagtt 250  
 gacctacccc ttgcacacct accctaagga agaggagttg tacgcatgtc 300  
 agagaggttg caggctgttt tcaatttgtc agtttgtgga tgatggaatt 350  
 gacttaaata gaactaaatt ggaatgtgaa totgcatgta cagaagcata 400  
 ttcccaatct gatgagcaat atgcttgcca tcttggttgc cagaatcagc 450  
 tgccattcgc tgaactgaga caagaacaac ttatgtccct gatgccaaaa 500  
 atgcacctac tctttcctct aactctggtg aggtcattct ggagtgcacat 550  
 gatggactcc gc 562

<210> 333  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 333  
 acaagctgag ctgctgtgac ag 22

<210> 334  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 334  
tgattctggc aaccaagatg gc 22

<210> 335  
<211> 40  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 335  
atggccttgg ccggagggtc ggggaccgct tcggctgaag 40

<210> 336  
<211> 1885  
<212> DNA  
<213> Homo sapiens

<400> 336  
gcgagggtggc gatcgctgag aggcaggagg gccgaggcgg gcctgggagg 50  
cgggccggag gtggggcgcc gctggggccg gcccgcacgg gcttcatctg 100  
agggcgcacg gcccgcgacc gagcgtgcgg actggcctcc caagcgtggg 150  
gcgacaagct gccggagctg caatggggccg cggttgggga ttcttgtttg 200  
gcctcctggg cgccgtgtgg ctgctcagct cgggccacgg agaggagcag 250  
cccccgaga cagcggcaca gaggtgcttc tgccaggtta gtggttactt 300  
ggatgattgt acctgtgatg ttgaaacat tgatagattt aataactaca 350  
ggctttttccc aagactacaa aaacttcttg aaagtgacta ctttaggtat 400  
tacaaggtaa acctgaagag gccgtgtcct ttctggaatg acatcagcca 450  
gtgtggaaga agggactgtg ctgtcaaacc atgtcaatct gatgaagttc 500  
ctgatggaat taaatctgcg agctacaagt attctgaaga agccaataat 550  
ctcattgaag aatgtgaaca agctgaacga cttggagcag tggatgaatc 600  
tctgagttag gaaacacaga aggtgttct tcagtggacc aagcatgatg 650  
attcttcaga taacttctgt gaagctgatg acattcagtc ccctgaagct 700  
gaatatgtag atttgcttct taatcctgag cgctacactg gttacaaggg 750  
accagatgct tggaaaatat ggaatgtcat ctacgaagaa aactgtttta 800  
agccacagac aattaaaaga cttttaaatc ctttggcttc tggtaaggg 850  
acaagtgaag agaacacttt ttacagttgg ctagaaggtc tctgtgtaga 900  
aaaaagagca ttctacagac ttatatctgg cctacatgca agcattaatg 950

tgcatttgag tgcaagatat cttttacaag agacctgggt agaaaagaaa 1000  
 tggggacaca acattacaga atttcaacag cgatttgatg gaattttgac 1050  
 tgaaggagaa ggtccaagaa ggcttaagaa cttgtatfff ctctacttaa 1100  
 tagaactaag ggctttatcc aaagtgttac cattcttoga gcgcccagat 1150  
 tttcaactct ttactggaaa taaaattcag gatgaggaaa acaaaatggt 1200  
 acttctggaa atacttcatg aaatcaagtc atttcctttg cattttgatg 1250  
 agaattcatt ttttgcggg gataaaaaag aagcacacaa actaaaggag 1300  
 gactttcgac tgcattttag aaatatttca agaattatgg attgtgttgg 1350  
 ttgttttaaa tgtcgtctgt ggggaaagct tcagactcag ggtttgggca 1400  
 ctgctctgaa gatcttattt tctgagaaat tgatagcaaa tatgccagaa 1450  
 agtggaccta gttatgaatt ccatctaacc agacaagaaa tagtatcatt 1500  
 attcaacgca tttggaagaa tttctacaag tgtgaaagaa ttagaaaact 1550  
 tcaggaactt gttacagaat attcattaaa gaaaacaagc tgatatgtgc 1600  
 ctgtttctgg acaatggagg cgaaagagtg gaatttcatt caaaggcata 1650  
 atagcaatga cagtcttaag ccaaacattt tatataaagt tgcttttgta 1700  
 aaggagaatt atattgtttt aagtaaacac atttttaaaa attgtgttaa 1750  
 gtctatgtat aatactactg tgagtaaaag taatacttta ataatgtggt 1800  
 acaaatttta aagtttaata ttgaataaaa ggaggattat caaattaata 1850  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1885

<210> 337  
 <211> 468  
 <212> PRT  
 <213> Homo sapiens

<400> 337  
 Met Gly Arg Gly Trp Gly Phe Leu Phe Gly Leu Leu Gly Ala Val  
   1                  5                  10                  15  
 Trp Leu Leu Ser Ser Gly His Gly Glu Glu Gln Pro Pro Glu Thr  
                   20                  25                  30  
 Ala Ala Gln Arg Cys Phe Cys Gln Val Ser Gly Tyr Leu Asp Asp  
                   35                  40                  45  
 Cys Thr Cys Asp Val Glu Thr Ile Asp Arg Phe Asn Asn Tyr Arg  
                   50                  55                  60  
 Leu Phe Pro Arg Leu Gln Lys Leu Leu Glu Ser Asp Tyr Phe Arg  
                   65                  70                  75

Tyr	Tyr	Lys	Val	Asn	Leu	Lys	Arg	Pro	Cys	Pro	Phe	Trp	Asn	Asp	
				80					85					90	
Ile	Ser	Gln	Cys	Gly	Arg	Arg	Asp	Cys	Ala	Val	Lys	Pro	Cys	Gln	
				95					100					105	
Ser	Asp	Glu	Val	Pro	Asp	Gly	Ile	Lys	Ser	Ala	Ser	Tyr	Lys	Tyr	
				110					115					120	
Ser	Glu	Glu	Ala	Asn	Asn	Leu	Ile	Glu	Glu	Cys	Glu	Gln	Ala	Glu	
				125					130					135	
Arg	Leu	Gly	Ala	Val	Asp	Glu	Ser	Leu	Ser	Glu	Glu	Thr	Gln	Lys	
				140					145					150	
Ala	Val	Leu	Gln	Trp	Thr	Lys	His	Asp	Asp	Ser	Ser	Asp	Asn	Phe	
				155					160					165	
Cys	Glu	Ala	Asp	Asp	Ile	Gln	Ser	Pro	Glu	Ala	Glu	Tyr	Val	Asp	
				170					175					180	
Leu	Leu	Leu	Asn	Pro	Glu	Arg	Tyr	Thr	Gly	Tyr	Lys	Gly	Pro	Asp	
				185					190					195	
Ala	Trp	Lys	Ile	Trp	Asn	Val	Ile	Tyr	Glu	Glu	Asn	Cys	Phe	Lys	
				200					205					210	
Pro	Gln	Thr	Ile	Lys	Arg	Pro	Leu	Asn	Pro	Leu	Ala	Ser	Gly	Gln	
				215					220					225	
Gly	Thr	Ser	Glu	Glu	Asn	Thr	Phe	Tyr	Ser	Trp	Leu	Glu	Gly	Leu	
				230					235					240	
Cys	Val	Glu	Lys	Arg	Ala	Phe	Tyr	Arg	Leu	Ile	Ser	Gly	Leu	His	
				245					250					255	
Ala	Ser	Ile	Asn	Val	His	Leu	Ser	Ala	Arg	Tyr	Leu	Leu	Gln	Glu	
				260					265					270	
Thr	Trp	Leu	Glu	Lys	Lys	Trp	Gly	His	Asn	Ile	Thr	Glu	Phe	Gln	
				275					280					285	
Gln	Arg	Phe	Asp	Gly	Ile	Leu	Thr	Glu	Gly	Glu	Gly	Pro	Arg	Arg	
				290					295					300	
Leu	Lys	Asn	Leu	Tyr	Phe	Leu	Tyr	Leu	Ile	Glu	Leu	Arg	Ala	Leu	
				305					310					315	
Ser	Lys	Val	Leu	Pro	Phe	Phe	Glu	Arg	Pro	Asp	Phe	Gln	Leu	Phe	
				320					325					330	
Thr	Gly	Asn	Lys	Ile	Gln	Asp	Glu	Glu	Asn	Lys	Met	Leu	Leu	Leu	
				335					340					345	
Glu	Ile	Leu	His	Glu	Ile	Lys	Ser	Phe	Pro	Leu	His	Phe	Asp	Glu	
				350					355					360	
Asn	Ser	Phe	Phe	Ala	Gly	Asp	Lys	Lys	Glu	Ala	His	Lys	Leu	Lys	

09978192-101501

	365		370		375
Glu Asp Phe Arg	Leu His Phe Arg Asn	Ile Ser Arg Ile Met	Asp		
	380		385		390
Cys Val Gly Cys	Phe Lys Cys Arg Leu	Trp Gly Lys Leu Gln	Thr		
	395		400		405
Gln Gly Leu Gly	Thr Ala Leu Lys Ile	Leu Phe Ser Glu Lys	Leu		
	410		415		420
Ile Ala Asn Met	Pro Glu Ser Gly Pro	Ser Tyr Glu Phe His	Leu		
	425		430		435
Thr Arg Gln Glu	Ile Val Ser Leu Phe	Asn Ala Phe Gly Arg	Ile		
	440		445		450
Ser Thr Ser Val	Lys Glu Leu Glu Asn	Phe Arg Asn Leu Leu	Gln		
	455		460		465

Asn Ile His

<210> 338  
 <211> 507  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 101, 263, 376, 397, 426  
 <223> unknown base

<400> 338  
 gctggaaata tggatgtcat ctacgagaaa ctgttttaag ccacagacaa 50  
 ttaaaagacc tttaaactct ttggcttctg gtcaagggac aagtgaagag 100  
 nacacttttt acagttggct agaaggtctc tgtgtagaaa aaagagcatt 150  
 ctacagactt atatctggcc tacatgcaag cattaatgtg catttgagtg 200  
 caagatatct tttaacaagag acctgggttag aaaagaaatg gggacacaac 250  
 attacagaat ttnaacagcg atttgatgga attttgactg aaggagaagg 300  
 tccaagaagg cttaagaact tgtattttct ctacttaata gaactaaggg 350  
 ctttatccaa agtgttacca ttcttngagc gccagattt tcaactnttt 400  
 actggaaata aaattcagga tgaggnaaac aaaatgttac ttttgaaaat 450  
 acttcatgaa atcaagtcatt ttcctttgca ttttgatgag aattcatttt 500  
 tttgctg 507

<210> 339  
 <211> 20

<212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 339  
 aagctgccgg agctgcaatg 20  
  
 <210> 340  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 340  
 ttgcttctta atcctgagcg c 21  
  
 <210> 341  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 341  
 aaaggaggac tttcgactgc 20  
  
 <210> 342  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 342  
 agagattcat ccactgctcc aagtcg 26  
  
 <210> 343  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 343  
 tgtccagaaa caggcacata tcagc 25  
  
 <210> 344  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 344

agacagcggc acagaggtgc ttctgccagg ttagtggtta cttggatgat 50

<210> 345

<211> 1486

<212> DNA

<213> Homo sapiens

<400> 345

cggacgcgtg ggcggacgcg tggcggacg cgtgggttgg gagggggcag 50

gatgggaggg aaagtgaaga aaacagaaaa ggagagggac agaggccaga 100

ggactttctca tactggacag aaaccgatca ggcatggaac tcccccttct 150

cactcacctg ttcttgcccc tgggtgttct gacaggtctc tgctccccct 200

ttaacctgga tgaacatcac ccacgcctat tcccagggcc accagaagct 250

gaatttggat acagtgtctt acaacatgtt gggggtggac agcgatggat 300

gctggtgggc gccccctggg atgggccttc aggcgaccgg aggggggacg 350

tttatcgctg ccctgtaggg ggggcccaaca atgccccatg tgccaagggc 400

cacttaggtg actaccaact gggaaattca tctcatctct ctgtgaatat 450

gcacctgggg atgtctctgt tagagacaga tggatgatgg ggattcatgg 500

tgagctaagg agaggggtgt ggcagtgtct ctgaagggtcc ataaaagaaa 550

aaagagaagt gtggtgaagg aaaatggtct gtgtggaggg gtcaaggagt 600

taaaaaccct agaaagcaaa aggtaggtaa tgtcaggag tagtcttcat 650

gcctccttca actgggagca tgttctgagg gtgccctccc aagcctggga 700

gtaactatct ccccatccc caggcctgtg cccctctctg gtctcgtgct 750

tgtggcagct ctgtcttcag ttctgggata tgtgccctgt tggatgcttc 800

attccagcct cagggaagcc tggcaccac tgcccaacgt gagccagagg 850

aaggctgagt acttggttcc cagaaggaga tactgggtgg gaaaaagatg 900

gggcaaagcg gtatgatgcc tggcaaagg cctgcatggc taccctcatt 950

gctacctaat gtgcttgcaa aagctccatg tttcctaaca gattcagact 1000

cctggccagg tgtggtggcc cacacctgta attctagcac tttgggaggc 1050

caaggtgggc agatcacttg aggtcaggag ttcaagacca gcctggccaa 1100

catggtgaaa ctccatctct actaaaaaaa aaaaaatata aaaattagct 1150

09978192.101501

gggtgcgcta gtgcatgcct gtaatctcat ctactcgga ggctaagaca 1200  
 ggagactctc acttcaaccc aggaggtgga ggttgcggtg agccaagatt 1250  
 gtgcctctgc actctagcgt gggtgacaga gtaagcgaga ctccatctca 1300  
 aaaataataa taataataat tcagactcct tatcaggagt ccatgatctg 1350  
 gcctggcaca gtaactcatg cctgtaatcc caacattttg ggaggccaac 1400  
 gcaggaggat tgcttgaggt ctggagggtt gagaccagcc tgggcaacat 1450  
 agaaagaccc catctctaaa taaatgtttt aaaaaat 1486

<210> 346  
 <211> 124  
 <212> PRT  
 <213> Homo sapiens

<400> 346  
 Met Glu Leu Pro Phe Val Thr His Leu Phe Leu Pro Leu Val Phe  
 1 5 10 15  
 Leu Thr Gly Leu Cys Ser Pro Phe Asn Leu Asp Glu His His Pro  
 20 25 30  
 Arg Leu Phe Pro Gly Pro Pro Glu Ala Glu Phe Gly Tyr Ser Val  
 35 40 45  
 Leu Gln His Val Gly Gly Gly Gln Arg Trp Met Leu Val Gly Ala  
 50 55 60  
 Pro Trp Asp Gly Pro Ser Gly Asp Arg Arg Gly Asp Val Tyr Arg  
 65 70 75  
 Cys Pro Val Gly Gly Ala His Asn Ala Pro Cys Ala Lys Gly His  
 80 85 90  
 Leu Gly Asp Tyr Gln Leu Gly Asn Ser Ser His Pro Ala Val Asn  
 95 100 105  
 Met His Leu Gly Met Ser Leu Leu Glu Thr Asp Gly Asp Gly Gly  
 110 115 120  
 Phe Met Val Ser

<210> 347  
 <211> 509  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 22  
 <223> unknown base

<400> 347



cacagttccc caccatcact cntcccatc cttccaactt tatttttagc 50  
 ttgccattgg gagggggcag gatgggaggg aaagtgaaga aaacagaaaa 100  
 ggagagggac agaggccaga ggactttctca tactggacag aaaccgatca 150  
 ggcatggaac tccccttcgt cactcacctg ttcttgcccc tgggtgttcct 200  
 gacaggtctc tgctccccct ttaacctgga tgaacatcac ccacgcctat 250  
 tcccagggcc accagaagct gaatttggat acagtgtctt acaacatggt 300  
 gggggtggac agcgatggat gctggtgggc gccccctggg atgggccttc 350  
 aggcgaccgg aggggggacg tttatcgctg ccctgtaggg ggggccca 400  
 atgccccatg tgccaagggc cacttaggtg actaccaact gggaaattca 450  
 tctcatcctg ctgtgaatat gcacctgggg atgtctctgt tagagacaga 500  
 tggatgatgg 509

<210> 348  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 348  
 agggacagag gccagaggac ttc 23

<210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 349  
 caggtgcata ttcacagcag gatg 24

<210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 350  
 ggaactcccc ttctgctc acctgttctt gccccctggtg ttct 45

<210> 351  
 <211> 2056  
 <212> DNA

<213> Homo sapiens

<400> 351

aaagttacat tttctctgga actctcctag gccactccct gctgatgcaa 50  
catctggggtt tgggcagaaa ggaggggtgct tcggagcccg ccctttctga 100  
gcttcctggg ccggctctag aacaattcag gcttcgctgc gactcagacc 150  
tcagctccaa catatgcatt ctgaagaaag atggctgaga tggacagaat 200  
gctttatttt ggaaagaaac aatgttctag gtcaaactga gtctaccaa 250  
tgcagacttt cacaatgggt ctagaagaaa tctggacaag tcttttcatg 300  
tggtttttct acgcattgat tccatgtttg ctacagatg aagtggccat 350  
tctgcctgcc cctcagaacc tctctgtact ctcaaccaac atgaagcatc 400  
tcttgatgtg gagcccagtg atcgcgcctg gagaaacagt gtactattct 450  
gtcgaatacc aggggggagta cgagagcctg tacacgagcc acatctggat 500  
ccccagcagc tgggtgctcac tcaactgaagg tcttgagtgt gatgtcactg 550  
atgacatcac ggccactgtg ccatacaacc ttcgtgtcag ggccacattg 600  
ggctcacaga cctcagcctg gagcatcctg aagcatccct ttaatagaaa 650  
ctcaaccatc cttaccogac ctgggatgga gatcaccaa gatggcttcc 700  
acctggttat tgagctggag gacctggggc ccagtttga gttccttctg 750  
gcctactgga ggaggagcc tggtgccgag gaacatgtca aaatgggtgag 800  
gagtgggggt attccagtc acctagaaac catggagcca ggggctgcat 850  
actgtgtgaa ggcccagaca ttcgtgaagg ccattgggag gtacagcgcc 900  
ttcagccaga cagaatgtgt ggaggtgcaa ggagaggcca tccccctggt 950  
actggccctg tttgcctttg ttggcttcat gctgacctt gtggctcgtgc 1000  
cactgttcgt ctggaaaatg ggccggctgc tccagtactc ctgttgcccc 1050  
gtggtggtcc tcccagacac cttgaaaata accaattcac cccagaagtt 1100  
aatcagctgc agaaggagg aggtggatgc ctgtgccacg gctgtgatgt 1150  
ctcctgagga actcctcagg gcctggatct cataggtttg cggaagggcc 1200  
caggtgaagc cgagaacctg gtctgcatga catggaaacc atgaggggac 1250  
aagttgtgtt tctgttttcc gccacggaca agggatgaga gaagtaggaa 1300  
gagcctgttg totacaagtc tagaagcaac catcagagga aggggtggtt 1350  
gtctaacaga aactgactg aggccttaggg gatgtgacct ctgactggg 1400

ggctgccact tgctggctga gcaaccctgg gaaaagtgac ttcattccctt 1450  
 cggtcctaag ttttctcatc tgtaatgggg gaattaccta cacacctgct 1500  
 aaacacacac acacagagtc tctctctata tatacacacg tacacataaa 1550  
 tacacccagc acttgcaagg ctagagggaa actgggtgaca ctctacagtc 1600  
 tgactgattc agtgtttctg gagagcagga cataaatgta tgatgagaat 1650  
 gatcaaggac tctacacact ggggtggcttg gagagcccac tttcccagaa 1700  
 taatccttga gagaaaagga atcatgggag caatgggtgtt gagttcactt 1750  
 caagcccaat gccggtgcag aggggaatgg cttagcgagc tctacagtag 1800  
 gtgacctgga ggaaggtcac agccacactg aaaatgggat gtgcatgaac 1850  
 acggaggatc catgaactac tgtaaagtgt tgacagtgtg tgcacactgc 1900  
 agacagcagg tgaaatgtat gtgtgcaatg cgacgagaat gcagaagtca 1950  
 gtaacatgtg catgtttgtt gtgctccttt tttctgttgg taaagtacag 2000  
 aattcagcaa ataaaaaggg ccaccctggc caaaagcggg aaaaaaaaaa 2050  
 aaaaaa 2056

<210> 352  
 <211> 311  
 <212> PRT  
 <213> Homo sapiens

<400> 352  
 Met Gln Thr Phe Thr Met Val Leu Glu Glu Ile Trp Thr Ser Leu  
 1 5 10 15  
 Phe Met Trp Phe Phe Tyr Ala Leu Ile Pro Cys Leu Leu Thr Asp  
 20 25 30  
 Glu Val Ala Ile Leu Pro Ala Pro Gln Asn Leu Ser Val Leu Ser  
 35 40 45  
 Thr Asn Met Lys His Leu Leu Met Trp Ser Pro Val Ile Ala Pro  
 50 55 60  
 Gly Glu Thr Val Tyr Tyr Ser Val Glu Tyr Gln Gly Glu Tyr Glu  
 65 70 75  
 Ser Leu Tyr Thr Ser His Ile Trp Ile Pro Ser Ser Trp Cys Ser  
 80 85 90  
 Leu Thr Glu Gly Pro Glu Cys Asp Val Thr Asp Asp Ile Thr Ala  
 95 100 105  
 Thr Val Pro Tyr Asn Leu Arg Val Arg Ala Thr Leu Gly Ser Gln  
 110 115 120

Thr	Ser	Ala	Trp	Ser	Ile	Leu	Lys	His	Pro	Phe	Asn	Arg	Asn	Ser	125	130	135
Thr	Ile	Leu	Thr	Arg	Pro	Gly	Met	Glu	Ile	Thr	Lys	Asp	Gly	Phe	140	145	150
His	Leu	Val	Ile	Glu	Leu	Glu	Asp	Leu	Gly	Pro	Gln	Phe	Glu	Phe	155	160	165
Leu	Val	Ala	Tyr	Trp	Arg	Arg	Glu	Pro	Gly	Ala	Glu	Glu	His	Val	170	175	180
Lys	Met	Val	Arg	Ser	Gly	Gly	Ile	Pro	Val	His	Leu	Glu	Thr	Met	185	190	195
Glu	Pro	Gly	Ala	Ala	Tyr	Cys	Val	Lys	Ala	Gln	Thr	Phe	Val	Lys	200	205	210
Ala	Ile	Gly	Arg	Tyr	Ser	Ala	Phe	Ser	Gln	Thr	Glu	Cys	Val	Glu	215	220	225
Val	Gln	Gly	Glu	Ala	Ile	Pro	Leu	Val	Leu	Ala	Leu	Phe	Ala	Phe	230	235	240
Val	Gly	Phe	Met	Leu	Ile	Leu	Val	Val	Val	Pro	Leu	Phe	Val	Trp	245	250	255
Lys	Met	Gly	Arg	Leu	Leu	Gln	Tyr	Ser	Cys	Cys	Pro	Val	Val	Val	260	265	270
Leu	Pro	Asp	Thr	Leu	Lys	Ile	Thr	Asn	Ser	Pro	Gln	Lys	Leu	Ile	275	280	285
Ser	Cys	Arg	Arg	Glu	Glu	Val	Asp	Ala	Cys	Ala	Thr	Ala	Val	Met	290	295	300
Ser	Pro	Glu	Glu	Leu	Leu	Arg	Ala	Trp	Ile	Ser					305	310	

<210> 353  
 <211> 864  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 654, 711, 748, 827  
 <223> unknown base

<400> 353  
 tcctgctgat gcacatctgg gtttggcaaa aggagggttg ttcgagccgc 50  
 cttttctagc ttcttgccg gctctagaac aattcaggct tcgctgcgac 100  
 tagacctcag ctccaacata tgcattctga agaaagatgg ctgagatgac 150  
 agaatgcttt attttggaaa gaaacaatgt tctaggtcaa actgagtcta 200

ccaaatgcag actttcacaa tggttctaga agaaatctgg acaagtcttt 250  
 tcatgtgggt tttctacgca ttgattccat gtttgctcac agatgaagtg 300  
 gccattctgc ctgcccctca gaacctctct gtactctcaa ccaacatgaa 350  
 gcatctcttg atgtggagcc cagtgatcgc gcctggagaa acagtgtact 400  
 attctgtcga ataccagggg gagtacgaga gcctgtacac gagccacatc 450  
 tggatcccca gcagctgggt ctcaactcact gaaggctctg agtgtgatgt 500  
 cactgatgac atcacggcca ctgtgccata caacctttgt gtcagggcca 550  
 cattgggctc acagacctca gcctggagca tcttgaagca tccctttaat 600  
 agaaactcaa ccatccttac ccgacctggg atggagatca ccaaagatgg 650  
 cttncacctg gttattgagc tggaggacct ggggccccag tttgagttcc 700  
 ttgtggccta ntggaggagg ggcgaacccc ttgcggcgca aggggttngc 750  
 gaacccttg cggccgctgg ggtatctctc gagaaaagag aggcccaata 800  
 tgaccacat actcaatatg gacgaantgc tattgtccac ctgtttgagt 850  
 ggcgctgggt tgat 864

- <210> 354
- <211> 23
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 354
- aggcttcgct gcgactagac ctc 23
- <210> 355
- <211> 24
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe
- <400> 355
- ccaggtcggg taaggatggt tgag 24
- <210> 356
- <211> 50
- <212> DNA
- <213> Artificial Sequence
- <220>
- <223> Synthetic oligonucleotide probe

<400> 356  
tttctacgca ttgattccat gtttgctcac agatgaagtg gccattctgc 50

<210> 357  
<211> 1670  
<212> DNA  
<213> Homo sapiens

<400> 357  
cccacgcgtc cgcccacgcg tccgagggac aagagagaag agagactgaa 50  
acagggagaa gaggcaggag aggaggaggt ggggagagca cgaagctgga 100  
ggccgacact gagggagggc gggaggaggt gaagaaggag agaggggaga 150  
agaggcagga gctggaaagg agagagggag gaggaggagg agatgcggga 200  
tgagagacct gagttaggtg gcttgggaga gcttaatgaa aagagaacgg 250  
agaggaggtg tgggttagga accaagaggt agccctgtgg gcagcagaag 300  
gctgagagga gtaggaagat caggagctag agggagactg gagggttccg 350  
ggaaaagagc agaggaaaga ggaaagacac agagagacgg gagagagaag 400  
aagagtgggt ttgaagggcg gatctcagtc cctggctgct ttggcatttg 450  
gggaactggg actccctgtg gggaggagag gaaagctgga agtcctggag 500  
ggacagggtc ccagaaggag gggacagagg agctgagaga ggggggcagg 550  
gcgttgggca ggggtccctc ggaggcctcc tggggatggg ggctgcagct 600  
cgtctgagcg cccctcgagc gctggtactc tgggctgcac tgggggcagc 650  
agctcacatc ggaccagcac ctgaccccga ggactggtgg agctacaagg 700  
ataatctcca gggaaacttc gtgccagggc ctcctttctg gggcctggtg 750  
aatgcagcgt ggagtctgtg tgctgtgggg aagcggcaga gcccctgga 800  
tgtggagctg aagagggttc tttatgacct ctttctgccc ccattaaggc 850  
tcagcactgg aggagagaag ctccggggaa ccttgtacaa caccggccga 900  
catgtctcct tcctgcctgc accccgacct gtggtcaatg tgtctggagg 950  
tcccctcctt tacagccacc gactcagtga actgcggctg ctgtttggag 1000  
ctcgcgacgg agccggctcg gaacatcaga tcaaccacca gggcttctct 1050  
gctgaggtgc agctcattca cttcaaccag gaactctacg ggaatttcag 1100  
cgctgcctcc cgcggcccca atggcctggc cattctcagc ctctttgtca 1150  
acgttgccag tacctctaac ccattcctca gtcgcctcct taaccgagac 1200  
accatcactc gcattctcta caagaatgat gcctactttc ttcaagacct 1250

09978192.10501

gagcctggag ctctgttcc ctgaatcctt cggcttcac acctatcagg 1300  
gctctctcag caccgcccc tgctccgaga ctgtcacctg gatcctcatt 1350  
gaccgggccc tcaatatcac ctcccttcag atgcactccc tgagactcct 1400  
gagccagaat cctccatctc agatcttcca gagcctcagc ggtaacagcc 1450  
ggcccctgca gcccttgccc cacagggcac tgaggggcaa cagggacccc 1500  
cggcaccgag agaggcgctg ccgaggcccc aactaccgcc tgcattgtga 1550  
tggtgtcccc catggtcgtt gagactcccc ttcgaggatt gcacccgccc 1600  
gtcctaagcc tccccacaag gcgaggggag ttaccacctaa aacaaagcta 1650  
ttaaaggagc agaatactta 1670

<210> 358  
<211> 328  
<212> PRT  
<213> Homo sapiens

<400> 358  
Met Gly Ala Ala Ala Arg Leu Ser Ala Pro Arg Ala Leu Val Leu  
1 5 10 15  
Trp Ala Ala Leu Gly Ala Ala Ala His Ile Gly Pro Ala Pro Asp  
20 25 30  
Pro Glu Asp Trp Trp Ser Tyr Lys Asp Asn Leu Gln Gly Asn Phe  
35 40 45  
Val Pro Gly Pro Pro Phe Trp Gly Leu Val Asn Ala Ala Trp Ser  
50 55 60  
Leu Cys Ala Val Gly Lys Arg Gln Ser Pro Val Asp Val Glu Leu  
65 70 75  
Lys Arg Val Leu Tyr Asp Pro Phe Leu Pro Pro Leu Arg Leu Ser  
80 85 90  
Thr Gly Gly Glu Lys Leu Arg Gly Thr Leu Tyr Asn Thr Gly Arg  
95 100 105  
His Val Ser Phe Leu Pro Ala Pro Arg Pro Val Val Asn Val Ser  
110 115 120  
Gly Gly Pro Leu Leu Tyr Ser His Arg Leu Ser Glu Leu Arg Leu  
125 130 135  
Leu Phe Gly Ala Arg Asp Gly Ala Gly Ser Glu His Gln Ile Asn  
140 145 150  
His Gln Gly Phe Ser Ala Glu Val Gln Leu Ile His Phe Asn Gln  
155 160 165  
Glu Leu Tyr Gly Asn Phe Ser Ala Ala Ser Arg Gly Pro Asn Gly

	170		175		180
Leu Ala Ile Leu Ser Leu Phe Val Asn Val Ala Ser Thr Ser Asn					
	185		190		195
Pro Phe Leu Ser Arg Leu Leu Asn Arg Asp Thr Ile Thr Arg Ile					
	200		205		210
Ser Tyr Lys Asn Asp Ala Tyr Phe Leu Gln Asp Leu Ser Leu Glu					
	215		220		225
Leu Leu Phe Pro Glu Ser Phe Gly Phe Ile Thr Tyr Gln Gly Ser					
	230		235		240
Leu Ser Thr Pro Pro Cys Ser Glu Thr Val Thr Trp Ile Leu Ile					
	245		250		255
Asp Arg Ala Leu Asn Ile Thr Ser Leu Gln Met His Ser Leu Arg					
	260		265		270
Leu Leu Ser Gln Asn Pro Pro Ser Gln Ile Phe Gln Ser Leu Ser					
	275		280		285
Gly Asn Ser Arg Pro Leu Gln Pro Leu Ala His Arg Ala Leu Arg					
	290		295		300
Gly Asn Arg Asp Pro Arg His Pro Glu Arg Arg Cys Arg Gly Pro					
	305		310		315
Asn Tyr Arg Leu His Val Asp Gly Val Pro His Gly Arg					
	320		325		

<210> 359

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 359

tctgctgagg tgcagctcat tcac 24

<210> 360

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 360

gaggctctgg aagatctgag atgg 24

<210> 361

<211> 50

<212> DNA

<213> Artificial Sequence



<220>

<223> Synthetic oligonucleotide probe

<400> 361

gcctctttgt caacgttgcc agtacctcta acccattcct cagtcgcctc 50

<210> 362

<211> 3038

<212> DNA

<213> Homo sapiens

<400> 362

ggcgcctggt tctgcgcgta ctggctgtac ggagcaggag caagaggctc 50

ccgccagcct ccgccgccga gcctcgttcg tgtccccgcc cctcgtcctc 100

gcagctactg ctcagaaaacg ctggggcgcc caccctggca gactaacgaa 150

gcagctccct tcccacccca actgcaggtc taattttgga cgctttgcct 200

gccatttctt ccaggttgag ggagccgcag aggcggaggc tcgcgtattc 250

ctgcagtcag caccacgctc gcccccgac gctcgtgct caggcccttc 300

gcgagcgggg ctctccgtct gcggtccctt gtgaaggctc tgggcggctg 350

cagaggccgg ccgtccggtt tggctcacct ctcccaggaa acttcacact 400

ggagagccaa aaggagtga agagcctgtc ttggagattt tcctggggaa 450

atcctgaggt cattcattat gaagtgtacc gcgcgggagt ggctcagagt 500

aaccacagtg ctgttcatgg ctagagcaat tccagccatg gtggttccca 550

atgccacttt attggagaaa cttttggaaa aatacatgga tgaggatggt 600

gagtgtgga tagccaaaca acgagggaaa agggccatca cagacaatga 650

catgcagagt attttggacc ttcataataa attacgaagt cagggtgtatc 700

caacagcctc taatatggag tatatgacat gggatgtaga gctggaaaga 750

tctgcagaat cctgggctga aagttgcttg tgggaacatg gacctgcaag 800

cttgcttcca tcaattggac agaatttggg agcacactgg ggaagatata 850

ggcccccgac gtttcatgta caatcgtggt atgatgaagt gaaagacttt 900

agctacccat atgaacatga atgcaaccca tattgtccat tcagggtgtc 950

tggccctgta tgtacacatt atacacaggc cgtgtgggca actagtaaca 1000

gaatcggttg tgccattaat ttgtgtcata acatgaacat ctgggggagc 1050

atatggccca aagctgtcta cctggtgtgc aattactccc caaagggaaa 1100

ctggtggggc catgcccctt acaaacatgg gcggccctgt tctgcttgcc 1150

cacctagttt tggagggggc tgtagagaaa atctgtgcta caaagaagg 1200  
tcagacaggt attatcccc tcgagaagag gaaacaaatg aaatagaacg 1250  
acagcagtca caagtccatg acacccatgt ccggacaaga tcagatgata 1300  
gtagcagaaa tgaagtcata agcgcacagc aaatgtccca aattgtttct 1350  
tgtgaagtaa gattaagaga tcagtgc aaa ggaacaacct gcaataggta 1400  
cgaatgtcct gctggctgtt tggatagtaa agctaaagtt attggcagtg 1450  
tacattatga aatgcaatcc agcatctgta gagctgcaat tcattatgg 1500  
ataatagaca atgatgggtg ctgggtagat atcactagac aaggaagaaa 1550  
gcattatttc atcaagtcca atagaaatgg tattcaaaca attggcaa 1600  
atcagtctgc taattccttc acagtctcta aagtaacagt tcaggctgtg 1650  
acttgtgaaa caactgtgga acagctctgt ccatttcata agcctgcttc 1700  
acattgccc agagtatact gtcctcgtaa ctgtatgcaa gcaaatccac 1750  
attatgctcg tgtaattgga actcgagttt attctgatct gtccagtatc 1800  
tgcagagcag cagtacatgc tggagtgggt cgaaatcacg gtgggttatgt 1850  
tgatgtaatg cctgtggaca aaagaaagac ctacattgct tcttttcaga 1900  
atggaatctt ctcagaaagt ttacagaatc ctccaggagg aaaggcattc 1950  
agagtgtttg ctgttgtgtg aaactgaata cttggaagag gaccataaag 2000  
actattccaa atgcaatatt tctgaatttt gtataaaaact gtaacattac 2050  
tgtacagagt acatcaacta ttttcagccc aaaaagggtgc caaatgcata 2100  
taaactctga taaacaaagt ctataaaaata aaacatggga cattagcttt 2150  
gggaaaagta atgaaaatat aatggtttta gaaatcctgt gttaaataatt 2200  
gctatatatt cttagcagtt atttctacag ttaattacat agtcatgatt 2250  
gttctacgtt tcatatatta tatggtgctt tgtatatgcc actaataaaa 2300  
tgaatctaaa cattgaatgt gaatggccct cagaaaatca tctagtgc 2350  
ttaaaaataa tcgactctaa aactgaaaga aaccttatca cattttcccc 2400  
agttcaatgc tatgccatta ccaactccaa ataatctcaa ataattttcc 2450  
acttaataac tgtaaagttt ttttctgtta atttaggc atagaatatt 2500  
aaattctgat attgcacttc ttattttata taaaataatc ctttaatatc 2550  
caaatgaatc tgttaaaatg tttgattcct tgggaatggc cttaaaaata 2600

aatgtaataa agtcagagtg gtggtatgaa aacattccta gtgatcatgt 2650  
 agtaaatgta gggttaagca tggacagcca gagctttcta tgtactgtta 2700  
 aaattgaggt cacatatattt cttttgtatc ctggcaaata ctctgcagg 2750  
 ccaggaagta taatagcaaa aagttgaaca aagatgaact aatgtattac 2800  
 attaccattg ccactgattt tttttaaatg gtaaatgacc ttgtatataa 2850  
 atattgccat atcatggtac ctataatggt gatataatttg tttctatgaa 2900  
 aaatgtattg tgctttgata ctaaaaaatct gtaaaatggt agttttggta 2950  
 attttttttc tgctggtgga tttacatatt aaattttttc tgctggtgga 3000  
 taaacattaa aattaatcat gtttcaaaaa aaaaaaaa 3038

<210> 363  
 <211> 500  
 <212> PRT  
 <213> Homo sapiens

<400> 363  
 Met Lys Cys Thr Ala Arg Glu Trp Leu Arg Val Thr Thr Val Leu  
 1 5 10 15  
 Phe Met Ala Arg Ala Ile Pro Ala Met Val Val Pro Asn Ala Thr  
 20 25 30  
 Leu Leu Glu Lys Leu Leu Glu Lys Tyr Met Asp Glu Asp Gly Glu  
 35 40 45  
 Trp Trp Ile Ala Lys Gln Arg Gly Lys Arg Ala Ile Thr Asp Asn  
 50 55 60  
 Asp Met Gln Ser Ile Leu Asp Leu His Asn Lys Leu Arg Ser Gln  
 65 70 75  
 Val Tyr Pro Thr Ala Ser Asn Met Glu Tyr Met Thr Trp Asp Val  
 80 85 90  
 Glu Leu Glu Arg Ser Ala Glu Ser Trp Ala Glu Ser Cys Leu Trp  
 95 100 105  
 Glu His Gly Pro Ala Ser Leu Leu Pro Ser Ile Gly Gln Asn Leu  
 110 115 120  
 Gly Ala His Trp Gly Arg Tyr Arg Pro Pro Thr Phe His Val Gln  
 125 130 135  
 Ser Trp Tyr Asp Glu Val Lys Asp Phe Ser Tyr Pro Tyr Glu His  
 140 145 150  
 Glu Cys Asn Pro Tyr Cys Pro Phe Arg Cys Ser Gly Pro Val Cys  
 155 160 165  
 Thr His Tyr Thr Gln Val Val Trp Ala Thr Ser Asn Arg Ile Gly

170					175					180				
Cys	Ala	Ile	Asn	Leu	Cys	His	Asn	Met	Asn	Ile	Trp	Gly	Gln	Ile
				185					190					195
Trp	Pro	Lys	Ala	Val	Tyr	Leu	Val	Cys	Asn	Tyr	Ser	Pro	Lys	Gly
				200					205					210
Asn	Trp	Trp	Gly	His	Ala	Pro	Tyr	Lys	His	Gly	Arg	Pro	Cys	Ser
				215					220					225
Ala	Cys	Pro	Pro	Ser	Phe	Gly	Gly	Gly	Cys	Arg	Glu	Asn	Leu	Cys
				230					235					240
Tyr	Lys	Glu	Gly	Ser	Asp	Arg	Tyr	Tyr	Pro	Pro	Arg	Glu	Glu	Glu
				245					250					255
Thr	Asn	Glu	Ile	Glu	Arg	Gln	Gln	Ser	Gln	Val	His	Asp	Thr	His
				260					265					270
Val	Arg	Thr	Arg	Ser	Asp	Asp	Ser	Ser	Arg	Asn	Glu	Val	Ile	Ser
				275					280					285
Ala	Gln	Gln	Met	Ser	Gln	Ile	Val	Ser	Cys	Glu	Val	Arg	Leu	Arg
				290					295					300
Asp	Gln	Cys	Lys	Gly	Thr	Thr	Cys	Asn	Arg	Tyr	Glu	Cys	Pro	Ala
				305					310					315
Gly	Cys	Leu	Asp	Ser	Lys	Ala	Lys	Val	Ile	Gly	Ser	Val	His	Tyr
				320					325					330
Glu	Met	Gln	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Ile	His	Tyr	Gly	Ile
				335					340					345
Ile	Asp	Asn	Asp	Gly	Gly	Trp	Val	Asp	Ile	Thr	Arg	Gln	Gly	Arg
				350					355					360
Lys	His	Tyr	Phe	Ile	Lys	Ser	Asn	Arg	Asn	Gly	Ile	Gln	Thr	Ile
				365					370					375
Gly	Lys	Tyr	Gln	Ser	Ala	Asn	Ser	Phe	Thr	Val	Ser	Lys	Val	Thr
				380					385					390
Val	Gln	Ala	Val	Thr	Cys	Glu	Thr	Thr	Val	Glu	Gln	Leu	Cys	Pro
				395					400					405
Phe	His	Lys	Pro	Ala	Ser	His	Cys	Pro	Arg	Val	Tyr	Cys	Pro	Arg
				410					415					420
Asn	Cys	Met	Gln	Ala	Asn	Pro	His	Tyr	Ala	Arg	Val	Ile	Gly	Thr
				425					430					435
Arg	Val	Tyr	Ser	Asp	Leu	Ser	Ser	Ile	Cys	Arg	Ala	Ala	Val	His
				440					445					450
Ala	Gly	Val	Val	Arg	Asn	His	Gly	Gly	Tyr	Val	Asp	Val	Met	Pro
				455					460					465

Val Asp Lys Arg Lys Thr Tyr Ile Ala Ser Phe Gln Asn Gly Ile  
 470 475 480

Phe Ser Glu Ser Leu Gln Asn Pro Pro Gly Gly Lys Ala Phe Arg  
 485 490 495

Val Phe Ala Val Val  
 500

<210> 364  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 364  
 ggacagaatt tgggagcaca ctgg 24

<210> 365  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 365  
 ccaagagtat actgtcctcg 20

<210> 366  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 366  
 agcacagatt ttctctacag ccccc 25

<210> 367  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 367  
 aaccactcca gcatgtactg ctgc 24

<210> 368  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 368

ccattcaggt gttctggccc tgtatgtaca cattatacac aggtcgtgtg 50

<210> 369

<211> 1685

<212> DNA

<213> Homo sapiens

<400> 369

gcggagacaa gcgcagagcg cagcgcacgg ccacagacag ccctgggcat 50

ccaccgacgg cgcagccgga gccagcagag ccggaaggcg cgccccgggc 100

agagaaaagcc gagcagagct ggggtggcgtc tccgggcccgc cgctccgacg 150

ggccagcgcc ctccccatgt ccctgctccc acgccgcgcc cctccggtca 200

gcatgaggct cctggcggcc gcgctgctcc tgctgctgct ggcgctgtac 250

accgcgcgtg tggacgggtc caaatgcaag tgctcccga agggacccaa 300

gatccgctac agcgacgtga agaagctgga aatgaagcca aagtacccgc 350

actgcgagga gaagatggtt atcatcacca ccaagagcgt gtccaggtac 400

cgaggtcagg agcactgcct gcacccaag ctgcagagca ccaagcgctt 450

catcaagtgg tacaacgcct ggaacgagaa gcgcagggtc tacgaagaat 500

agggtgaaaa acctcagaag ggaaaactcc aaaccagttg ggagacttgt 550

gcaaaggact ttgcagatta aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600

aaaaaaaaaa aaagcctttc tttctcacag gcataagaca caaattatat 650

attgttatga agcacttttt accaacggtc agtttttaca ttttatagct 700

gcgtgcgaaa ggcttccaga tgggagaccc atctctcttg tgctccagac 750

ttcatcacag gctgcttttt atcaaaaagg ggaaaactca tgcctttcct 800

ttttaaaaaa tgcttttttg tatttgtcca tacgtcacta tacatctgag 850

ctttataagc gcccgaggag aacaatgagc ttggtggaca catttcattg 900

cagtgttgct ccattcctag cttgggaagc ttccgcttag aggtcctggc 950

gcctcggcac agctgccacg ggctctcctg ggcttatggc cggtcacagc 1000

ctcagtgtga ctccacagtg gccctgtag ccgggcaagc aggagcaggt 1050

ctctctgcat ctgttctctg aggaactcaa gtttggttgc cagaaaaatg 1100

tgcttcattc cccctgggtt aatttttaca caccctagga aacatttcca 1150

09978192.10501

agatcctgtg atggcgagac aaatgacct taaagaaggt gtggggtctt 1200  
 tcccaacctg aggatttctg aaagggtcac aggttcaata tttaatgctt 1250  
 cagaagcatg tgagggtccc aacactgtca gcaaaaacct taggagaaaa 1300  
 cttaaaaata tatgaatata tgcgcaatac acagctacag acacacattc 1350  
 tgttgacaag ggaaaacctt caaagcatgt ttctttccct caccacaaca 1400  
 gaacatgcag tactaaagca atatatttgt gattcccat gtaattcttc 1450  
 aatgttaaag agtgagtc tctttcgaaa gctaagatga ccatgcgccc 1500  
 tttcctctgt acatataccc ttaagaacgc cccctccaca cactgcccc 1550  
 cagtatatgc cgcattgtac tgctgtgtta tatgctatgt acatgtcaga 1600  
 aaccattagc attgcatgca ggtttcatat tctttctaag atggaaagta 1650  
 ataaaatata tttgaaatgt aaaaaaaaaa aaaaa 1685

<210> 370  
 <211> 111  
 <212> PRT  
 <213> Homo sapiens

<400> 370  
 Met Ser Leu Leu Pro Arg Arg Ala Pro Pro Val Ser Met Arg Leu  
 1 5 10 15  
 Leu Ala Ala Ala Leu Leu Leu Leu Leu Ala Leu Tyr Thr Ala  
 20 25 30  
 Arg Val Asp Gly Ser Lys Cys Lys Cys Ser Arg Lys Gly Pro Lys  
 35 40 45  
 Ile Arg Tyr Ser Asp Val Lys Lys Leu Glu Met Lys Pro Lys Tyr  
 50 55 60  
 Pro His Cys Glu Glu Lys Met Val Ile Ile Thr Thr Lys Ser Val  
 65 70 75  
 Ser Arg Tyr Arg Gly Gln Glu His Cys Leu His Pro Lys Leu Gln  
 80 85 90  
 Ser Thr Lys Arg Phe Ile Lys Trp Tyr Asn Ala Trp Asn Glu Lys  
 95 100 105  
 Arg Arg Val Tyr Glu Glu  
 110

<210> 371  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 371

cagcgccctc cccatgtccc tg 22

<210> 372

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 372

tcccaactgg tttggagttt tccc 24

<210> 373

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 373

ctccggtcag catgaggctc ctggcggccg ctgctcctgc tgctg 45

<210> 374

<211> 3113

<212> DNA

<213> Homo sapiens

<400> 374

gccccaggga ctgctatggc ttcctttgtt gttcaccccg gtctgctca 50

tggttaaactc caatgtctc ctgtgggttaa ctgctcttgc catcaagttc 100

accctcattg acagccaagc acagtatcca gttgtcaaca caaattatgg 150

caaaatccgg ggcctaagaa caccgttacc caatgagatc ttgggtccag 200

tggagcagta cttaggggtc ccctatgcct cccccccac tggagagagg 250

cggtttcagc cccagaacc cccgtcctcc tggactggca tccgaaatac 300

tactcagttt gctgctgtgt gccccagca cctggatgag agatccttac 350

tgcatgacat gctgcccac tgggtttaccg ccaatttgga tactttgatg 400

acctatgttc aagatcaaaa tgaagactgc ctttacttaa acatctacgt 450

gcccacggaa gatggagcca acacaaagaa aaacgcagat gatataacga 500

gtaatgaccg tgggtgaagac gaagatattc atgatcagaa cagtaagaag 550

cccgatcatgg tctatatcca tgggggatct tacatggagg gcaccggcaa 600

catgattgac ggcagcattt tggcaagcta cggaacgctc atcgtgatca 650



ccattaacta ccgtctgga atactaggt ttttaagtac cggtagaccag 700  
gcagcaaaag gcaactatgg gtccttgat cagattcaag cactgcggtg 750  
gattgaggag aatgtgggag cctttggcgg ggacccaag agagtgaacca 800  
tctttggctc gggggctggg gcctcctgtg tcagcctgtt gaccctgtcc 850  
cactactcag aaggtctctt ccagaaggcc atcattcaga gcggcaccgc 900  
cctgtccagc tgggcagtga actaccagcc ggccaagtac actcggatat 950  
tggcagacaa ggtaggctgc aacatgctgg acaccacgga catggtagaa 1000  
tgctgcgga acaagaacta caaggagctc atccagcaga ccatcacccc 1050  
ggccacctac cacatagcct tcggggccggt gatcgacggc gacgtcatcc 1100  
cagacgaccc ccagatcctg atggagcaag gcgagttcct caactacgac 1150  
atcatgctgg gcgtcaacca aggggaaggc ctgaagtctg tggacggcat 1200  
cgtggataac gaggacggtg tgacgccaa cgactttgac ttctccgtgt 1250  
ccaacttcgt ggacaacott tacggctacc ctgaaggga agacactttg 1300  
cgggagacta tcaagttcat gtacacagac tggggcgata aggaaaaccc 1350  
ggagacgcgg cggaacccc tgggtggctct ctttactgac caccagtggg 1400  
tggccccgc cgtggccgcc gacctgcacg cgcagtagcg ctccccacc 1450  
tacttctatg ccttctatca tcaactgcaa agcgaaatga agcccagctg 1500  
ggcagattcg gcccatggtg atgaggtccc ctatgtcttc ggcatcccca 1550  
tgatcggctc caccgagctc ttcagttgta acttttccaa gaacgacgtc 1600  
atgctcagcg ccgtggtcat gacctactgg acgaacttcg ccaaaactgg 1650  
tgatccaaat caaccagttc ctcaggatac caagttcatt cacacaaaac 1700  
ccaaccgctt tgaagaagtg gcctgggtcca agtataatcc caaagaccag 1750  
ctctatctgc atattggctt gaaaccaga gtgagagatc actaccgggc 1800  
aacgaaagtg gctttctggt tggaactcgt tcctcatttg cacaacttga 1850  
acgagatatt ccagtatggt tcaacaacca caaaggttcc tccaccagac 1900  
atgacatcat ttccctatgg caccggcgga tctcccgcca agatatggcc 1950  
aaccacaaa cgccagcaa tcaactcctg caacaatccc aaacactcta 2000  
aggaccctca caaacaggg cctgaggaca caactgtcct cattgaaacc 2050  
aaacgagatt attccaccga attaagtgtc accattgccg tcggggcgctc 2100

gctcctcttc ctcaacatct tagcttttgc ggcgctgtac tacaaaaagg 2150  
acaagaggcg ccatgagact cacaggcgcc ccagtcccca gagaaacacc 2200  
acaaatgata tcgctcacat ccagaacgaa gagatcatgt ctctgcagat 2250  
gaagcagctg gaacacgac acgagtgtga gtcgctgcag gcacacgaca 2300  
cactgaggct cacctgcccg ccagactaca ccctcacgct gcgcccgtcg 2350  
ccagatgaca tcccacttat gacgccaaac accatcacca tgattccaaa 2400  
cacactgacg gggatgcagc ctttgcacac tttaaacc ttcagtggag 2450  
gacaaaacag tacaaattta cccacggac attccaccac tagagtatag 2500  
ctttgcccta tttcccttcc tatccctctg ccctaccgc tcagcaacat 2550  
agaagagga aggaaagaga gaaggaaaga gagagagaaa gaaagtctcc 2600  
agaccaggaa tgtttttgtc ccaactgactt aagacaaaaa tgcaaaaagg 2650  
cagtcatccc atcccggcag acccttatcg ttggtgtttt ccagtattac 2700  
aagatcaact tctgaccctg tgaaatgtga gaagtacaca tttctgttaa 2750  
aataactgct ttaagatctc taccactcca atcaatgttt agtgtgatag 2800  
gacatcacca tttcaaggcc ccgggtgttt ccaacgtcat ggaagcagct 2850  
gacacttctg aaactcagcc aaggacactt gatatttttt aattacaatg 2900  
gaagtttaaa catttctttc tgtgccacac aatggatggc tctccttaag 2950  
tgaagaaaga gtcaatgaga ttttgcccag cacatggagc tgtaatccag 3000  
agagaaggaa acgtagaaat ttattattaa aagaatggac tgtgcagcga 3050  
aatctgtacg gttctgtgca aagaggtgtt ttgccagcct gaactatatt 3100  
taagagactt tgt 3113

<210> 375

<211> 816

<212> PRT

<213> Homo sapiens

<400> 375

Met	Leu	Asn	Ser	Asn	Val	Leu	Leu	Trp	Leu	Thr	Ala	Leu	Ala	Ile
1				5				10						15

Lys	Phe	Thr	Leu	Ile	Asp	Ser	Gln	Ala	Gln	Tyr	Pro	Val	Val	Asn
			20					25						30

Thr	Asn	Tyr	Gly	Lys	Ile	Arg	Gly	Leu	Arg	Thr	Pro	Leu	Pro	Asn
			35					40						45

Glu	Ile	Leu	Gly	Pro	Val	Glu	Gln	Tyr	Leu	Gly	Val	Pro	Tyr	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

	50		55		60
Ser Pro Pro Thr	Gly 65	Glu Arg Arg Phe	Gln 70	Pro Pro Glu Pro	Pro 75
Ser Ser Trp Thr	Gly 80	Ile Arg Asn Thr	Thr 85	Gln Phe Ala Ala	Val 90
Cys Pro Gln His	Leu 95	Asp Glu Arg Ser	Leu 100	Leu His Asp Met	Leu 105
Pro Ile Trp Phe	Thr 110	Ala Asn Leu Asp	Thr 115	Leu Met Thr Tyr	Val 120
Gln Asp Gln Asn	Glu 125	Asp Cys Leu Tyr	Leu 130	Asn Ile Tyr Val	Pro 135
Thr Glu Asp Gly	Ala 140	Asn Thr Lys Lys	Asn 145	Ala Asp Asp Ile	Thr 150
Ser Asn Asp Arg	Gly 155	Glu Asp Glu Asp	Ile 160	His Asp Gln Asn	Ser 165
Lys Lys Pro Val	Met 170	Val Tyr Ile His	Gly 175	Gly Ser Tyr Met	Glu 180
Gly Thr Gly Asn	Met 185	Ile Asp Gly Ser	Ile 190	Leu Ala Ser Tyr	Gly 195
Asn Val Ile Val	Ile 200	Thr Ile Asn Tyr	Arg 205	Leu Gly Ile Leu	Gly 210
Phe Leu Ser Thr	Gly 215	Asp Gln Ala Ala	Lys 220	Gly Asn Tyr Gly	Leu 225
Leu Asp Gln Ile	Gln 230	Ala Leu Arg Trp	Ile 235	Glu Glu Asn Val	Gly 240
Ala Phe Gly Gly	Asp 245	Pro Lys Arg Val	Thr 250	Ile Phe Gly Ser	Gly 255
Ala Gly Ala Ser	Cys 260	Val Ser Leu Leu	Thr 265	Leu Ser His Tyr	Ser 270
Glu Gly Leu Phe	Gln 275	Lys Ala Ile Ile	Gln 280	Ser Gly Thr Ala	Leu 285
Ser Ser Trp Ala	Val 290	Asn Tyr Gln Pro	Ala 295	Lys Tyr Thr Arg	Ile 300
Leu Ala Asp Lys	Val 305	Gly Cys Asn Met	Leu 310	Asp Thr Thr Asp	Met 315
Val Glu Cys Leu	Arg 320	Asn Lys Asn Tyr	Lys 325	Glu Leu Ile Gln	Gln 330
Thr Ile Thr Pro	Ala 335	Thr Tyr His Ile	Ala 340	Phe Gly Pro Val	Ile 345

Asp Gly Asp Val	Ile Pro Asp Asp Pro	Gln Ile Leu Met Glu Gln	350	355	360
Gly Glu Phe Leu	Asn Tyr Asp Ile Met	Leu Gly Val Asn Gln Gly	365	370	375
Glu Gly Leu Lys	Phe Val Asp Gly Ile	Val Asp Asn Glu Asp Gly	380	385	390
Val Thr Pro Asn	Asp Phe Asp Phe Ser	Val Ser Asn Phe Val Asp	395	400	405
Asn Leu Tyr Gly	Tyr Pro Glu Gly Lys	Asp Thr Leu Arg Glu Thr	410	415	420
Ile Lys Phe Met	Tyr Thr Asp Trp Ala	Asp Lys Glu Asn Pro Glu	425	430	435
Thr Arg Arg Lys	Thr Leu Val Ala Leu	Phe Thr Asp His Gln Trp	440	445	450
Val Ala Pro Ala	Val Ala Ala Asp Leu	His Ala Gln Tyr Gly Ser	455	460	465
Pro Thr Tyr Phe	Tyr Ala Phe Tyr His	His Cys Gln Ser Glu Met	470	475	480
Lys Pro Ser Trp	Ala Asp Ser Ala His	Gly Asp Glu Val Pro Tyr	485	490	495
Val Phe Gly Ile	Pro Met Ile Gly Pro	Thr Glu Leu Phe Ser Cys	500	505	510
Asn Phe Ser Lys	Asn Asp Val Met Leu	Ser Ala Val Val Met Thr	515	520	525
Tyr Trp Thr Asn	Phe Ala Lys Thr Gly	Asp Pro Asn Gln Pro Val	530	535	540
Pro Gln Asp Thr	Lys Phe Ile His Thr	Lys Pro Asn Arg Phe Glu	545	550	555
Glu Val Ala Trp	Ser Lys Tyr Asn Pro	Lys Asp Gln Leu Tyr Leu	560	565	570
His Ile Gly Leu	Lys Pro Arg Val Arg	Asp His Tyr Arg Ala Thr	575	580	585
Lys Val Ala Phe	Trp Leu Glu Leu Val	Pro His Leu His Asn Leu	590	595	600
Asn Glu Ile Phe	Gln Tyr Val Ser Thr	Thr Thr Lys Val Pro Pro	605	610	615
Pro Asp Met Thr	Ser Phe Pro Tyr Gly	Thr Arg Arg Ser Pro Ala	620	625	630
Lys Ile Trp Pro	Thr Thr Lys Arg Pro	Ala Ile Thr Pro Ala Asn			

635	640	645
Asn Pro Lys His Ser Lys Asp Pro His Lys Thr Gly Pro Glu Asp		
650	655	660
Thr Thr Val Leu Ile Glu Thr Lys Arg Asp Tyr Ser Thr Glu Leu		
665	670	675
Ser Val Thr Ile Ala Val Gly Ala Ser Leu Leu Phe Leu Asn Ile		
680	685	690
Leu Ala Phe Ala Ala Leu Tyr Tyr Lys Lys Asp Lys Arg Arg His		
695	700	705
Glu Thr His Arg Arg Pro Ser Pro Gln Arg Asn Thr Thr Asn Asp		
710	715	720
Ile Ala His Ile Gln Asn Glu Glu Ile Met Ser Leu Gln Met Lys		
725	730	735
Gln Leu Glu His Asp His Glu Cys Glu Ser Leu Gln Ala His Asp		
740	745	750
Thr Leu Arg Leu Thr Cys Pro Pro Asp Tyr Thr Leu Thr Leu Arg		
755	760	765
Arg Ser Pro Asp Asp Ile Pro Leu Met Thr Pro Asn Thr Ile Thr		
770	775	780
Met Ile Pro Asn Thr Leu Thr Gly Met Gln Pro Leu His Thr Phe		
785	790	795
Asn Thr Phe Ser Gly Gly Gln Asn Ser Thr Asn Leu Pro His Gly		
800	805	810
His Ser Thr Thr Arg Val		
815		

<210> 376  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 376  
 ggcaagctac ggaaacgtca tcgtg 25

<210> 377  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 377

aacccccgag ccaaaagatg gtcac 25

<210> 378

<211> 47

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 378

gtaccggtga ccaggcagca aaaggcaact atgggctcct ggatcag 47

<210> 379

<211> 2461

<212> DNA

<213> Homo sapiens

<400> 379

gggaaagatg gcggcgactc tgggacccct tgggtcgtgg cagcagtggc 50

ggcgatgttt gtcggctcgg gatgggtcca ggatgttact ccttcttctt 100

ttgttggggc ctgggcaggg gccacagcaa gtcggggcgg gtcaaacgtt 150

cgagtacttg aaacgggagc actcgctgtc gaagccctac cagggtgtgg 200

gcacaggcag ttcctcactg tggaaatctga tgggcaatgc catggtgatg 250

accaggtata tccgccttac ccagatatg caaagtaaac aggggtgcctt 300

gtggaaccgg gtgccatgtt tcctgagaga ctgggagttg cagggtgcact 350

tcaaaatcca tggacaagga aagaagaatc tgcatgggga tggcttggca 400

atctggtaca caaaggatcg gatgcagcca gggcctgtgt ttggaaacat 450

ggacaaatth gtggggctgg gagtatttgt agacacctac cccaatgagg 500

agaagcagca agagcgggta ttcccctaca tctcagccat ggtgaacaac 550

ggctccctca gctatgatca tgagcgggat gggcggccta cagagctggg 600

aggctgcaca gccattgtcc gcaatcttca ttacgacacc ttcctggtga 650

ttcgctacgt caagaggcat ttgacgataa tgatggatat tgatggcaag 700

catgagtgga gggactgcat tgaagtgccg ggagtccgcc tgccccgcgg 750

ctactacttc ggcacctcct ccatcactgg ggatctctca gataatcatg 800

atgtcatttc cttgaagttg tttgaactga cagtggagag aaccccagaa 850

gaggaaaagc tccatcgaga tgtgttcttg ccctcagtgg acaatatgaa 900

gctgcctgag atgacagctc cactgccgcc cctgagtggc ctggccctct 950

tcctcatcgt ctttttctcc ctggtgtttt ctgtatttgc catagtcatt 1000

ggtatcatatc tctacaacaa atggcaggaa cagagccgaa agcgcttcta 1050  
 ctgagccctc ctgctgccac cacttttgtg actgtcaccc atgaggtatg 1100  
 gaaggagcag gcactggcct gagcatgcag cctggagagt gttcttgtct 1150  
 ctagcagctg gttggggact atattctgtc actggagttt tgaatgcagg 1200  
 gaccccgcat tcccatgggt gtgcatgggg acatctaact ctggtctggg 1250  
 aagccaccca cccagggca atgctgctgt gatgtgcctt tccctgcagt 1300  
 ccttccatgt gggagcagag gtgtgaagag aatttacgtg gttgtgatgc 1350  
 caaaatcaca gaacagaatt tcatagccca ggctgccgtg ttgtttgact 1400  
 cagaaggccc ttctacttca gttttgaatc cacaaagaat taaaaactgg 1450  
 taacaccaca ggctttctga ccattccattc gttgggtttt gcatttgacc 1500  
 caaccctctg cctacctgag gagctttctt tggaaaccag gatggaaact 1550  
 tcttccctgc cttaccttcc ttctactcca ttctattgtcc tctctgtgtg 1600  
 caacctgagc tgggaaaggc atttggtatgc ctctctgttg gggcctgggg 1650  
 ctgcagaaca cacctgcgtt tcaactggcct tcattaggtg gccctaggga 1700  
 gatggctttc tgctttggat cactgttccc tagcatgggt ctgggtcta 1750  
 ttggcatgtc catggccttc ccaatcaagt ctcttcaggc cctcagtga 1800  
 gtttggttaa aggttgggtg aaaaatcaag agaagcctgg aagacatcat 1850  
 ggatgccatg gattagctgt gcaactgacc agctccaggt ttgatcaaac 1900  
 caaaagcaac atttgtcatg tggctgacc atgtggagat gtttctggac 1950  
 ttgctagagc ctgcttagct gcatgttttg tagttacgat ttttggaaac 2000  
 ccactttgag tgctgaaagt gtaagggaagc tttcttctta caccttgggc 2050  
 ttggatattg cccagagaag aaatttggct ttttttttct taatggacaa 2100  
 gagacagtgt ctgttctcat gttccaagtc tgagagcaac agaccctcat 2150  
 catctgtgcc tggaagagtt cactgtcatt gagcagcaca gcctgagtgc 2200  
 tggcctctgt caacccttat tccactgcct tatttgacaa ggggttacat 2250  
 gctgtcacc ttactgccct gggattaaat cagttacagg ccagagtctc 2300  
 cttggagggc ctggaactct gagtcctcct atgaacctct gtagcctaaa 2350  
 tgaaattctt aaaatcaccc atggaaccaa aaaaaaaaaa aaaaagggcg 2400  
 gccgcgactc tagagtcgac ctgcagtagg gataacaggg taataagctt 2450

ggccgcatg g 2461

<210> 380

<211> 348

<212> PRT

<213> Homo sapiens

<400> 380

Met Ala Ala Thr Leu Gly Pro Leu Gly Ser Trp Gln Gln Trp Arg  
1 5 10 15

Arg Cys Leu Ser Ala Arg Asp Gly Ser Arg Met Leu Leu Leu Leu  
20 25 30

Leu Leu Leu Gly Ser Gly Gln Gly Pro Gln Gln Val Gly Ala Gly  
35 40 45

Gln Thr Phe Glu Tyr Leu Lys Arg Glu His Ser Leu Ser Lys Pro  
50 55 60

Tyr Gln Gly Val Gly Thr Gly Ser Ser Ser Leu Trp Asn Leu Met  
65 70 75

Gly Asn Ala Met Val Met Thr Gln Tyr Ile Arg Leu Thr Pro Asp  
80 85 90

Met Gln Ser Lys Gln Gly Ala Leu Trp Asn Arg Val Pro Cys Phe  
95 100 105

Leu Arg Asp Trp Glu Leu Gln Val His Phe Lys Ile His Gly Gln  
110 115 120

Gly Lys Lys Asn Leu His Gly Asp Gly Leu Ala Ile Trp Tyr Thr  
125 130 135

Lys Asp Arg Met Gln Pro Gly Pro Val Phe Gly Asn Met Asp Lys  
140 145 150

Phe Val Gly Leu Gly Val Phe Val Asp Thr Tyr Pro Asn Glu Glu  
155 160 165

Lys Gln Gln Glu Arg Val Phe Pro Tyr Ile Ser Ala Met Val Asn  
170 175 180

Asn Gly Ser Leu Ser Tyr Asp His Glu Arg Asp Gly Arg Pro Thr  
185 190 195

Glu Leu Gly Gly Cys Thr Ala Ile Val Arg Asn Leu His Tyr Asp  
200 205 210

Thr Phe Leu Val Ile Arg Tyr Val Lys Arg His Leu Thr Ile Met  
215 220 225

Met Asp Ile Asp Gly Lys His Glu Trp Arg Asp Cys Ile Glu Val  
230 235 240

Pro Gly Val Arg Leu Pro Arg Gly Tyr Tyr Phe Gly Thr Ser Ser  
245 250 255



Ile Thr Gly Asp	Leu Ser Asp Asn His Asp Val Ile Ser Leu Lys	
	260	265 270
Leu Phe Glu Leu Thr Val Glu Arg Thr	Pro Glu Glu Glu Lys Leu	
	275	280 285
His Arg Asp Val Phe Leu Pro Ser Val	Asp Asn Met Lys Leu Pro	
	290	295 300
Glu Met Thr Ala Pro Leu Pro Pro Leu	Ser Gly Leu Ala Leu Phe	
	305	310 315
Leu Ile Val Phe Phe Ser Leu Val Phe	Ser Val Phe Ala Ile Val	
	320	325 330
Ile Gly Ile Ile Leu Tyr Asn Lys Trp	Gln Glu Gln Ser Arg Lys	
	335	340 345

Arg Phe Tyr

<210> 381  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 381  
 ccttgggtcg tggcagcagt gg 22

<210> 382  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 382  
 cactctccag gctgcatgct cagg 24

<210> 383  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 383  
 gtcaaacggtt cgagtacttg aaacgggagc actcgctgtc gaagc 45

<210> 384  
 <211> 3150  
 <212> DNA  
 <213> Homo sapiens

<400> 384

ccgagccggg cgcgcagcga cggagctggg gccggcctgg gaccatgggc 50  
 gtgagtgcaa tctacggatc agtctctgat ggtgggtcgt taacctcagt 100  
 ggggactcca agatttccat gaagaaaatc agttgtcttc attcaagaat 150  
 tggggctctgg ctcaagaattc ctgcagctgg tgaaaatctg ttttctagaa 200  
 gaggtttaat taatgcctgc agtctgacat gttcccgatt tgaggtgaaa 250  
 ccatgaagag aaaatagaat acttaataat gcttttccgc aaccgcttct 300  
 tgctgctgct ggccctggct gcgctgctgg cctttgtgag cctcagcctg 350  
 cagttcttcc acctgatccc ggtgtcgact cctaagaatg gaatgagtag 400  
 caagagtoga aagagaatca tgcccgaccc tgtgacggag cccctgtga 450  
 cagaccccggt ttatgaagct cttttgtact gcaacatccc cagtgtggcc 500  
 gagcgcagca tggaagggtca tgccccgcac cattttaagc tgggtctcagt 550  
 gcatgtgttc attcgccacg gagacaggta cccactgtat gtcattccca 600  
 aaacaaagcg accagaaatt gactgcactc tgggtggctaa caggaaaccg 650  
 tatcacccaa aactggaagc ttctattagt cacatgtcaa aaggatccgg 700  
 agcctctttc gaaagccctt tgaactcctt gcctctttac ccaaatacacc 750  
 cattgtgtga gatgggagag ctcacacaga caggagtgtg gcagcatttg 800  
 cagaacggtc agctgctgag ggatatctat ctaaagaaac acaaactcct 850  
 gcccaatgat tgggtctgcag accagctcta tttagagacc actgggaaaa 900  
 gccggaccct acaaagtggg ctggccttgc tttatggctt tctcccagat 950  
 tttgactgga agaagattta ttccaggcac cagccaagtg cgctgttctg 1000  
 ctctggaagc tgctattgcc cggtaagaaa ccagtatctg gaaaaggagc 1050  
 agcgtcgtca gtacctcta cgtttgaaaa acagccagct ggagaagacc 1100  
 tacggggaga tggccaagat cgtggatgtc cccaccaagc agcttagagc 1150  
 tgccaacccc atagaactcca tgctctgcca cttctgccac aatgtcagct 1200  
 ttccctgtac cagaaatggc tgtgttgaca tggagcactt caaggtaatt 1250  
 aagaccatc agatcgagga tgaaaggga agacgggaga agaaattgta 1300  
 cttcgggtat tctctcctgg gtgcccaccc catcctgaac caaaccatcg 1350  
 gccgatgca gcgtgccacc gagggcagga aagaagagct ctttgccctc 1400  
 tactctgctc atgatgtcac tctgtcacca gttctcagt ccttgggcct 1450

ttcagaagcc aggttcccaa ggtttgcagc caggttgatc tttgagcttt 1500  
 ggcaagacag agaaaagccc agtgaacatt ccgcccgat tctttacaat 1550  
 ggcgtcgatg tcacattcca cacctctttc tgccaagacc accacaagcg 1600  
 ttctcccaag cccatgtgcc cgcttgaaaa cttggtccgc tttgtgaaaa 1650  
 gggacatggt ttagccctg ggtggcagtg gtacaaatta ttatgatgca 1700  
 tgtcacaggg aaggattcta aaaggatgc agtacagcag tatagaatcc 1750  
 atgccaatac agagcatagg gaaaggcca cttctagttt tgtctgttac 1800  
 taagggtaga agattattgc tttttaaagg ctaaatttg tttgtgggaa 1850  
 ccacagatgg ttgggggtga acagtaagca cattgctgca atgtggtacg 1900  
 tgaattgctt ggtacaaaat ggccagttca cagaggaata gaaggactt 1950  
 tatcatagcc agacttcgct tagaatgcca gaataatata gttcaagacc 2000  
 tgaagttgcc aatccaagtt tgcactcttc tggcctgccc catgttacta 2050  
 tgtgatggaa ccagcacacc tcaacaaaaa tttttttaat cttagacatt 2100  
 tttacctgt ccttgtaag aatttcttga agtgatttat ctaaaataaa 2150  
 ggttggcaaa ctttttctgt aaagggccag attgtaaata tttcagactg 2200  
 tgtggaccaa aaggccacat acagtctctg tcataactac tcaactctgt 2250  
 ttctgaagca ggaaagccac cacagacagt acataaagga atatgtgtag 2300  
 ctgggttccc aggccagaca aaacagatgg tgaccagact tggcccctgg 2350  
 gctgtagttt gctgaccct catctaaaaa ataggctata ctacaattgc 2400  
 acttccagca ctttgagaac gagttgaata ccaagaatta ttcaatgggt 2450  
 cctccagtaa cttctgctag aaacacagaa tttggtctgt atctgacact 2500  
 agaacaaaac ttgagggtaa ataaacattg aattagaatg aatcatagaa 2550  
 aactgattag aagaatactt gatgtttatg atgattgtgg tacaagatag 2600  
 ttttaagtat gttctaaata tttgtctgct gtagtctatt tgctgtatat 2650  
 gctgaaattt ttgtatgcca tttagtattt ttatagttaa ggaaaatatt 2700  
 ttctaagacc agtttttagat gactcttatt cctgtagtaa tattcaattt 2750  
 gctgtacctg cttggtggtt agaaggaggc tagaagatga attcaggcac 2800  
 tttcttccaa taaaactaat tatggctcat tcccttgac aagctgtaga 2850  
 actggattca tttttaaacc attttcatca gtttcaaag gtaaattctg 2900

attgattttt aaatgcgttt ttggaagaac ttgctatta ggtagtttac 2950  
 agatctttat aagggtgtttt atatattaga agcaattata attacatctg 3000  
 tgatttctga actaatggtg ctaattcaga gaaatggaaa gtgaaagtga 3050  
 gattctctgt tgtcatcggc attccaactt tttctctttg tttttgtcca 3100  
 gtgttgcatt tgaatatgtc tgtttctata aataaatttt ttaagaataa 3150

<210> 385  
 <211> 480  
 <212> PRT  
 <213> Homo sapiens

<400> 385  
 Met Leu Phe Arg Asn Arg Phe Leu Leu Leu Leu Ala Leu Ala Ala  
 1 5 10 15  
 Leu Leu Ala Phe Val Ser Leu Ser Leu Gln Phe Phe His Leu Ile  
 20 25 30  
 Pro Val Ser Thr Pro Lys Asn Gly Met Ser Ser Lys Ser Arg Lys  
 35 40 45  
 Arg Ile Met Pro Asp Pro Val Thr Glu Pro Pro Val Thr Asp Pro  
 50 55 60  
 Val Tyr Glu Ala Leu Leu Tyr Cys Asn Ile Pro Ser Val Ala Glu  
 65 70 75  
 Arg Ser Met Glu Gly His Ala Pro His His Phe Lys Leu Val Ser  
 80 85 90  
 Val His Val Phe Ile Arg His Gly Asp Arg Tyr Pro Leu Tyr Val  
 95 100 105  
 Ile Pro Lys Thr Lys Arg Pro Glu Ile Asp Cys Thr Leu Val Ala  
 110 115 120  
 Asn Arg Lys Pro Tyr His Pro Lys Leu Glu Ala Phe Ile Ser His  
 125 130 135  
 Met Ser Lys Gly Ser Gly Ala Ser Phe Glu Ser Pro Leu Asn Ser  
 140 145 150  
 Leu Pro Leu Tyr Pro Asn His Pro Leu Cys Glu Met Gly Glu Leu  
 155 160 165  
 Thr Gln Thr Gly Val Val Gln His Leu Gln Asn Gly Gln Leu Leu  
 170 175 180  
 Arg Asp Ile Tyr Leu Lys Lys His Lys Leu Leu Pro Asn Asp Trp  
 185 190 195  
 Ser Ala Asp Gln Leu Tyr Leu Glu Thr Thr Gly Lys Ser Arg Thr  
 200 205 210

09978192.104501

Leu Gln Ser Gly	Leu Ala Leu Leu Tyr	Gly Phe Leu Pro Asp	Phe
215		220	225
Asp Trp Lys Lys	Ile Tyr Phe Arg His	Gln Pro Ser Ala Leu	Phe
230		235	240
Cys Ser Gly Ser	Cys Tyr Cys Pro Val	Arg Asn Gln Tyr Leu	Glu
245		250	255
Lys Glu Gln Arg	Arg Gln Tyr Leu Leu	Arg Leu Lys Asn Ser	Gln
260		265	270
Leu Glu Lys Thr	Tyr Gly Glu Met Ala	Lys Ile Val Asp Val	Pro
275		280	285
Thr Lys Gln Leu	Arg Ala Ala Asn Pro	Ile Asp Ser Met Leu	Cys
290		295	300
His Phe Cys His	Asn Val Ser Phe Pro	Cys Thr Arg Asn Gly	Cys
305		310	315
Val Asp Met Glu	His Phe Lys Val Ile	Lys Thr His Gln Ile	Glu
320		325	330
Asp Glu Arg Glu	Arg Arg Glu Lys Lys	Leu Tyr Phe Gly Tyr	Ser
335		340	345
Leu Leu Gly Ala	His Pro Ile Leu Asn	Gln Thr Ile Gly Arg	Met
350		355	360
Gln Arg Ala Thr	Glu Gly Arg Lys Glu	Glu Leu Phe Ala Leu	Tyr
365		370	375
Ser Ala His Asp	Val Thr Leu Ser Pro	Val Leu Ser Ala Leu	Gly
380		385	390
Leu Ser Glu Ala	Arg Phe Pro Arg Phe	Ala Ala Arg Leu Ile	Phe
395		400	405
Glu Leu Trp Gln	Asp Arg Glu Lys Pro	Ser Glu His Ser Val	Arg
410		415	420
Ile Leu Tyr Asn	Gly Val Asp Val Thr	Phe His Thr Ser Phe	Cys
425		430	435
Gln Asp His His	Lys Arg Ser Pro Lys	Pro Met Cys Pro Leu	Glu
440		445	450
Asn Leu Val Arg	Phe Val Lys Arg Asp	Met Phe Val Ala Leu	Gly
455		460	465
Gly Ser Gly Thr	Asn Tyr Tyr Asp Ala	Cys His Arg Glu Gly	Phe
470		475	480

<210> 386

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 386  
ccaagcagct tagagctcca gacc 24

<210> 387  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 387  
ttccctatgc tctgtattgg catgg 25

<210> 388  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 388  
gccacttctg ccacaatgtc agctttccct gtaccagaaa tggctgtgtt 50

<210> 389  
<211> 3313  
<212> DNA  
<213> Homo sapiens

<400> 389  
aaaaaagctc actaaagttt ctattagagc gaatacggta gatttccatc 50  
cccttttgaa gaacagtact gtggagctat ttaagagata aaaacgaaat 100  
atcctttctg ggagttcaag attgtgcagt aattggttag gactctgagc 150  
gccgctgttc accaatcggg gagagaaaag cggagatcct gctcgccttg 200  
cacgcgcctg aagcacaaag cagatagcta ggaatgaacc atccctggga 250  
gtatgtggaa acaacggagg agctctgact tcccaactgt cccattctat 300  
gggcgaagga actgctcctg acttcagtgg ttaagggcag aattgaaaat 350  
aattctggag gaagataaga atgattcctg cgcgactgca ccgggactac 400  
aaagggcttg tcctgctggg aatcctcctg gggactctgt gggagaccgg 450  
atgcacccag atacgtatt cagttccgga agagctggag aaaggctcta 500  
gggtgggcga catctccagg gacctggggc tggagccccg ggagctcgcg 550  
gagcgcggag tccgcatcat cccagaggt aggacgcagc ttttcgcctt 600

gaatccgcgc agcggcagct tggtcacggc gggcaggata gaccgggagg 650  
 agctctgtat gggggccatc aagtgtcaat taaatctaga cattctgatg 700  
 gaggataaag tgaaaatata tggagtagaa gtagaagtaa gggacattaa 750  
 cgacaatgcg ccttactttc gtgaaagtga attagaaata aaaattagtg 800  
 aaaatgcagc cactgagatg cggttccctc taccacacgc ctgggatccg 850  
 gatatcggga agaactctct gcagagctac gagctcagcc cgaacactca 900  
 cttctccctc atcgtgcaaa atggagccga cggtagtaag taccocgaat 950  
 tggtgctgaa acgcgccctg gaccgcgaag aaaaggctgc tcaccacctg 1000  
 gtccttacgg cctccgacgg gggcgacccg gtgcgcacag gcaccgcgcg 1050  
 catccgcgtg atggttctgg atgcgaacga caacgcacca gcgtttgctc 1100  
 agcccagagta ccgcgcgagc gttccggaga atctggcctt gggcacgcag 1150  
 ctgctttagt tcaacgctac cgaccctgac gaaggagtca atgcggaagt 1200  
 gaggtattcc ttccggtatg tggacgacaa ggcggcccaa gttttcaaac 1250  
 tagattgtaa ttcagggaca atatcaacaa taggggagtt ggaccacgag 1300  
 gagtcaggat tctaccagat ggaagtgcaa gcaatggata atgcaggata 1350  
 ttctgcgcga gccaaaagtcc tgatcactgt tctggacgtg aacgacaatg 1400  
 cccagaagt ggtcctcacc tctctcgcca gctcggttcc cgaaaactct 1450  
 ccagagggga cattaattgc ctttttaa atgaaatgacc aagattctga 1500  
 ggaaaacgga caggatgatc gtttcatcca aggaaatctg ccctttaaat 1550  
 tagaaaaatc ttacggaaat tactatagtt tagtcacaga catagtcttg 1600  
 gatagggaa acggttcctag ctacaacatc acagtgaccg ccactgaccg 1650  
 gggaaacccg cccctatcca cggaactca tatctcgtg aacgtggcag 1700  
 acaccaacga caaccgcgcg gtcttccctc aggcctccta ttccgcttat 1750  
 atcccagaga acaatcccag aggagtttcc ctctctctg tgaccgcccc 1800  
 cgaccccgac tgtgaagaga acgcccagat cacttattcc ctggctgaga 1850  
 acaccatcca aggggcaagc ctatcgtcct acgtgtccat caactccgac 1900  
 actgggttac tgtatgcgct gagctccttc gactacgagc agttccgaga 1950  
 cttgcaagtg aaagtgatgg cgcgggacaa cgggcacccg cccctcagca 2000  
 gcaacgtgtc gttgagcctg ttcgtgctgg accagaacga caatgcgccc 2050

gagatcctgt accccgcctt cccacaggac ggttccactg gcgtggagct 2100  
 ggctccccgc tccgcagagc ccggctacct ggtgaccaag gtggtggcgg 2150  
 tggacagaga ctccggccag aacgcctggc tgtcctaccg tctgctcaag 2200  
 gccagcgagc cgggactctt ctcggtgggt ctgcacacgg gcgaggtgcg 2250  
 cacggcgaga gccctgctgg acagagacgc gctcaagcag agcctcgtag 2300  
 tggccgtcca ggaccacggc cagccccctc tctccgccac tgtcacgctc 2350  
 accgtggccg tggccgacag catcccccaa gtcctggcgg acctcggcag 2400  
 cctcgagtct ccagctaact ctgaaacctc agacctcact ctgtacctgg 2450  
 tggtagcggg ggccgcgggc tcttgctgtt tcttgccctt cgtcatcttg 2500  
 ctgctggcgc tcaggctgcg gcgctggcac aagtcacgcc tgctgcaggc 2550  
 ttcaggaggc ggcttgacag gagcgccggc gtcgcacttt gtgggcgtgg 2600  
 acggggtgca ggctttcttg cagacctatt cccacgaggt ttccctcacc 2650  
 acggactcgc ggaagagtca cctgatcttc cccagccca actatgcaga 2700  
 catgctcgtc agccaggaga gctttgaaaa aagcgagccc cttttgctgt 2750  
 caggtgattc ggtatcttct aaagacagtc atgggttaat tgaggtgagt 2800  
 ttatatcaaa tcttcttctt tttttttttt aattgctctg tctccaagc 2850  
 tggagtgcag cggtaacgac atagctcact gcggcctcaa actcctaggc 2900  
 tcaagcaatt atcccacctt tgccctccgg gtaacaggga ctacagggtc 2950  
 aagccacctt ctgtctgcct atctatctat ctatctatct atctatctat 3000  
 ctatctatct atctatctat tactttcttg tacagacggg agtctcacgc 3050  
 ctgtaatccc agtacttttg gaggccgagg cgggtggatc acctgaggtt 3100  
 gggagtgtga gaccagcctg accaaccatg agaaaccccg tctatactaa 3150  
 aaaaatacaa aattagccgg gcgtggtggt gcatgtctgt aatcccagct 3200  
 acttgggagg ctgagtcagg agaattgctt taacctggga ggtggagggt 3250  
 gcaatgagct gagattgtgc cattgcactc cagcctgggc aacaagagtg 3300  
 aaactctatc tca 3313

<210> 390  
 <211> 916  
 <212> PRT  
 <213> Homo sapiens  
 <400> 390



Met	Ile	Pro	Ala	Arg	Leu	His	Arg	Asp	Tyr	Lys	Gly	Leu	Val	Leu
1				5					10					15
Leu	Gly	Ile	Leu	Leu	Gly	Thr	Leu	Trp	Glu	Thr	Gly	Cys	Thr	Gln
				20					25					30
Ile	Arg	Tyr	Ser	Val	Pro	Glu	Glu	Leu	Glu	Lys	Gly	Ser	Arg	Val
				35					40					45
Gly	Asp	Ile	Ser	Arg	Asp	Leu	Gly	Leu	Glu	Pro	Arg	Glu	Leu	Ala
				50					55					60
Glu	Arg	Gly	Val	Arg	Ile	Ile	Pro	Arg	Gly	Arg	Thr	Gln	Leu	Phe
				65					70					75
Ala	Leu	Asn	Pro	Arg	Ser	Gly	Ser	Leu	Val	Thr	Ala	Gly	Arg	Ile
				80					85					90
Asp	Arg	Glu	Glu	Leu	Cys	Met	Gly	Ala	Ile	Lys	Cys	Gln	Leu	Asn
				95					100					105
Leu	Asp	Ile	Leu	Met	Glu	Asp	Lys	Val	Lys	Ile	Tyr	Gly	Val	Glu
				110					115					120
Val	Glu	Val	Arg	Asp	Ile	Asn	Asp	Asn	Ala	Pro	Tyr	Phe	Arg	Glu
				125					130					135
Ser	Glu	Leu	Glu	Ile	Lys	Ile	Ser	Glu	Asn	Ala	Ala	Thr	Glu	Met
				140					145					150
Arg	Phe	Pro	Leu	Pro	His	Ala	Trp	Asp	Pro	Asp	Ile	Gly	Lys	Asn
				155					160					165
Ser	Leu	Gln	Ser	Tyr	Glu	Leu	Ser	Pro	Asn	Thr	His	Phe	Ser	Leu
				170					175					180
Ile	Val	Gln	Asn	Gly	Ala	Asp	Gly	Ser	Lys	Tyr	Pro	Glu	Leu	Val
				185					190					195
Leu	Lys	Arg	Ala	Leu	Asp	Arg	Glu	Glu	Lys	Ala	Ala	His	His	Leu
				200					205					210
Val	Leu	Thr	Ala	Ser	Asp	Gly	Gly	Asp	Pro	Val	Arg	Thr	Gly	Thr
				215					220					225
Ala	Arg	Ile	Arg	Val	Met	Val	Leu	Asp	Ala	Asn	Asp	Asn	Ala	Pro
				230					235					240
Ala	Phe	Ala	Gln	Pro	Glu	Tyr	Arg	Ala	Ser	Val	Pro	Glu	Asn	Leu
				245					250					255
Ala	Leu	Gly	Thr	Gln	Leu	Leu	Val	Val	Asn	Ala	Thr	Asp	Pro	Asp
				260					265					270
Glu	Gly	Val	Asn	Ala	Glu	Val	Arg	Tyr	Ser	Phe	Arg	Tyr	Val	Asp
				275					280					285
Asp	Lys	Ala	Ala	Gln	Val	Phe	Lys	Leu	Asp	Cys	Asn	Ser	Gly	Thr

				290					295					300
Ile	Ser	Thr	Ile	Gly	Glu	Leu	Asp	His	Glu	Glu	Ser	Gly	Phe	Tyr
				305					310					315
Gln	Met	Glu	Val	Gln	Ala	Met	Asp	Asn	Ala	Gly	Tyr	Ser	Ala	Arg
				320					325					330
Ala	Lys	Val	Leu	Ile	Thr	Val	Leu	Asp	Val	Asn	Asp	Asn	Ala	Pro
				335					340					345
Glu	Val	Val	Leu	Thr	Ser	Leu	Ala	Ser	Ser	Val	Pro	Glu	Asn	Ser
				350					355					360
Pro	Arg	Gly	Thr	Leu	Ile	Ala	Leu	Leu	Asn	Val	Asn	Asp	Gln	Asp
				365					370					375
Ser	Glu	Glu	Asn	Gly	Gln	Val	Ile	Cys	Phe	Ile	Gln	Gly	Asn	Leu
				380					385					390
Pro	Phe	Lys	Leu	Glu	Lys	Ser	Tyr	Gly	Asn	Tyr	Tyr	Ser	Leu	Val
				395					400					405
Thr	Asp	Ile	Val	Leu	Asp	Arg	Glu	Gln	Val	Pro	Ser	Tyr	Asn	Ile
				410					415					420
Thr	Val	Thr	Ala	Thr	Asp	Arg	Gly	Thr	Pro	Pro	Leu	Ser	Thr	Glu
				425					430					435
Thr	His	Ile	Ser	Leu	Asn	Val	Ala	Asp	Thr	Asn	Asp	Asn	Pro	Pro
				440					445					450
Val	Phe	Pro	Gln	Ala	Ser	Tyr	Ser	Ala	Tyr	Ile	Pro	Glu	Asn	Asn
				455					460					465
Pro	Arg	Gly	Val	Ser	Leu	Val	Ser	Val	Thr	Ala	His	Asp	Pro	Asp
				470					475					480
Cys	Glu	Glu	Asn	Ala	Gln	Ile	Thr	Tyr	Ser	Leu	Ala	Glu	Asn	Thr
				485					490					495
Ile	Gln	Gly	Ala	Ser	Leu	Ser	Ser	Tyr	Val	Ser	Ile	Asn	Ser	Asp
				500					505					510
Thr	Gly	Val	Leu	Tyr	Ala	Leu	Ser	Ser	Phe	Asp	Tyr	Glu	Gln	Phe
				515					520					525
Arg	Asp	Leu	Gln	Val	Lys	Val	Met	Ala	Arg	Asp	Asn	Gly	His	Pro
				530					535					540
Pro	Leu	Ser	Ser	Asn	Val	Ser	Leu	Ser	Leu	Phe	Val	Leu	Asp	Gln
				545					550					555
Asn	Asp	Asn	Ala	Pro	Glu	Ile	Leu	Tyr	Pro	Ala	Leu	Pro	Thr	Asp
				560					565					570
Gly	Ser	Thr	Gly	Val	Glu	Leu	Ala	Pro	Arg	Ser	Ala	Glu	Pro	Gly
				575					580					585

Tyr	Leu	Val	Thr	Lys	Val	Val	Ala	Val	Asp	Arg	Asp	Ser	Gly	Gln	590	595	600
Asn	Ala	Trp	Leu	Ser	Tyr	Arg	Leu	Leu	Lys	Ala	Ser	Glu	Pro	Gly	605	610	615
Leu	Phe	Ser	Val	Gly	Leu	His	Thr	Gly	Glu	Val	Arg	Thr	Ala	Arg	620	625	630
Ala	Leu	Leu	Asp	Arg	Asp	Ala	Leu	Lys	Gln	Ser	Leu	Val	Val	Ala	635	640	645
Val	Gln	Asp	His	Gly	Gln	Pro	Pro	Leu	Ser	Ala	Thr	Val	Thr	Leu	650	655	660
Thr	Val	Ala	Val	Ala	Asp	Ser	Ile	Pro	Gln	Val	Leu	Ala	Asp	Leu	665	670	675
Gly	Ser	Leu	Glu	Ser	Pro	Ala	Asn	Ser	Glu	Thr	Ser	Asp	Leu	Thr	680	685	690
Leu	Tyr	Leu	Val	Val	Ala	Val	Ala	Ala	Val	Ser	Cys	Val	Phe	Leu	695	700	705
Ala	Phe	Val	Ile	Leu	Leu	Leu	Ala	Leu	Arg	Leu	Arg	Arg	Trp	His	710	715	720
Lys	Ser	Arg	Leu	Leu	Gln	Ala	Ser	Gly	Gly	Gly	Leu	Thr	Gly	Ala	725	730	735
Pro	Ala	Ser	His	Phe	Val	Gly	Val	Asp	Gly	Val	Gln	Ala	Phe	Leu	740	745	750
Gln	Thr	Tyr	Ser	His	Glu	Val	Ser	Leu	Thr	Thr	Asp	Ser	Arg	Lys	755	760	765
Ser	His	Leu	Ile	Phe	Pro	Gln	Pro	Asn	Tyr	Ala	Asp	Met	Leu	Val	770	775	780
Ser	Gln	Glu	Ser	Phe	Glu	Lys	Ser	Glu	Pro	Leu	Leu	Leu	Ser	Gly	785	790	795
Asp	Ser	Val	Phe	Ser	Lys	Asp	Ser	His	Gly	Leu	Ile	Glu	Val	Ser	800	805	810
Leu	Tyr	Gln	Ile	Phe	Phe	Leu	Phe	Phe	Phe	Asn	Cys	Ser	Val	Ser	815	820	825
Gln	Ala	Gly	Val	Gln	Arg	Tyr	Asp	His	Ser	Ser	Leu	Arg	Pro	Gln	830	835	840
Thr	Pro	Arg	Leu	Lys	Gln	Leu	Ser	His	Leu	Cys	Leu	Arg	Cys	Asn	845	850	855
Arg	Asp	Tyr	Arg	Cys	Lys	Pro	Pro	Thr	Val	Cys	Leu	Ser	Ile	Tyr	860	865	870
Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Ser	Ile	Tyr	Leu	Leu	Leu			

	875		880		885
Ser Cys Thr Asp	Gly Ser Leu Thr Pro	Val Ile Pro Val Leu Trp			
	890	895	900		
Glu Ala Glu Ala	Gly Gly Ser Pro Glu	Val Gly Ser Leu Arg Pro			
	905	910	915		

Ala

<210> 391  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 391  
 tccgtctctg tgaaccgccc cac 23

<210> 392  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 392  
 ctcgggcgca ttgtcgttct ggtc 24

<210> 393  
 <211> 40  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 393  
 ccgactgtga aagagaacgc ccagatcca cttgttcccc 40

<210> 394  
 <211> 999  
 <212> DNA  
 <213> Homo sapiens

<400> 394  
 ccaggctct agtgcaggag gagaaggagg aggagcagga ggtggagatt 50  
 ccagttaaa aggtccaga atcgtgtacc aggcagagaa ctgaagtact 100  
 ggggcctcct ccactgggtc cgaatcagta ggtgaccccg cccctggatt 150  
 ctggaagacc tcaccatggg acgccccga cctcgtgcgg ccaagacgtg 200

gatgttcctg ctcttgctgg ggggagcctg ggcaggacac tccagggcac 250  
aggaggacaa ggtgctgggg ggtcatgagt gccaaaccca ttcgcagcct 300  
tggcaggcgg ccttggtcca gggccagcaa ctactctgtg gcggtgtcct 350  
tgtaggtggc aactgggtcc ttacagctgc cactgtaaa aaaccgaaat 400  
acacagtacg cctgggagac cacagcctac agaataaaga tggcccagag 450  
caagaaatac ctgtggttca gtccatccca caccctgtct acaacagcag 500  
cgatgtggag gaccacaacc atgatctgat gcttcttcaa ctgcgtgacc 550  
aggcatccct ggggtccaaa gtgaagccca tcagcctggc agatcattgc 600  
accagcctg gccagaagtg caccgtctca ggctggggca ctgtcaccag 650  
tccccgagag aattttcctg acactctcaa ctgtgcagaa gtaaaaatct 700  
ttccccagaa gaagtgtgag gatgcttacc cggggcagat cacagatggc 750  
atggtctgtg caggcagcag caaaggggct gacacgtgcc agggcgattc 800  
tggaggcccc ctggtgtgtg atggtgcaact ccagggcata acatcctggg 850  
gctcagaccc ctgtgggagg tccgacaaac ctggcgtcta taccaacatc 900  
tgccgctacc tggactggat caagaagatc ataggcagca agggctgatt 950  
ctaggataag cactagatct cccttaataa actcacaact ctctggttc 999

<210> 395

<211> 260

<212> PRT

<213> Homo sapiens

<400> 395

Met	Gly	Arg	Pro	Arg	Pro	Arg	Ala	Ala	Lys	Thr	Trp	Met	Phe	Leu
1				5					10					15
Leu	Leu	Leu	Gly	Gly	Ala	Trp	Ala	Gly	His	Ser	Arg	Ala	Gln	Glu
			20						25					30
Asp	Lys	Val	Leu	Gly	Gly	His	Glu	Cys	Gln	Pro	His	Ser	Gln	Pro
			35						40					45
Trp	Gln	Ala	Ala	Leu	Phe	Gln	Gly	Gln	Gln	Leu	Leu	Cys	Gly	Gly
			50						55					60
Val	Leu	Val	Gly	Gly	Asn	Trp	Val	Leu	Thr	Ala	Ala	His	Cys	Lys
			65						70					75
Lys	Pro	Lys	Tyr	Thr	Val	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn
			80						85					90
Lys	Asp	Gly	Pro	Glu	Gln	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro
			95						100					105

His	Pro	Cys	Tyr	Asn	Ser	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	110	115	120
Leu	Met	Leu	Leu	Gln	Leu	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	125	130	135
Val	Lys	Pro	Ile	Ser	Leu	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	140	145	150
Lys	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	155	160	165
Asn	Phe	Pro	Asp	Thr	Leu	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	170	175	180
Gln	Lys	Lys	Cys	Glu	Asp	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	185	190	195
Met	Val	Cys	Ala	Gly	Ser	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	200	205	210
Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Asp	Gly	Ala	Leu	Gln	Gly	Ile	215	220	225
Thr	Ser	Trp	Gly	Ser	Asp	Pro	Cys	Gly	Arg	Ser	Asp	Lys	Pro	Gly	230	235	240
Val	Tyr	Thr	Asn	Ile	Cys	Arg	Tyr	Leu	Asp	Trp	Ile	Lys	Lys	Ile	245	250	255
Ile	Gly	Ser	Lys	Gly											260		

<210> 396  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 396  
 cagcctacag aataaagatg gcc 24

<210> 397  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 397  
 ggtgcaatga tctgccaggc tgat 24

<210> 398  
 <211> 48  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 398

agaaatacct gtggttcagt ccatcccaaa cccctgctac aacagcag 48

<210> 399

<211> 2236

<212> DNA

<213> Homo sapiens

<400> 399

ggcgccggtg caccgggagg gctgagcgcc tcctgcggcc cggcctgcgc 50

gccccggccc gccgcgccc ccacgcccc accccggccc gcgcccccta 100

gccccgccc gggcccgccc ccgcgcccgc gccaggtga gcgctccgcc 150

cgccgcgagg ccccgcccc gcccgcccc gcccgcccc ggccggcggg 200

ggaaccgggc ggattcctcg cgcgtcaaac cacctgatcc cataaaacat 250

tcctcctccc ggcgccccgc gctgcgagcg ccccgccagt ccgcgccgcc 300

gccgccctcg cctgtgcgc cctgcgcgcc ctgcgcaccc gcggcccgag 350

cccagccaga gccgggagg gaggagcgcg ccgagcctcg tcccgcggcc 400

gggcccgggc cgggcccgtg cggcgccgcc tggatgcgga cccggccgcg 450

gggagacggg cggccgcccc gaaacgactt tcagtcccc acgcgccccg 500

cccaaccct acgatgaaga gggcgtccgc tggagggagc cggctgctgg 550

catgggtgct gtggctgcag gcctggcagg tggcagcccc atgccagggt 600

gcctgcgtat gctacaatga gccaagggtg acgacaagct gccccagca 650

gggcctgcag gctgtgccc tgggcatccc tgctgccagc cagcgcattct 700

tcctgcacgg caaccgcac tcgcatgtgc cagctgccag cttccgtgcc 750

tgccgaacc tcaccatcct gtggctgcac tcgaatgtgc tggcccgaat 800

tgatgcggct gccttcaact gcctggccct cctggagcag ctggacctca 850

gcgataatgc acagctccg tctgtggacc ctgccacatt ccacggcctg 900

ggccgcctac acacgtgca cctggaccgc tgcggcctgc aggagctggg 950

ccgggggctg ttccggggcc tggtgccct gcagtacctc tacctgcagg 1000

acaacgcgt gcaggcactg cctgatgaca cttccgcga cctgggcaac 1050

ctcacacacc tcttctgca cggcaaccgc atctccagcg tgcccagagc 1100

09978192.101501

cgcttccgt gggctgcaca gcctcgaccg tctcctactg caccagaacc 1150  
 gcgtggccca tgtgcaccgc catgccttcc gtgaccttgg ccgcctcatg 1200  
 acactctatc tgtttgccaa caatctatca gcgctgcccc ctgaggccct 1250  
 ggccccctg cgtgccctgc agtacctgag gctcaacgac aacccttggg 1300  
 tgtgtgactg ccggggcacgc ccaactctggg cctggctgca gaagttccgc 1350  
 ggctcctcct ccgaggtgcc ctgcagcctc ccgcaacgcc tggctggccg 1400  
 tgacctcaaa cgcctagctg ccaatgacct gcagggctgc gctgtggcca 1450  
 ccggccctta ccatcccatc tggaccggca gggccaccga tgaggagccg 1500  
 ctggggcttc ccaagtgtctg ccagccagat gccgctgaca aggcctcagt 1550  
 actggagcct ggaagaccag cttcggcagg caatgcgctg aaggagcgcg 1600  
 tgccgcccgg tgacagcccg ccgggcaacg gctctggccc acggcacatc 1650  
 aatgactcac cctttgggac tctgcctggc tctgctgagc ccccgctcac 1700  
 tgcaagtgcg cccgagggct ccgagccacc aggggttccc acctcgggcc 1750  
 ctcgccggag gccaggtgtg tcacgcaaga accgcacccg cagccactgc 1800  
 cgtctgggcc aggcaggcag cgggggtggc gggactggtg actcagaagg 1850  
 ctcaggtgcc ctaccagcc tcacctgcag cctcaccccc ctgggccttg 1900  
 cgctggtgct gtggacagtg cttgggccct gctgaccccc agcggacaca 1950  
 agagcgtgct cagcagccag gtgtgtgtac atacggggtc tctctccacg 2000  
 ccgccaagcc agccgggcg ccgaccctg gggcaggcca ggccaggtcc 2050  
 tccctgatgg acgcctgccg cccgccaccc ccatctccac cccatcatgt 2100  
 ttacagggtt cggcggcagc gtttgttcca gaacgccgc tcccaccag 2150  
 atcgcggtat atagagatat gcattttatt ttacttgtgt aaaaatatcg 2200  
 gacgacgtgg aataaagagc tcttttctta aaaaaa 2236

<210> 400

<211> 473

<212> PRT

<213> Homo sapiens

<400> 400

Met Lys Arg Ala Ser Ala Gly Gly Ser Arg Leu Leu Ala Trp Val  
 1 5 10 15

Leu Trp Leu Gln Ala Trp Gln Val Ala Ala Pro Cys Pro Gly Ala  
 20 25 30



Cys	Val	Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	35	40	45
Gln	Gly	Leu	Gln	Ala	Val	Pro	Val	Gly	Ile	Pro	Ala	Ala	Ser	Gln	50	55	60
Arg	Ile	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	His	Val	Pro	Ala	Ala	65	70	75
Ser	Phe	Arg	Ala	Cys	Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	80	85	90
Asn	Val	Leu	Ala	Arg	Ile	Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Ala	95	100	105
Leu	Leu	Glu	Gln	Leu	Asp	Leu	Ser	Asp	Asn	Ala	Gln	Leu	Arg	Ser	110	115	120
Val	Asp	Pro	Ala	Thr	Phe	His	Gly	Leu	Gly	Arg	Leu	His	Thr	Leu	125	130	135
His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu	Leu	Gly	Pro	Gly	Leu	Phe	140	145	150
Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	Ala	155	160	165
Leu	Gln	Ala	Leu	Pro	Asp	Asp	Thr	Phe	Arg	Asp	Leu	Gly	Asn	Leu	170	175	180
Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Ser	Ser	Val	Pro	Glu	185	190	195
Arg	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu	Leu	His	200	205	210
Gln	Asn	Arg	Val	Ala	His	Val	His	Pro	His	Ala	Phe	Arg	Asp	Leu	215	220	225
Gly	Arg	Leu	Met	Thr	Leu	Tyr	Leu	Phe	Ala	Asn	Asn	Leu	Ser	Ala	230	235	240
Leu	Pro	Thr	Glu	Ala	Leu	Ala	Pro	Leu	Arg	Ala	Leu	Gln	Tyr	Leu	245	250	255
Arg	Leu	Asn	Asp	Asn	Pro	Trp	Val	Cys	Asp	Cys	Arg	Ala	Arg	Pro	260	265	270
Leu	Trp	Ala	Trp	Leu	Gln	Lys	Phe	Arg	Gly	Ser	Ser	Ser	Glu	Val	275	280	285
Pro	Cys	Ser	Leu	Pro	Gln	Arg	Leu	Ala	Gly	Arg	Asp	Leu	Lys	Arg	290	295	300
Leu	Ala	Ala	Asn	Asp	Leu	Gln	Gly	Cys	Ala	Val	Ala	Thr	Gly	Pro	305	310	315
Tyr	His	Pro	Ile	Trp	Thr	Gly	Arg	Ala	Thr	Asp	Glu	Glu	Pro	Leu			

	320		325		330
Gly Leu Pro Lys	Cys Cys Gln Pro Asp	Ala Ala Asp Lys Ala	Ser		
	335		340		345
Val Leu Glu Pro	Gly Arg Pro Ala Ser	Ala Gly Asn Ala Leu	Lys		
	350		355		360
Gly Arg Val Pro	Pro Gly Asp Ser Pro	Pro Gly Asn Gly Ser	Gly		
	365		370		375
Pro Arg His Ile	Asn Asp Ser Pro Phe	Gly Thr Leu Pro Gly	Ser		
	380		385		390
Ala Glu Pro Pro	Leu Thr Ala Val Arg	Pro Glu Gly Ser Glu	Pro		
	395		400		405
Pro Gly Phe Pro	Thr Ser Gly Pro Arg	Arg Arg Pro Gly Cys	Ser		
	410		415		420
Arg Lys Asn Arg	Thr Arg Ser His Cys	Arg Leu Gly Gln Ala	Gly		
	425		430		435
Ser Gly Gly Gly	Gly Thr Gly Asp Ser	Glu Gly Ser Gly Ala	Leu		
	440		445		450
Pro Ser Leu Thr	Cys Ser Leu Thr Pro	Leu Gly Leu Ala Leu	Val		
	455		460		465
Leu Trp Thr Val	Leu Gly Pro Cys				
	470				

<210> 401  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 401  
 tggctgccct gcagtacctc tacc 24

<210> 402  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 402  
 ccctgcaggt cattggcagc tagg 24

<210> 403  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 403

aggcactgcc tgatgacacc ttccgcgacc tgggcaacct cacac 45

<210> 404

<211> 2738

<212> DNA

<213> Homo sapiens

<400> 404

ggaagtccac ggggagcttg gatgccaaag ggaggacggc tgggtcctct 50  
ggagaggact actcactggc atatttctga ggtatctgta gaataaccac 100  
agcctcagat actggggact ttacagtccc acagaaccgt cctcccagga 150  
agctgaatcc agcaagaaca atggaggcca gcgggaagct catttgcaga 200  
caaaggcaag tccttttttc ctttctcctt ttgggcttat ctctggcggg 250  
cgcggcggaa cctagaagct attctgtggt ggaggaaact gagggcagct 300  
cctttgtcac caatttagca aaggacctgg gtctggagca gagggaattc 350  
tccaggcggg gggttagggt tgtttccaga ggaacaaac tacatttgca 400  
gctcaatcag gagaccgcgg atttgttgct aaatgagaaa ttggaccgtg 450  
aggatctgtg cggtcacaca gagccctgtg tgctacgttt ccaagtgttg 500  
ctagagagtc ccttcgagtt ttttcaagct gagctgcaag taatagacat 550  
aaacgaccac tctccagtat ttctggacaa acaaagtgtg gtgaaagtat 600  
cagagagcag tcctcctggg actacgtttc ctctgaagaa tgccgaagac 650  
ttagatgtag gccaaaacaa tattgagaac tatataatca gcccactc 700  
ctattttcgg gtcctcaccg gcaaacgcag tgatggcagg aaatacccag 750  
agctggtgct ggacaaagcg ctggaccgag aggaagaagc tgagctcagg 800  
ttaacactca cagcactgga tgggtggtct cgcgccagat ctggcactgc 850  
tcaggtctac atcgaagtcc tggatgtcaa cgataatgcc cctgaatttg 900  
agcagccttt ctatagagtg cagatctctg aggacagtcc ggtaggcttc 950  
ctggttgtga aggtctctgc cacggatgta gacacaggag tcaacggaga 1000  
gatttcctat tcacttttcc aagcttcaga agagattggc aaaaccttta 1050  
agatcaatcc cttgacagga gaaattgaac taaaaaaca actcgatttc 1100  
gaaaaacttc agtcctatga agtcaatatt gaggcaagag atgctggaac 1150

cttttctgga aaatgcaccg ttctgattca agtgatagat gtgaacgacc 1200  
atgccccaga agttaccatg tctgcattta ccagcccaat acctgagaac 1250  
gcgctgaaa ctgtggttgc acttttcagt gtttcagatc ttgattcagg 1300  
agaaaatggg aaaattagtt gctccattca ggaggatcta cccttcctcc 1350  
tgaaatccgc ggaaaacttt tacaccctac taacggagag accactagac 1400  
agagaaagca gagcggaata caacatcact atcactgtca ctgacttggg 1450  
gaccctatg ctgataacac agtcaatat gaccgtgctg atcgccgatg 1500  
tcaatgacaa cgctcccgcc ttcacccaaa cctcctacac cctgttcgtc 1550  
cgcgagaaca acagccccgc cctgcacatc cgcagcgtca gcgctacaga 1600  
cagagactca ggcaccaacg cccaggtcac ctactcgtg ctgccgcccc 1650  
aggacccgca cctgcccctc acatccctgg tctccatcaa cgcggacaac 1700  
ggccacctgt tcgccctcag gtctctggac tacgaggccc tgcaggggtt 1750  
ccagttccgc gtgggcgctt cagaccacgg ctccccggcg ctgagcagcg 1800  
aggcgctggt gcgctggtg gtgctggacg ccaacgacaa ctcgcccttc 1850  
gtgctgtacc cgctgcagaa cggctccgcg ccctgcaccg agctggtgcc 1900  
ccgggcggcc gagccgggct acctggtgac caaggtggtg gcggtggacg 1950  
gcgactcggg ccagaacgcc tggctgtcgt accagctgct caaggccacg 2000  
gagctcggtc tgttcggcgt gtgggcgcac aatggcgagg tgcgcaccgc 2050  
caggctgctg agcgagcgcg acgcggccaa gcacaggctg gtggtgctgg 2100  
tcaaggacaa tggcgagcct ccgcgctcgg ccaccgccac gctgcacgtg 2150  
ctcctggtgg acggcttctc ccagccctac ctgcctctcc cggaggcggc 2200  
cccgacccag gccagggcg acttgctcac cgtctacctg gtggtggcgt 2250  
tggcctcggg gtcttcgctc ttcctctttt cgggtgctct gtctgtggcg 2300  
gtgcggctgt gtaggaggag cagggcggcc tcggtgggtc gctgcttggg 2350  
gcccgagggc ccccttccag ggcattctgt ggacatgagc ggcaccagga 2400  
ccctatccca gagctaccag tatgaggtgt gtctggcagg aggctcaggg 2450  
accaatgagt tcaagttcct gaagccgatt atccccaact tccctccca 2500  
gtgccctggg aaagaaatac aaggaaattc taccttcccc aataactttg 2550  
ggttcaatat tcagtacca tagttgactt ttacattcca taggtatttt 2600

attttgtggc atttccatgc caatgtttat ttcccccaat ttgtgtgtat 2650  
gtaatattgt acggattttac tcttgatttt tctcatgttc tttctccctt 2700  
tgtttttaaag tgaacattta cctttattcc tggttctt 2738

<210> 405  
<211> 798  
<212> PRT  
<213> Homo sapiens

<400> 405  
Met Glu Ala Ser Gly Lys Leu Ile Cys Arg Gln Arg Gln Val Leu  
1 5 10 15  
Phe Ser Phe Leu Leu Leu Gly Leu Ser Leu Ala Gly Ala Ala Glu  
20 25 30  
Pro Arg Ser Tyr Ser Val Val Glu Glu Thr Glu Gly Ser Ser Phe  
35 40 45  
Val Thr Asn Leu Ala Lys Asp Leu Gly Leu Glu Gln Arg Glu Phe  
50 55 60  
Ser Arg Arg Gly Val Arg Val Val Ser Arg Gly Asn Lys Leu His  
65 70 75  
Leu Gln Leu Asn Gln Glu Thr Ala Asp Leu Leu Leu Asn Glu Lys  
80 85 90  
Leu Asp Arg Glu Asp Leu Cys Gly His Thr Glu Pro Cys Val Leu  
95 100 105  
Arg Phe Gln Val Leu Leu Glu Ser Pro Phe Glu Phe Phe Gln Ala  
110 115 120  
Glu Leu Gln Val Ile Asp Ile Asn Asp His Ser Pro Val Phe Leu  
125 130 135  
Asp Lys Gln Met Leu Val Lys Val Ser Glu Ser Ser Pro Pro Gly  
140 145 150  
Thr Thr Phe Pro Leu Lys Asn Ala Glu Asp Leu Asp Val Gly Gln  
155 160 165  
Asn Asn Ile Glu Asn Tyr Ile Ile Ser Pro Asn Ser Tyr Phe Arg  
170 175 180  
Val Leu Thr Arg Lys Arg Ser Asp Gly Arg Lys Tyr Pro Glu Leu  
185 190 195  
Val Leu Asp Lys Ala Leu Asp Arg Glu Glu Glu Ala Glu Leu Arg  
200 205 210  
Leu Thr Leu Thr Ala Leu Asp Gly Gly Ser Pro Pro Arg Ser Gly  
215 220 225  
Thr Ala Gln Val Tyr Ile Glu Val Leu Asp Val Asn Asp Asn Ala

230	235	240
Pro Glu Phe Glu Gln	Pro Phe Tyr Arg Val Gln Ile Ser Glu Asp	
245	250	255
Ser Pro Val Gly Phe	Leu Val Val Lys Val Ser Ala Thr Asp Val	
260	265	270
Asp Thr Gly Val Asn	Gly Glu Ile Ser Tyr Ser Leu Phe Gln Ala	
275	280	285
Ser Glu Glu Ile Gly	Lys Thr Phe Lys Ile Asn Pro Leu Thr Gly	
290	295	300
Glu Ile Glu Leu Lys	Lys Gln Leu Asp Phe Glu Lys Leu Gln Ser	
305	310	315
Tyr Glu Val Asn Ile	Glu Ala Arg Asp Ala Gly Thr Phe Ser Gly	
320	325	330
Lys Cys Thr Val Leu	Ile Gln Val Ile Asp Val Asn Asp His Ala	
335	340	345
Pro Glu Val Thr Met	Ser Ala Phe Thr Ser Pro Ile Pro Glu Asn	
350	355	360
Ala Pro Glu Thr Val	Val Ala Leu Phe Ser Val Ser Asp Leu Asp	
365	370	375
Ser Gly Glu Asn Gly	Lys Ile Ser Cys Ser Ile Gln Glu Asp Leu	
380	385	390
Pro Phe Leu Leu Lys	Ser Ala Glu Asn Phe Tyr Thr Leu Leu Thr	
395	400	405
Glu Arg Pro Leu Asp	Arg Glu Ser Arg Ala Glu Tyr Asn Ile Thr	
410	415	420
Ile Thr Val Thr Asp	Leu Gly Thr Pro Met Leu Ile Thr Gln Leu	
425	430	435
Asn Met Thr Val Leu	Ile Ala Asp Val Asn Asp Asn Ala Pro Ala	
440	445	450
Phe Thr Gln Thr Ser	Tyr Thr Leu Phe Val Arg Glu Asn Asn Ser	
455	460	465
Pro Ala Leu His Ile	Arg Ser Val Ser Ala Thr Asp Arg Asp Ser	
470	475	480
Gly Thr Asn Ala Gln	Val Thr Tyr Ser Leu Leu Pro Pro Gln Asp	
485	490	495
Pro His Leu Pro Leu	Thr Ser Leu Val Ser Ile Asn Ala Asp Asn	
500	505	510
Gly His Leu Phe Ala	Leu Arg Ser Leu Asp Tyr Glu Ala Leu Gln	
515	520	525

Gly	Phe	Gln	Phe	Arg	Val	Gly	Ala	Ser	Asp	His	Gly	Ser	Pro	Ala	
				530					535					540	
Leu	Ser	Ser	Glu	Ala	Leu	Val	Arg	Val	Val	Val	Leu	Asp	Ala	Asn	
				545					550					555	
Asp	Asn	Ser	Pro	Phe	Val	Leu	Tyr	Pro	Leu	Gln	Asn	Gly	Ser	Ala	
				560					565					570	
Pro	Cys	Thr	Glu	Leu	Val	Pro	Arg	Ala	Ala	Glu	Pro	Gly	Tyr	Leu	
				575					580					585	
Val	Thr	Lys	Val	Val	Ala	Val	Asp	Gly	Asp	Ser	Gly	Gln	Asn	Ala	
				590					595					600	
Trp	Leu	Ser	Tyr	Gln	Leu	Leu	Lys	Ala	Thr	Glu	Leu	Gly	Leu	Phe	
				605					610					615	
Gly	Val	Trp	Ala	His	Asn	Gly	Glu	Val	Arg	Thr	Ala	Arg	Leu	Leu	
				620					625					630	
Ser	Glu	Arg	Asp	Ala	Ala	Lys	His	Arg	Leu	Val	Val	Leu	Val	Lys	
				635					640					645	
Asp	Asn	Gly	Glu	Pro	Pro	Arg	Ser	Ala	Thr	Ala	Thr	Leu	His	Val	
				650					655					660	
Leu	Leu	Val	Asp	Gly	Phe	Ser	Gln	Pro	Tyr	Leu	Pro	Leu	Pro	Glu	
				665					670					675	
Ala	Ala	Pro	Thr	Gln	Ala	Gln	Ala	Asp	Leu	Leu	Thr	Val	Tyr	Leu	
				680					685					690	
Val	Val	Ala	Leu	Ala	Ser	Val	Ser	Ser	Leu	Phe	Leu	Phe	Ser	Val	
				695					700					705	
Leu	Leu	Phe	Val	Ala	Val	Arg	Leu	Cys	Arg	Arg	Ser	Arg	Ala	Ala	
				710					715					720	
Ser	Val	Gly	Arg	Cys	Leu	Val	Pro	Glu	Gly	Pro	Leu	Pro	Gly	His	
				725					730					735	
Leu	Val	Asp	Met	Ser	Gly	Thr	Arg	Thr	Leu	Ser	Gln	Ser	Tyr	Gln	
				740					745					750	
Tyr	Glu	Val	Cys	Leu	Ala	Gly	Gly	Ser	Gly	Thr	Asn	Glu	Phe	Lys	
				755					760					765	
Phe	Leu	Lys	Pro	Ile	Ile	Pro	Asn	Phe	Pro	Pro	Gln	Cys	Pro	Gly	
				770					775					780	
Lys	Glu	Ile	Gln	Gly	Asn	Ser	Thr	Phe	Pro	Asn	Asn	Phe	Gly	Phe	
				785					790					795	

Asn Ile Gln

<210> 406

<211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 406  
 ctgagaacgc gcctgaaact gtg 23

<210> 407  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 407  
 agcgttgtca ttgacatcgg cg 22

<210> 408  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 408  
 ttagttgctc cattcaggag gatctaccct tcctcctgaa atccgcggaa 50

<210> 409  
 <211> 1379  
 <212> DNA  
 <213> Homo sapiens

<400> 409  
 acccacgcgt ccgcccacgc gtccgcccac gcgtccgccc acgcgtccgc 50  
 gcgtagccgt gcgccgattg cctctcggcc tgggcaatgg tcccggctgc 100  
 cggtcgacga ccgccccgcg tcatgcggct cctcggctgg tggcaagtat 150  
 tgctgtgggt gctgggactt cccgtccgcg gcgtggaggt tgcagaggaa 200  
 agtggtcgct tatggtcaga ggagcagcct gctcaccctc tccaggtggg 250  
 ggctgtgtac ctgggtgagg aggagctcct gcatgaccgc atgggcccagg 300  
 acagggcagc agaagaggcc aatgcggtgc tggggctgga caccgaaggc 350  
 gatcacatgg tgatgctgtc tgtgattcct ggggaagctg aggacaaagt 400  
 gagttcagag cctagcggcg tcacctgtgg tgctggagga gcggaggact 450  
 caaggtgcaa cgtccgagag agccttttct ctctggatgg cgctggagca 500



cacttccctg acagagaaga ggagtattac acagagccag aagtggcgga 550  
 atctgacgca gccccgacag aggactccaa taactactgaa agtctgaaat 600  
 ccccaaaggt gaactgtgag gagagaaaca ttacaggatt agaaaatttc 650  
 actctgaaaa ttttaaataat gtcacaggac cttatggatt ttctgaaccc 700  
 aaacggtagt gactgtactc tagtcctggt ttacaccccg tggcgccgct 750  
 tttctgccag tttggcccct cactttaact ctctgccccg ggcatttcca 800  
 gctcttcaact ttttggcact ggatgcatct cagcacagca gcctttctac 850  
 caggtttggc accgtagctg ttcctaataat tttattattt caaggagcta 900  
 aaccaatggc cagattttaat catacagatc gaacactgga aacactgaaa 950  
 atcttcattt ttaatcagac aggtatagaa gccagaaga atgtggtggt 1000  
 aactcaagcc gaccaaatac gccctcttcc cagcactttg ataaaaagt 1050  
 tggactgggt gcttgtattt tccttattct ttttaattag ttttattatg 1100  
 tatgctacca ttcgaactga gagtattcgg tggctaattc caggacaaga 1150  
 gcaggaacat gtggagtagt gatggtctga aagaagttgg aaagaggaac 1200  
 ttcaatcctt cgtttcagaa attagtgcga cagtttcata cttttctcc 1250  
 agtgacgtgt tgacttgaaa cttcaggcag attaaaagaa tcatttggtg 1300  
 aacaactgaa tgtataaaaa aattataaac tgggtgttta actagtattg 1350  
 caataagcaa atgcaaaaat attcaatag 1379

<210> 410  
 <211> 360  
 <212> PRT  
 <213> Homo sapiens

<400> 410  
 Met Val Pro Ala Ala Gly Arg Arg Pro Pro Arg Val Met Arg Leu  
 1 5 10 15  
 Leu Gly Trp Trp Gln Val Leu Leu Trp Val Leu Gly Leu Pro Val  
 20 25 30  
 Arg Gly Val Glu Val Ala Glu Glu Ser Gly Arg Leu Trp Ser Glu  
 35 40 45  
 Glu Gln Pro Ala His Pro Leu Gln Val Gly Ala Val Tyr Leu Gly  
 50 55 60  
 Glu Glu Glu Leu Leu His Asp Pro Met Gly Gln Asp Arg Ala Ala  
 65 70 75  
 Glu Glu Ala Asn Ala Val Leu Gly Leu Asp Thr Gln Gly Asp His

80										85					90				
Met	Val	Met	Leu	Ser	Val	Ile	Pro	Gly	Glu	Ala	Glu	Asp	Lys	Val					
				95					100					105					
Ser	Ser	Glu	Pro	Ser	Gly	Val	Thr	Cys	Gly	Ala	Gly	Gly	Ala	Glu					
				110					115					120					
Asp	Ser	Arg	Cys	Asn	Val	Arg	Glu	Ser	Leu	Phe	Ser	Leu	Asp	Gly					
				125					130					135					
Ala	Gly	Ala	His	Phe	Pro	Asp	Arg	Glu	Glu	Glu	Tyr	Tyr	Thr	Glu					
				140					145					150					
Pro	Glu	Val	Ala	Glu	Ser	Asp	Ala	Ala	Pro	Thr	Glu	Asp	Ser	Asn					
				155					160					165					
Asn	Thr	Glu	Ser	Leu	Lys	Ser	Pro	Lys	Val	Asn	Cys	Glu	Glu	Arg					
				170					175					180					
Asn	Ile	Thr	Gly	Leu	Glu	Asn	Phe	Thr	Leu	Lys	Ile	Leu	Asn	Met					
				185					190					195					
Ser	Gln	Asp	Leu	Met	Asp	Phe	Leu	Asn	Pro	Asn	Gly	Ser	Asp	Cys					
				200					205					210					
Thr	Leu	Val	Leu	Phe	Tyr	Thr	Pro	Trp	Cys	Arg	Phe	Ser	Ala	Ser					
				215					220					225					
Leu	Ala	Pro	His	Phe	Asn	Ser	Leu	Pro	Arg	Ala	Phe	Pro	Ala	Leu					
				230					235					240					
His	Phe	Leu	Ala	Leu	Asp	Ala	Ser	Gln	His	Ser	Ser	Leu	Ser	Thr					
				245					250					255					
Arg	Phe	Gly	Thr	Val	Ala	Val	Pro	Asn	Ile	Leu	Leu	Phe	Gln	Gly					
				260					265					270					
Ala	Lys	Pro	Met	Ala	Arg	Phe	Asn	His	Thr	Asp	Arg	Thr	Leu	Glu					
				275					280					285					
Thr	Leu	Lys	Ile	Phe	Ile	Phe	Asn	Gln	Thr	Gly	Ile	Glu	Ala	Lys					
				290					295					300					
Lys	Asn	Val	Val	Val	Thr	Gln	Ala	Asp	Gln	Ile	Gly	Pro	Leu	Pro					
				305					310					315					
Ser	Thr	Leu	Ile	Lys	Ser	Val	Asp	Trp	Leu	Leu	Val	Phe	Ser	Leu					
				320					325					330					
Phe	Phe	Leu	Ile	Ser	Phe	Ile	Met	Tyr	Ala	Thr	Ile	Arg	Thr	Glu					
				335					340					345					
Ser	Ile	Arg	Trp	Leu	Ile	Pro	Gly	Gln	Glu	Gln	Glu	His	Val	Glu					
				350					355					360					

<210> 411  
 <211> 24

<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 411  
cacagagcca gaagtggcgg aatc 24

<210> 412  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 412  
ccacatgttc ctgctcttgc cctgg 25

<210> 413  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 413  
cggtagtgc tgtactctag tctgtttta caccocgtgg tgccg 45

<210> 414  
<211> 1196  
<212> DNA  
<213> Homo sapiens

<400> 414  
cccggctccg ctccctctgc cccctcgggg tcgcgcgccc acgatgctgc 50  
agggccctgg ctgcgtgctg ctgctcttcc tcgcctcgca ctgctgcctg 100  
ggctcggcgc gcgggctctt cctctttggc cagcccgact tctcctacaa 150  
gcgcagcaat tgcaagccca tcccggtcaa cctgcagctg tgccacggca 200  
tcgaatacca gaacatgcgg ctgcccacc tcgctgggcca cgagaccatg 250  
aaggaggtgc tggagcaggc cggcgcttgg atcccgctgg tcatgaagca 300  
gtgccacccg gacaccaaga agttcctgtg ctgcgtcttc gccccgtct 350  
gctcgatga cctagacgag accatccagc catgccactc gctctgcgtg 400  
caggtgaagg accgctgcgc cccggtcatg tccgccttcg gcttcccctg 450  
gcccagacatg cttgagtgcg accgtttccc ccaggacaac gacctttgca 500  
tccccctcgc tagcagcgac cacctcctgc cagccaccga ggaagctcca 550

aaggtatgtg aagcctgcaa aaataaaaat gatgatgaca acgacataat 600  
 ggaaacgctt tgtaaaaatg attttgcact gaaaataaaa gtgaaggaga 650  
 taacctacat caaccgagat accaaaatca tcctggagac caagagcaag 700  
 accatttaca agctgaacgg tgtgtccgaa agggacctga agaaatcggg 750  
 gctgtggctc aaagacagct tgcagtgcac ctgtgaggag atgaacgaca 800  
 tcaacgcgcc ctatctggtc atgggacaga aacaggggtg ggagctgggtg 850  
 atcacctcgg tgaagcgggtg gcagaagggg cagagagagt tcaagcgcac 900  
 ctcccgcagc atccgcaagc tgcagtgcta gtcccggcat cctgatgggt 950  
 ccgacaggcc tgctccagag cacggctgac catttctgct ccgggatctc 1000  
 agctcccgtt ccccaagcac actcctagct gctccagtct cagcctgggc 1050  
 agcttcccc tgccttttgc acgtttgcat cccagcatt tcctgagtta 1100  
 taaggccaca ggagtggata gctgttttca cctaaaggaa aagcccaccc 1150  
 gaatcttgta gaaatattca aactaataaa atcatgaata ttttaa 1196

<210> 415  
 <211> 295  
 <212> PRT  
 <213> Homo sapiens

<400> 415  
 Met Leu Gln Gly Pro Gly Ser Leu Leu Leu Leu Phe Leu Ala Ser  
 1 5 10 15  
 His Cys Cys Leu Gly Ser Ala Arg Gly Leu Phe Leu Phe Gly Gln  
 20 25 30  
 Pro Asp Phe Ser Tyr Lys Arg Ser Asn Cys Lys Pro Ile Pro Val  
 35 40 45  
 Asn Leu Gln Leu Cys His Gly Ile Glu Tyr Gln Asn Met Arg Leu  
 50 55 60  
 Pro Asn Leu Leu Gly His Glu Thr Met Lys Glu Val Leu Glu Gln  
 65 70 75  
 Ala Gly Ala Trp Ile Pro Leu Val Met Lys Gln Cys His Pro Asp  
 80 85 90  
 Thr Lys Lys Phe Leu Cys Ser Leu Phe Ala Pro Val Cys Leu Asp  
 95 100 105  
 Asp Leu Asp Glu Thr Ile Gln Pro Cys His Ser Leu Cys Val Gln  
 110 115 120  
 Val Lys Asp Arg Cys Ala Pro Val Met Ser Ala Phe Gly Phe Pro  
 125 130 135

Trp	Pro	Asp	Met	Leu	Glu	Cys	Asp	Arg	Phe	Pro	Gln	Asp	Asn	Asp	
				140					145					150	
Leu	Cys	Ile	Pro	Leu	Ala	Ser	Ser	Asp	His	Leu	Leu	Pro	Ala	Thr	
				155					160					165	
Glu	Glu	Ala	Pro	Lys	Val	Cys	Glu	Ala	Cys	Lys	Asn	Lys	Asn	Asp	
				170					175					180	
Asp	Asp	Asn	Asp	Ile	Met	Glu	Thr	Leu	Cys	Lys	Asn	Asp	Phe	Ala	
				185					190					195	
Leu	Lys	Ile	Lys	Val	Lys	Glu	Ile	Thr	Tyr	Ile	Asn	Arg	Asp	Thr	
				200					205					210	
Lys	Ile	Ile	Leu	Glu	Thr	Lys	Ser	Lys	Thr	Ile	Tyr	Lys	Leu	Asn	
				215					220					225	
Gly	Val	Ser	Glu	Arg	Asp	Leu	Lys	Lys	Ser	Val	Leu	Trp	Leu	Lys	
				230					235					240	
Asp	Ser	Leu	Gln	Cys	Thr	Cys	Glu	Glu	Met	Asn	Asp	Ile	Asn	Ala	
				245					250					255	
Pro	Tyr	Leu	Val	Met	Gly	Gln	Lys	Gln	Gly	Gly	Glu	Leu	Val	Ile	
				260					265					270	
Thr	Ser	Val	Lys	Arg	Trp	Gln	Lys	Gly	Gln	Arg	Glu	Phe	Lys	Arg	
				275					280					285	
Ile	Ser	Arg	Ser	Ile	Arg	Lys	Leu	Gln	Cys						
				290					295						

<210> 416  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 416  
 cctggctcgc tgctgctgct c 21

<210> 417  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 417  
 cctcacaggt gcactgcaag ctgtc 25

<210> 418  
 <211> 47  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 418

ctcttcctct ttggccagcc cgacttctcc tacaagcgca gaattgc 47

<210> 419

<211> 1830

<212> DNA

<213> Homo sapiens

<400> 419

gtggaggccg ccgacgatgg cggggccgac ggaggccgag acgggggttg 50

ccgagccccc ggccctgtgc gcgcagcggg gccaccgcac ctacgcgcgc 100

cgctgggtgt tcctgctcgc gatcagcctg ctcaactgct ccaacgccac 150

gctgtggctc agctttgcac ctgtggctga cgtcattgct gaggacttgg 200

tcctgtccat ggagcagatc aactggctgt cactggtcta cctcgtggta 250

tccaccccat ttggcgtggc ggccatctgg atcctggact ccgtcgggct 300

ccgtgcggcg accatcctgg gtgcgtggct gaactttgcc gggagtgtgc 350

tacgcatggt gccctgcatg gttgttggga cccaaaaccc atttgccttc 400

ctcatgggtg gccagagcct ctgtgccctt gccagagacc tggatcatctt 450

ctctccagcc aagctggctg ccttgtgggt cccagagcac cagcagacca 500

cggccaacat gctcgccacc atgtcgaacc ctctgggcgt ccttgtggcc 550

aatgtgctgt cccctgtgct ggtcaagaag ggtgaggaca ttccgttaat 600

gctcgggtgc tataccatcc ctgctggcgt cgtctgcctg ctgtccacca 650

tctgcctgtg ggagagtgtg cccccaccc cgccctctgc cggggctgcc 700

agctccacct cagagaagtt cctggatggg ctcaagctgc agctcatgtg 750

gaacaaggcc tatgtcatcc tggctgtgtg cttgggggga atgatcggga 800

tctctgccag cttctcagcc ctctggagc agatcctctg tgcaagcggc 850

cactccagtg ggttttcgg cctctgtggc gctctcttca tcacgtttgg 900

gatcctgggg gcactggctc tcggccccta tgtggaccgg accaagcact 950

tcactgaggc caccaagatt ggctgtgcc tgttctctct ggctgcgtg 1000

ccctttgccc tgggtgtcca gctgcaggga cagacccttg ccctggctgc 1050

cacctgctcg ctgctcgggc tgtttggctt ctcggtgggc ccctggcca 1100

09978192.101501

tggagttggc ggtcgagtgt tccttccccg tgggggaggg ggctgccaca 1150  
 ggcatgatct ttgtgctggg gcaggccgag ggaataactca tcatgctggc 1200  
 aatgacggca ctgactgtgc gacgctcgga gccgtccttg tccacctgcc 1250  
 agcaggggga ggatccactt gactggacag tgtctctgct gctgatggcc 1300  
 ggctgtgca ccttcttcag ctgcatactg gcggtcttct tccacacccc 1350  
 ataccggcgc ctgcaggccg agtctgggga gccccctcc acccgtaacg 1400  
 ccgtgggcgg cgcagactca gggccgggtg tggaccgagg gggagcagga 1450  
 agggctgggg tcctggggcc cagcacggcg actccggagt gcacggcgag 1500  
 gggggcctcg ctagaggacc ccagagggcc cgggagcccc caccagcct 1550  
 gccaccgagc gactccccgt gcgcaaggcc cagcagccac cgacgcgccc 1600  
 tcccgccccg gcagactcgc aggcagggtc caagcgtcca ggtttattga 1650  
 cccggctggg tctcactcct ccttctctc cccgtgggtg atcacgtagc 1700  
 tgagcgcctt gtagtccagg ttgcccgcca catcgatgga ggcgaactgg 1750  
 aacatctggt ccacctgcgg gcgggggcga aagggtcctt tgcgggctcc 1800  
 gggagcgaat tacaagcgcg cacctgaaaa 1830

<210> 420

<211> 560

<212> PRT

<213> Homo sapiens

<400> 420

Met	Ala	Gly	Pro	Thr	Glu	Ala	Glu	Thr	Gly	Leu	Ala	Glu	Pro	Arg
1				5					10					15
Ala	Leu	Cys	Ala	Gln	Arg	Gly	His	Arg	Thr	Tyr	Ala	Arg	Arg	Trp
				20					25					30
Val	Phe	Leu	Leu	Ala	Ile	Ser	Leu	Leu	Asn	Cys	Ser	Asn	Ala	Thr
				35					40					45
Leu	Trp	Leu	Ser	Phe	Ala	Pro	Val	Ala	Asp	Val	Ile	Ala	Glu	Asp
				50					55					60
Leu	Val	Leu	Ser	Met	Glu	Gln	Ile	Asn	Trp	Leu	Ser	Leu	Val	Tyr
				65					70					75
Leu	Val	Val	Ser	Thr	Pro	Phe	Gly	Val	Ala	Ala	Ile	Trp	Ile	Leu
				80					85					90
Asp	Ser	Val	Gly	Leu	Arg	Ala	Ala	Thr	Ile	Leu	Gly	Ala	Trp	Leu
				95					100					105
Asn	Phe	Ala	Gly	Ser	Val	Leu	Arg	Met	Val	Pro	Cys	Met	Val	Val

	110		115		120
Gly Thr Gln Asn	Pro Phe Ala Phe Leu	Met Gly Gly Gln Ser	Leu		
	125		130		135
Cys Ala Leu Ala	Gln Ser Leu Val Ile	Phe Ser Pro Ala Lys	Leu		
	140		145		150
Ala Ala Leu Trp	Phe Pro Glu His Gln	Arg Ala Thr Ala Asn	Met		
	155		160		165
Leu Ala Thr Met	Ser Asn Pro Leu Gly	Val Leu Val Ala Asn	Val		
	170		175		180
Leu Ser Pro Val	Leu Val Lys Lys Gly	Glu Asp Ile Pro Leu	Met		
	185		190		195
Leu Gly Val Tyr	Thr Ile Pro Ala Gly	Val Val Cys Leu Leu	Ser		
	200		205		210
Thr Ile Cys Leu	Trp Glu Ser Val Pro	Pro Thr Pro Pro Ser	Ala		
	215		220		225
Gly Ala Ala Ser	Ser Thr Ser Glu Lys	Phe Leu Asp Gly Leu	Lys		
	230		235		240
Leu Gln Leu Met	Trp Asn Lys Ala Tyr	Val Ile Leu Ala Val	Cys		
	245		250		255
Leu Gly Gly Met	Ile Gly Ile Ser Ala	Ser Phe Ser Ala Leu	Leu		
	260		265		270
Glu Gln Ile Leu	Cys Ala Ser Gly His	Ser Ser Gly Phe Ser	Gly		
	275		280		285
Leu Cys Gly Ala	Leu Phe Ile Thr Phe	Gly Ile Leu Gly Ala	Leu		
	290		295		300
Ala Leu Gly Pro	Tyr Val Asp Arg Thr	Lys His Phe Thr Glu	Ala		
	305		310		315
Thr Lys Ile Gly	Leu Cys Leu Phe Ser	Leu Ala Cys Val Pro	Phe		
	320		325		330
Ala Leu Val Ser	Gln Leu Gln Gly Gln	Thr Leu Ala Leu Ala	Ala		
	335		340		345
Thr Cys Ser Leu	Leu Gly Leu Phe Gly	Phe Ser Val Gly Pro	Val		
	350		355		360
Ala Met Glu Leu	Ala Val Glu Cys Ser	Phe Pro Val Gly Glu	Gly		
	365		370		375
Ala Ala Thr Gly	Met Ile Phe Val Leu	Gly Gln Ala Glu Gly	Ile		
	380		385		390
Leu Ile Met Leu	Ala Met Thr Ala Leu	Thr Val Arg Arg Ser	Glu		
	395		400		405



Pro Ser Leu Ser Thr Cys Gln Gln Gly Glu Asp Pro Leu Asp Trp  
410 415 420

Thr Val Ser Leu Leu Leu Met Ala Gly Leu Cys Thr Phe Phe Ser  
425 430 435

Cys Ile Leu Ala Val Phe Phe His Thr Pro Tyr Arg Arg Leu Gln  
440 445 450

Ala Glu Ser Gly Glu Pro Pro Ser Thr Arg Asn Ala Val Gly Gly  
455 460 465

Ala Asp Ser Gly Pro Gly Val Asp Arg Gly Gly Ala Gly Arg Ala  
470 475 480

Gly Val Leu Gly Pro Ser Thr Ala Thr Pro Glu Cys Thr Ala Arg  
485 490 495

Gly Ala Ser Leu Glu Asp Pro Arg Gly Pro Gly Ser Pro His Pro  
500 505 510

Ala Cys His Arg Ala Thr Pro Arg Ala Gln Gly Pro Ala Ala Thr  
515 520 525

Asp Ala Pro Ser Arg Pro Gly Arg Leu Ala Gly Arg Val Gln Ala  
530 535 540

Ser Arg Phe Ile Asp Pro Ala Gly Ser His Ser Ser Phe Ser Ser  
545 550 555

Pro Trp Val Ile Thr  
560

<210> 421  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 421  
agcttctcag ccctcctgga gcag 24

<210> 422  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 422  
cgggtcaata aacctggacg cttgg 25

<210> 423  
<211> 43  
<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 423

tatgtggacc ggaccaagca cttcactgag gccaccaaga ttg 43

<210> 424

<211> 4313

<212> DNA

<213> Homo sapiens

<400> 424

gtcccacatc ctgctcaact gggtcaggtc cctcttagac cagctcttgt 50

ccatcatttg ctgaagtgga ccaactagtt cccagtagg gggctctccc 100

tggcaattct tgatcggcgt ttggacatct cagatcgctt ccaatgaaga 150

tggccttgcc ttggggctct gcttgtttca taatcatcta actatgggac 200

aaggttgtgc cggcagctct gggggaagga gcacggggct gatcaagcca 250

tccaggaaac actggaggac ttgtccagcc ttgaaagaac tctagtgggt 300

tctgaatcta gccacttg cggtaagcat gatgcaactt ctgcaacttc 350

tgctggggct tttggggcca ggtggctact tatttctttt aggggattgt 400

caggaggtga ccactctcac ggtgaaatac caagtgtcag aggaagtgcc 450

atcrggtaca gtgatcggga agctgtccca ggaactgggc cgggaggaga 500

ggcggaggca agctggggcc gccttcacag tggtgcagct gcctcaggcg 550

ctccccattc aggtggactc tgaggaaggc ttgctcagca caggcaggcg 600

gctggatcga gagcagctgt gccgacagtg ggatccctgc ctggtttct 650

ttgatgtgct tgccacaggg gatttggtc tgatccatgt ggagatccaa 700

gtgctggaca tcaatgacca ccagccacgg tttcccaaag gcgagcagga 750

gctggaaatc tctgagagcg cctctctgcg aaccggatc cccctggaca 800

gagctcttga cccagacaca ggccctaaca cctgcacac ctacactctg 850

tctcccagtg agcactttgc cttggatgtc attgtgggccc ctgatgagac 900

caaacatgca gaactcatag tggatgaagga gctggacagg gaaatccatt 950

catttttttga tctgggtgta actgcctatg acaatgggaa ccccccaag 1000

tcaggtacca gcttgggtcaa ggtcaacgtc ttggactcca atgacaatag 1050

ccctgcgttt gctgagagtt cactggcact ggaaatccaa gaagatgctg 1100

09978192-101501

cacctggtac gcttctcata aaactgaccg ccacagaccc tgaccaaggc 1150  
cccaatgggg aggtggagtt cttoctcagt aagcacatgc ctccagaggt 1200  
gctggacacc ttcagtattg atgccaagac aggccaggtc attctgcgtc 1250  
gacctctaga ctatgaaaag aacctgcct acgaggtgga tgttcaggca 1300  
agggacctgg gtoccaatcc tatcccagcc cattgcaaag ttctcatcaa 1350  
ggttctggat gtcaatgaca acatcccaag catccacgtc acatgggcct 1400  
cccagccatc actggtgtca gaagctcttc ccaaggacag ttttattgct 1450  
cttgtcatgg cagatgactt ggattcagga cacaatgggt tggtcactg 1500  
ctggctgagc caagagctgg gccacttcag gctgaaaaga actaatggca 1550  
acacatacat gttgctaacc aatgccacac tggacagaga gcagtggccc 1600  
aaatataccc tcaactctgtt agcccaagac caaggactcc agcccttate 1650  
agccaagaaa cagctcagca ttcagatcag tgacatcaac gacaatgcac 1700  
ctgtgtttga gaaaagcagg tatgaagtct ccacgoggga aaacaactta 1750  
ccctctcttc acctcattac catcaaggct catgatgcag acttgggcat 1800  
taatggaaaa gtctcatacc gcatccagga ctcccagtt gctcacttag 1850  
tagctattga ctccaacaca ggagaggtca ctgctcagag gtcactgaac 1900  
tatgaagaga tggccggctt tgagttccag gtgatgcag aggacagcgg 1950  
gcaacccatg cttgcatcca gtgtctctgt gtgggtcagc ctcttggtg 2000  
ccaatgataa tgccccagag gtggtccagc ctgtgctcag cgatggaaaa 2050  
gccagcctct ccgtgcttgt gaatgcctcc acaggccacc tgctggtgcc 2100  
catcgagact cccaatggct tgggcccagc gggcactgac acacctccac 2150  
tggccactca cagctcccg ccattccttt tgacaaccat tgtggcaaga 2200  
gatgcagact cgggggcaaa tggagagccc ctctacagca tccgcaatgg 2250  
aaatgaagcc cacctcttca tcctcaaccc tcatacgggg cagctgttcg 2300  
tcaatgtcac caatgccagc agcctcattg ggagtgagtg ggagctggag 2350  
atagtagtag aggaccaggg aagccccccc ttacagaccc gagccctgtt 2400  
gagggtcagt tttgtcacca gtgtggacca cctgagggac tcagcccga 2450  
agcctggggc cttgagcatg tcgatgctga cggatgatctg cctggctgta 2500  
ctgttgggca tcttcgggtt gatcctggct ttgttcatgt ccatctgccg 2550

gacagaaaag aaggacaaca gggcctacaa ctgtcgggag gccgagtcca 2600  
 cctaccgcca gcagcccaag aggccccaga aacacattca gaaggcagac 2650  
 atccacctcg tgcctgtgct caggggtcag gcagggtgagc cttgtgaagt 2700  
 cgggcagtc cacaagatg tggacaagga ggcgatgatg gaagcaggct 2750  
 gggaccctg cctgcaggcc cccttccacc tcaccccgac cctgtacagg 2800  
 acgctgcgta atcaaggcaa ccaggaggca ccggcggaga gccgagaggt 2850  
 gctgcaagac acggtcaacc tccttttcaa ccatcccagg cagaggaatg 2900  
 cctcccggga gaacctgaac cttcccagc ccagcctgc cacaggccag 2950  
 ccacgttcca ggcctctgaa ggttgcaggc agccccacag ggaggctggc 3000  
 tggagaccag ggcagtgagg aagccccaca gaggccacca gcctcctctg 3050  
 caaccctgag acggcagcga catctcaatg gcaaagtgtc ccctgagaaa 3100  
 gaatcagggc cccgtcagat cctgcggagc ctggtccggc tgtctgtggc 3150  
 tgccttcgcc gagcggaaacc ccgtggagga gctcactgtg gattctcctc 3200  
 ctgttcagca aatctcccag ctgctgtcct tgctgcatca gggccaattc 3250  
 cagcccaaac caaaccaccg aggaaataag tacttggcca agccaggagg 3300  
 cagcaggagt gcaatcccag acacagatgg cccaagtga agggctggag 3350  
 gccagacaga ccagaacag gaggaagggc ctttggatcc tgaagaggac 3400  
 ctctctgtga agcaactgct agaagaagag ctgtcaagtc tgctggaccc 3450  
 cagcacaggt ctggccctgg accggctgag cggccctgac ccggcctgga 3500  
 tggcgagact ctctttgccc ctcaccacca actaccgtga caatgtgatc 3550  
 tccccgatg ctgcagccac ggaggagccg aggaccttcc agacgttcgg 3600  
 caaggcagag gcaccagagc tgagcccaac aggcacgagg ctggccagca 3650  
 cctttgtctc ggagatgagc tcaactgtgg agatgctgct ggaacagcgc 3700  
 tccagcatgc ccgtggaggc cgcctccgag gcgctgcggc ggctctcgg 3750  
 ctgcgggagg accctcagtt tagacttggc caccagtga gcctcaggca 3800  
 tgaaagtga aggggaccca ggtggaaaga cggggactga gggcaagagc 3850  
 agaggcagca gcagcagcag caggtgcctg tgaacatacc tcagacgcct 3900  
 ctggatccaa gaaccagggg cctgaggatc tgtggacaag agctggtttc 3950  
 taaaatcttg taactcacta gctagcggcg gcctgagaac tttagggtga 4000

ctgatgctac cccacagag gaggcaagag cccaggact aacagctgac 4050  
 tgaccaaagc agcccttgt aagcagctct gagtcttttg gaggacaggg 4100  
 acggtttgtg gctgagataa gtgtttcctg gcaaacata tgtggagcac 4150  
 aaagggtcag tcctctggca gaacagatgc cacggagtat cacaggcagg 4200  
 aaagggtggc cttcttgggt agcaggagtc agggggctgt accctggggg 4250  
 tgccaggaaa tgctctctga cctatcaata aaggaaaagc agtaaaaaaa 4300  
 aaaaaaaaaa aaa 4313

<210> 425

<211> 1184

<212> PRT

<213> Homo sapiens

<400> 425

Met	Met	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Gly	Leu	Leu	Gly	Pro	Gly	
1				5					10					15	
Gly	Tyr	Leu	Phe	Leu	Leu	Gly	Asp	Cys	Gln	Glu	Val	Thr	Thr	Leu	
				20					25					30	
Thr	Val	Lys	Tyr	Gln	Val	Ser	Glu	Glu	Val	Pro	Ser	Gly	Thr	Val	
				35					40					45	
Ile	Gly	Lys	Leu	Ser	Gln	Glu	Leu	Gly	Arg	Glu	Glu	Arg	Arg	Arg	
				50					55					60	
Gln	Ala	Gly	Ala	Ala	Phe	Gln	Val	Leu	Gln	Leu	Pro	Gln	Ala	Leu	
				65					70					75	
Pro	Ile	Gln	Val	Asp	Ser	Glu	Glu	Gly	Leu	Leu	Ser	Thr	Gly	Arg	
				80					85					90	
Arg	Leu	Asp	Arg	Glu	Gln	Leu	Cys	Arg	Gln	Trp	Asp	Pro	Cys	Leu	
				95					100					105	
Val	Ser	Phe	Asp	Val	Leu	Ala	Thr	Gly	Asp	Leu	Ala	Leu	Ile	His	
				110					115					120	
Val	Glu	Ile	Gln	Val	Leu	Asp	Ile	Asn	Asp	His	Gln	Pro	Arg	Phe	
				125					130					135	
Pro	Lys	Gly	Glu	Gln	Glu	Leu	Glu	Ile	Ser	Glu	Ser	Ala	Ser	Leu	
				140					145					150	
Arg	Thr	Arg	Ile	Pro	Leu	Asp	Arg	Ala	Leu	Asp	Pro	Asp	Thr	Gly	
				155					160					165	
Pro	Asn	Thr	Leu	His	Thr	Tyr	Thr	Leu	Ser	Pro	Ser	Glu	His	Phe	
				170					175					180	
Ala	Leu	Asp	Val	Ile	Val	Gly	Pro	Asp	Glu	Thr	Lys	His	Ala	Glu	
				185					190					195	

Leu Ile Val Val	Lys Glu Leu Asp Arg	Glu Ile His Ser Phe	Phe
200		205	210
Asp Leu Val Leu	Thr Ala Tyr Asp Asn	Gly Asn Pro Pro Lys	Ser
215		220	225
Gly Thr Ser Leu	Val Lys Val Asn Val	Leu Asp Ser Asn Asp	Asn
230		235	240
Ser Pro Ala Phe	Ala Glu Ser Ser Leu	Ala Leu Glu Ile Gln	Glu
245		250	255
Asp Ala Ala Pro	Gly Thr Leu Leu Ile	Lys Leu Thr Ala Thr	Asp
260		265	270
Pro Asp Gln Gly	Pro Asn Gly Glu Val	Glu Phe Phe Leu Ser	Lys
275		280	285
His Met Pro Pro	Glu Val Leu Asp Thr	Phe Ser Ile Asp Ala	Lys
290		295	300
Thr Gly Gln Val	Ile Leu Arg Arg Pro	Leu Asp Tyr Glu Lys	Asn
305		310	315
Pro Ala Tyr Glu	Val Asp Val Gln Ala	Arg Asp Leu Gly Pro	Asn
320		325	330
Pro Ile Pro Ala	His Cys Lys Val Leu	Ile Lys Val Leu Asp	Val
335		340	345
Asn Asp Asn Ile	Pro Ser Ile His Val	Thr Trp Ala Ser Gln	Pro
350		355	360
Ser Leu Val Ser	Glu Ala Leu Pro Lys	Asp Ser Phe Ile Ala	Leu
365		370	375
Val Met Ala Asp	Asp Leu Asp Ser Gly	His Asn Gly Leu Val	His
380		385	390
Cys Trp Leu Ser	Gln Glu Leu Gly His	Phe Arg Leu Lys Arg	Thr
395		400	405
Asn Gly Asn Thr	Tyr Met Leu Leu Thr	Asn Ala Thr Leu Asp	Arg
410		415	420
Glu Gln Trp Pro	Lys Tyr Thr Leu Thr	Leu Leu Ala Gln Asp	Gln
425		430	435
Gly Leu Gln Pro	Leu Ser Ala Lys Lys	Gln Leu Ser Ile Gln	Ile
440		445	450
Ser Asp Ile Asn	Asp Asn Ala Pro Val	Phe Glu Lys Ser Arg	Tyr
455		460	465
Glu Val Ser Thr	Arg Glu Asn Asn Leu	Pro Ser Leu His Leu	Ile
470		475	480
Thr Ile Lys Ala	His Asp Ala Asp Leu	Gly Ile Asn Gly Lys	Val

	485	490	495
Ser Tyr Arg Ile	Gln Asp Ser Pro Val	Ala His Leu Val Ala	Ile
	500	505	510
Asp Ser Asn Thr	Gly Glu Val Thr Ala	Gln Arg Ser Leu Asn Tyr	
	515	520	525
Glu Glu Met Ala	Gly Phe Glu Phe Gln	Val Ile Ala Glu Asp Ser	
	530	535	540
Gly Gln Pro Met	Leu Ala Ser Ser Val	Ser Val Trp Val Ser Leu	
	545	550	555
Leu Asp Ala Asn	Asp Asn Ala Pro Glu	Val Val Gln Pro Val Leu	
	560	565	570
Ser Asp Gly Lys	Ala Ser Leu Ser Val	Leu Val Asn Ala Ser Thr	
	575	580	585
Gly His Leu Leu	Val Pro Ile Glu Thr	Pro Asn Gly Leu Gly Pro	
	590	595	600
Ala Gly Thr Asp	Thr Pro Pro Leu Ala	Thr His Ser Ser Arg Pro	
	605	610	615
Phe Leu Leu Thr	Thr Ile Val Ala Arg	Asp Ala Asp Ser Gly Ala	
	620	625	630
Asn Gly Glu Pro	Leu Tyr Ser Ile Arg	Asn Gly Asn Glu Ala His	
	635	640	645
Leu Phe Ile Leu	Asn Pro His Thr Gly	Gln Leu Phe Val Asn Val	
	650	655	660
Thr Asn Ala Ser	Ser Leu Ile Gly Ser	Glu Trp Glu Leu Glu Ile	
	665	670	675
Val Val Glu Asp	Gln Gly Ser Pro Pro	Leu Gln Thr Arg Ala Leu	
	680	685	690
Leu Arg Val Met	Phe Val Thr Ser Val	Asp His Leu Arg Asp Ser	
	695	700	705
Ala Arg Lys Pro	Gly Ala Leu Ser Met	Ser Met Leu Thr Val Ile	
	710	715	720
Cys Leu Ala Val	Leu Leu Gly Ile Phe	Gly Leu Ile Leu Ala Leu	
	725	730	735
Phe Met Ser Ile	Cys Arg Thr Glu Lys	Lys Asp Asn Arg Ala Tyr	
	740	745	750
Asn Cys Arg Glu	Ala Glu Ser Thr Tyr	Arg Gln Gln Pro Lys Arg	
	755	760	765
Pro Gln Lys His	Ile Gln Lys Ala Asp	Ile His Leu Val Pro Val	
	770	775	780

Leu Arg Gly Gln Ala Gly Glu Pro Cys Glu Val Gly Gln Ser His	785	790	795
Lys Asp Val Asp Lys Glu Ala Met Met Glu Ala Gly Trp Asp Pro	800	805	810
Cys Leu Gln Ala Pro Phe His Leu Thr Pro Thr Leu Tyr Arg Thr	815	820	825
Leu Arg Asn Gln Gly Asn Gln Gly Ala Pro Ala Glu Ser Arg Glu	830	835	840
Val Leu Gln Asp Thr Val Asn Leu Leu Phe Asn His Pro Arg Gln	845	850	855
Arg Asn Ala Ser Arg Glu Asn Leu Asn Leu Pro Glu Pro Gln Pro	860	865	870
Ala Thr Gly Gln Pro Arg Ser Arg Pro Leu Lys Val Ala Gly Ser	875	880	885
Pro Thr Gly Arg Leu Ala Gly Asp Gln Gly Ser Glu Glu Ala Pro	890	895	900
Gln Arg Pro Pro Ala Ser Ser Ala Thr Leu Arg Arg Gln Arg His	905	910	915
Leu Asn Gly Lys Val Ser Pro Glu Lys Glu Ser Gly Pro Arg Gln	920	925	930
Ile Leu Arg Ser Leu Val Arg Leu Ser Val Ala Ala Phe Ala Glu	935	940	945
Arg Asn Pro Val Glu Glu Leu Thr Val Asp Ser Pro Pro Val Gln	950	955	960
Gln Ile Ser Gln Leu Leu Ser Leu Leu His Gln Gly Gln Phe Gln	965	970	975
Pro Lys Pro Asn His Arg Gly Asn Lys Tyr Leu Ala Lys Pro Gly	980	985	990
Gly Ser Arg Ser Ala Ile Pro Asp Thr Asp Gly Pro Ser Ala Arg	995	1000	1005
Ala Gly Gly Gln Thr Asp Pro Glu Gln Glu Glu Gly Pro Leu Asp	1010	1015	1020
Pro Glu Glu Asp Leu Ser Val Lys Gln Leu Leu Glu Glu Glu Leu	1025	1030	1035
Ser Ser Leu Leu Asp Pro Ser Thr Gly Leu Ala Leu Asp Arg Leu	1040	1045	1050
Ser Ala Pro Asp Pro Ala Trp Met Ala Arg Leu Ser Leu Pro Leu	1055	1060	1065
Thr Thr Asn Tyr Arg Asp Asn Val Ile Ser Pro Asp Ala Ala Ala			



1070	1075	1080
Thr Glu Glu Pro Arg Thr Phe Gln Thr Phe Gly Lys Ala Glu Ala		
1085	1090	1095
Pro Glu Leu Ser Pro Thr Gly Thr Arg Leu Ala Ser Thr Phe Val		
1100	1105	1110
Ser Glu Met Ser Ser Leu Leu Glu Met Leu Leu Glu Gln Arg Ser		
1115	1120	1125
Ser Met Pro Val Glu Ala Ala Ser Glu Ala Leu Arg Arg Leu Ser		
1130	1135	1140
Val Cys Gly Arg Thr Leu Ser Leu Asp Leu Ala Thr Ser Ala Ala		
1145	1150	1155
Ser Gly Met Lys Val Gln Gly Asp Pro Gly Gly Lys Thr Gly Thr		
1160	1165	1170
Glu Gly Lys Ser Arg Gly Ser Ser Ser Ser Ser Arg Cys Leu		
1175	1180	

<210> 426  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 426  
 gtaagcacat gcctccagag gtgc 24

<210> 427  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 427  
 gtgacgtgga tgcttgggat gttg 24

<210> 428  
 <211> 50  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 428  
 tggacacctt cagtattgat gccagacag gccaggtcat tctgcgtcga 50

<210> 429  
 <211> 2037

<212> DNA  
<213> Homo sapiens

<400> 429  
cggacgcgtg ggcggacgcg tgggggagag ccgcagtccc ggctgcagca 50  
cctgggagaa ggcagaccgt gtgagggggc ctgtggcccc agcgtgctgt 100  
ggcctcgggg agtgggaagt ggaggcagga gccttcctta cacttcgcca 150  
tgagtttcct catcgactcc agcatcatga ttacctcca gatactattt 200  
tttggatttg ggtggctttt cttcatgcgc caattgttta aagactatga 250  
gatacgtcag tatgttgtag aggtgatctt ctccgtgacg tttgcatttt 300  
cttgacccat gtttgagctc atcatctttg aaatcttagg agtattgaat 350  
agcagctccc gttattttca ctggaaaatg aacctgtgtg taattctgct 400  
gatcctgggtt ttcattggtgc ctttttacat tggctatttt attgtgagca 450  
atatccgact actgcataaa caacgactgc ttttttctg tctcttatgg 500  
ctgaccttta tgtatttctt ctggaaacta ggagatccct tccccattct 550  
cagcccaaaa catgggatct tatccataga acagctcatc agccgggttg 600  
gtgtgattgg agtgactctc atggctcttc tttctggatt tgggtgctgtc 650  
aactgcccat acacttacat gtcttacttc ctcaggaatg tgactgacac 700  
ggatattcta gccctggaac ggcgactgct gcaaaccatg gatatgatca 750  
taagcaaaaa gaaaaggatg gcaatggcac ggagaacaat gttccagaag 800  
ggggaagtgc ataacaaacc atcaggtttc tggggaatga taaaaagtgt 850  
taccacttca gcatcaggaa gtgaaaatct tactcttatt caacaggaag 900  
tggatgcttt ggaagaatta agcaggcagc tttttctgga aacagctgat 950  
ctatatgcta ccaaggagag aatagaatac tccaaaacct tcaaggggaa 1000  
atattttaat tttcttggtt actttttctc tatttactgt gtttggaata 1050  
ttttcatggc taccatcaat attgtttttg atcgagttgg gaaaacggat 1100  
cctgtcacia gaggcattga gatcactgtg aattatctgg gaatccaatt 1150  
tgatgtgaag ttttgggtccc aacacatttc cttcattctt gttggaataa 1200  
tcactgtcac atccatcaga ggattgctga tcaactctac caagttcttt 1250  
tatgccatct ctagcagtaa gtcctccaat gtcattgtcc tgctattagc 1300  
acagataatg ggcattgtact ttgtctctc tgtgctgctg atccgaatga 1350

gtatgccttt agaataccgc accataatca ctgaagtcct tggagaactg 1400  
cagttcaact tctatcaccg ttggtttgat gtgatcttcc tggtcagcgc 1450  
tctctctagc atactcttcc tctatattggc tcacaaacag gcaccagaga 1500  
agcaaatggc accttgaact taagcctact acagactgtt agaggccagt 1550  
ggtttcaaaa tttagatata agaggggggga aaaatggaac cagggcctga 1600  
cattttataa acaaacaaaa tgctatggta gcatttttca ccttcatagc 1650  
atactccttc cccgtcaggt gatactatga ccatgagtag catcagccag 1700  
aacatgagag ggagaactaa ctcaagacaa tactcagcag agagcatccc 1750  
gtgtggatat gaggctggtg tagaggcgga gaggagccaa gaaactaaag 1800  
gtgaaaaata cactggaact ctgggggcaag acatgtctat ggtagctgag 1850  
ccaaacacgt aggatttccg ttttaagggtt cacatggaaa aggttatagc 1900  
tttgccttga gattgactca ttaaaatcag agactgtaac aaaaaaaaaa 1950  
aaaaaaaaaa agggcgggccg cgactctaga gtcgacctgc agaagcttgg 2000  
ccgccatggc ccaacttggt tattgcagct tataatg 2037

<210> 430  
<211> 455  
<212> PRT  
<213> Homo sapiens

<400> 430  
Met Ser Phe Leu Ile Asp Ser Ser Ile Met Ile Thr Ser Gln Ile  
1 5 10 15  
Leu Phe Phe Gly Phe Gly Trp Leu Phe Phe Met Arg Gln Leu Phe  
20 25 30  
Lys Asp Tyr Glu Ile Arg Gln Tyr Val Val Gln Val Ile Phe Ser  
35 40 45  
Val Thr Phe Ala Phe Ser Cys Thr Met Phe Glu Leu Ile Ile Phe  
50 55 60  
Glu Ile Leu Gly Val Leu Asn Ser Ser Ser Arg Tyr Phe His Trp  
65 70 75  
Lys Met Asn Leu Cys Val Ile Leu Leu Ile Leu Val Phe Met Val  
80 85 90  
Pro Phe Tyr Ile Gly Tyr Phe Ile Val Ser Asn Ile Arg Leu Leu  
95 100 105  
His Lys Gln Arg Leu Leu Phe Ser Cys Leu Leu Trp Leu Thr Phe  
110 115 120

Met Tyr Phe Phe Trp Lys Leu Gly Asp	Pro Phe Pro Ile Leu Ser	125	130	135
Pro Lys His Gly Ile Leu Ser Ile Glu	Gln Leu Ile Ser Arg Val	140	145	150
Gly Val Ile Gly Val Thr Leu Met Ala	Leu Leu Ser Gly Phe Gly	155	160	165
Ala Val Asn Cys Pro Tyr Thr Tyr Met	Ser Tyr Phe Leu Arg Asn	170	175	180
Val Thr Asp Thr Asp Ile Leu Ala Leu	Glu Arg Arg Leu Leu Gln	185	190	195
Thr Met Asp Met Ile Ile Ser Lys Lys	Lys Arg Met Ala Met Ala	200	205	210
Arg Arg Thr Met Phe Gln Lys Gly Glu	Val His Asn Lys Pro Ser	215	220	225
Gly Phe Trp Gly Met Ile Lys Ser Val	Thr Thr Ser Ala Ser Gly	230	235	240
Ser Glu Asn Leu Thr Leu Ile Gln Gln	Glu Val Asp Ala Leu Glu	245	250	255
Glu Leu Ser Arg Gln Leu Phe Leu Glu	Thr Ala Asp Leu Tyr Ala	260	265	270
Thr Lys Glu Arg Ile Glu Tyr Ser Lys	Thr Phe Lys Gly Lys Tyr	275	280	285
Phe Asn Phe Leu Gly Tyr Phe Phe Ser	Ile Tyr Cys Val Trp Lys	290	295	300
Ile Phe Met Ala Thr Ile Asn Ile Val	Phe Asp Arg Val Gly Lys	305	310	315
Thr Asp Pro Val Thr Arg Gly Ile Glu	Ile Thr Val Asn Tyr Leu	320	325	330
Gly Ile Gln Phe Asp Val Lys Phe Trp	Ser Gln His Ile Ser Phe	335	340	345
Ile Leu Val Gly Ile Ile Ile Val Thr	Ser Ile Arg Gly Leu Leu	350	355	360
Ile Thr Leu Thr Lys Phe Phe Tyr Ala	Ile Ser Ser Ser Lys Ser	365	370	375
Ser Asn Val Ile Val Leu Leu Leu Ala	Gln Ile Met Gly Met Tyr	380	385	390
Phe Val Ser Ser Val Leu Leu Ile Arg	Met Ser Met Pro Leu Glu	395	400	405
Tyr Arg Thr Ile Ile Thr Glu Val Leu	Gly Glu Leu Gln Phe Asn			

410 415 420

Phe Tyr His Arg Trp Phe Asp Val Ile Phe Leu Val Ser Ala Leu  
425 430 435

Ser Ser Ile Leu Phe Leu Tyr Leu Ala His Lys Gln Ala Pro Glu  
440 445 450

Lys Gln Met Ala Pro  
455

<210> 431  
<211> 407  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 78, 81, 113, 157, 224, 297  
<223> unknown base

<400> 431  
catgggaagt ggagccggag ccttccttac actcgccatg agtttccctca 50  
tcgactccag catcatgatt acctcccnga nactattttt tggatttggg 100  
tggcttttct tcngcgccaa tgtttaaaga ctatgagata cgtcagtatg 150  
ttgtacnggt gatctttctcc gtgacgtttg ccattttcttg caccatgttt 200  
gagctcatca tctttgaaat cttinggagta ttgaatagca gctcccgta 250  
ttttcactgg aaaatgaacc tgtgtgtaat tctgctgata ctgggtntca 300  
tgggtgccttt ttacattggc tattttattg tgagcaatat ccgactactg 350  
cataaacaac gactgctttt ttctgtctc ttatggctga cctttatgta 400  
tttccag 407

<210> 432  
<211> 457  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 31, 66, 81-82, 84, 122, 184, 187, 232, 241, 400, 424, 427, 434  
<223> unknown base

<400> 432  
gtgttgccct tggggagggg aaggggagcc nggccccttc ctaaaatttg 50  
gccaaagggtt tctttnttga attccgggtt nngnatacct tcccagaaaa 100  
tatttttttg atttggggta gnttttttcc atgcgccaat tgtttaaaga 150  
ctatgagata cgtcagtatg ttgtacaggt gatnttntcc gtgacgtttg 200

cattttcttg caccatgttt gagctcatca tntttgaaat nttaggagta 250  
 ttgaatagca gctcccgtta ttttactggg aaaatgaacc tgtgtgtaat 300  
 tctgctgac ctggttttca tggcgcttt ttacattggc tattttattg 350  
 tgagcaatat ccgactactg cataaacaac gactgctttt ttctgtctn 400  
 ttatggctga cctttatgta tttntntg aaantaggag atccctttcc 450  
 cattctc 457

<210> 433  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 433  
 aagtggagcc ggagccttcc 20

<210> 434  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 434  
 tcgttggtta tgcagtagtc gg 22

<210> 435  
 <211> 41  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 435  
 attgtttaaa gactatgaga tacgtcagta tgttgtagag g 41

<210> 436  
 <211> 3951  
 <212> DNA  
 <213> Homo sapiens

<400> 436  
 ctgcgcagg gatcgtccca tggccggggc tcggagccgc gacccttggg 50  
 gggcctccgg gatttgctac ctttttggct ccctgctcgt cgaactgctc 100  
 ttctcacggg ctgtcgctt caatctggac gtgatgggtg ccttgcgcaa 150  
 ggagggcgag ccaggcagcc tcttcggctt ctctgtggcc ctgcaccggc 200

agttgcagcc ccgacccccag agctggctgc tgggtgggtgc tccccaggcc 250  
 ctggctcttc ctgggcagca ggogaatcgc actggaggcc tcttcgcttg 300  
 cccgttgagc ctggaggaga ctgactgcta cagagtggac atcgaccagg 350  
 gagctgatat gcaaaaaggaa agcaaggaga accagtgggtt gggagtcagt 400  
 gttcggagcc aggggcctgg gggcaagatt gttacctgtg cacaccgata 450  
 tgaggcaagg cagcgagtgg accagatcct ggagacgcgg gatatgattg 500  
 gtcgctgctt tgtgctcagc caggacctgg ccatccggga tgagttggat 550  
 ggtgggggaat ggaagtctctg tgaggggacgc ccccaaggcc atgaacaatt 600  
 tgggttctgc cagcagggca cagctgccgc cttctcccct gatagccact 650  
 acctcctctt tggggcccca ggaacctata attggaaggc cacggccagg 700  
 gtggagctct gtgcacaggc ctccagcggc ctggcacacc tggacgacgg 750  
 tccctacgag gcgggggggag agaaggagca ggacccccgc ctcatcccgg 800  
 tccctgccaa cagctacttt ggcttctcta ttgactcggg gaaaggctctg 850  
 gtgcgtgcag aagagctgag ctttgtggct ggagcccccc gcgccaacca 900  
 caagggtgct gtggtcatcc tgcgcaagga cagcgccagt cgcctggtgc 950  
 ccgaggttat gctgtctggg gagcgccctga cctccggctt tggctactca 1000  
 ctggctgttg ctgacctcaa cagtgatggc tggccagacc tgatagtggg 1050  
 tgccccctac ttctttgagc gccagaaga gctgggggggt gctgtgtatg 1100  
 tgtacttgaa ccaggggggt cactgggctg ggatctcccc tctccggctc 1150  
 tgcggtccc ctgactccat gttcgggatc agcctggctg tcttggggga 1200  
 cctcaaccaa gatggctttc cagatattgc agtgggtgcc ccctttgatg 1250  
 gtgatgggaa agtcttcac taccatggga gcagcctggg ggttgctgcc 1300  
 aaaccttcac aggtgctgga gggcgaggct gtgggcatca agagcttcgg 1350  
 ctactccctg tcaggcagct tggatatgga tgggaaccaa taccctgacc 1400  
 tgctggtggg ctccctggct gacaccgcag tgctcttcag ggccagacct 1450  
 atcctccatg tctcccatga ggtctctatt gctccacgaa gcacgacct 1500  
 ggagcagccc aactgtgctg gcggccactc ggtctgtgtg gacctaaggg 1550  
 tctgtttcag ctacattgca gtccccagca gctatagccc tactgtggcc 1600  
 ctggactatg tgttagatgc ggacacagac cggaggctcc ggggccaggt 1650

tccccgtgtg acgttcctga gccgtaacct ggaagaaccc aagcaccagg 1700  
 cctcggggcac cgtgtggctg aagcaccagc atgaccgagt ctgtggagac 1750  
 gccatgttcc agctccagga aaatgtcaaa gacaagcttc gggccattgt 1800  
 agtgaccttg tcctacagtc tcacagacccc tcggctccgg cgacaggctc 1850  
 ctggccaggg gctgcctcca gtggccccca tcctcaatgc ccaccagccc 1900  
 agcaccacagc gggcagagat ccacttcctg aagcaaggct gtggtgaaga 1950  
 caagatctgc cagagcaatc tgcagctggc ccacgcccgc ttctgtaccc 2000  
 gggtcagcga cacggaattc caacctctgc ccatggatgt ggatggaaca 2050  
 acagccctgt ttgcaactgag tgggcagcca gtcattggcc tggagctgat 2100  
 ggtcaccaac ctgccatcgg acccagccca gcccagggct gatggggatg 2150  
 atgcccataa agcccagctc ctggatcatg ttcttgactc actgcactac 2200  
 tcaggggtcc gggccctgga cctgcggag aagccactct gcctgtccaa 2250  
 tgagaatgcc tcccatgttg agtgtgagct ggggaacccc atgaagagag 2300  
 gtgcccaggc caccttctac ctcatcctta gcacctccgg gatcagcatt 2350  
 gagaccacgg aactggaggt agagctgctg ttggccacga tcagttagca 2400  
 ggagctgcat ccagtctctg cagcagcccg tgtcttcatt gagctgccac 2450  
 tgtccattgc aggaatggcc attccccagc aactcttctt ctctggtgtg 2500  
 gtgagggggc agagagccat gcagtctgag cgggatgtgg gcagcaaggc 2550  
 caagtatgag gtcacgggtt ccaaccaagg ccagtcgctc agaaccctgg 2600  
 gctctgcctt cctcaacatc atgtggcctc atgagattgc caatgggaag 2650  
 tggttgctgt acccaatgca ggttgagctg gagggcgggc aggggcctgg 2700  
 gcagaaaggc ctttgcctc ccaggcccaa catcctccac ctggatgtgg 2750  
 acagtaggga taggaggcgg cgggagctgg agccacctga gcagcaggag 2800  
 cctggtgagc ggcaggagcc cagcatgtcc tggcggccag tgcctctgc 2850  
 tgagaagaag aaaaacatca cctggactg cggccggggc acggccaact 2900  
 gtgtggtgtt cagctgcccc ctctacagct ttgaccgccc ggctgtgctg 2950  
 catgtctggg gccgtctctg gaacagcacc tttctggagg agtactcagc 3000  
 tgtgaagtcc ctggaagtga ttgtccgggc caacatcaca gtgaagtcct 3050  
 ccataaagaa cttgatgctc cgagatgcct ccacagtgat ccagtgatg 3100



gtatacttgg accccatggc tgtggtggca gaaggagtgc cctggtgggt 3150  
catcctcctg gctgtactgg ctgggctgct ggtgctagca ctgctggtgc 3200  
tgctcctgtg gaagatggga ttcttcaaac gggcgaagca ccccgaggcc 3250  
accgtgcccc agtaccatgc ggtgaagatt cctcggggaag accgacagca 3300  
gttcaaggag gagaagacgg gcaccatcct gaggaacaac tggggcagcc 3350  
cccggcggga gggcccggat gcacacccca tcctggctgc tgacgggcat 3400  
cccgagctgg gccccgatgg gcatccaggg ccaggcaccg cctaggttcc 3450  
catgtcccag cctggcctgt ggctgccctc catcccttcc ccagagatgg 3500  
ctccttggga tgaagagggt agagtgggct gctggtgtcg catcaagatt 3550  
tggcaggatc ggcttcctca ggggcacaga cctctccac ccacaagaac 3600  
tcctcccacc caacttcccc ttagagtgtc gtgagatgag agtgggtaaa 3650  
tcagggacag ggccatgggg tagggtgaga agggcagggg tgcctgatg 3700  
caaaggtggg gagaagggat cctaatacct tcctctcca ttcacctgt 3750  
gtaacaggac cccaaggacc tgctccccg gaagtgcctt aacctagagg 3800  
gtcggggagg aggttgtgtc actgactcag gctgtcctt ctctagtttc 3850  
ccctctcatc tgaccttagt ttgctgccat cagtctagt gtttcgtggt 3900  
ttcgtctatt tattaataaa tatttgagaa caaaaaaaaa aaaaaaaaaa 3950

a 3951

<210> 437  
<211> 1141  
<212> PRT  
<213> Homo sapiens

<400> 437

Met	Ala	Gly	Ala	Arg	Ser	Arg	Asp	Pro	Trp	Gly	Ala	Ser	Gly	Ile
1				5					10					15
Cys	Tyr	Leu	Phe	Gly	Ser	Leu	Leu	Val	Glu	Leu	Leu	Phe	Ser	Arg
				20					25					30
Ala	Val	Ala	Phe	Asn	Leu	Asp	Val	Met	Gly	Ala	Leu	Arg	Lys	Glu
				35					40					45
Gly	Glu	Pro	Gly	Ser	Leu	Phe	Gly	Phe	Ser	Val	Ala	Leu	His	Arg
				50					55					60
Gln	Leu	Gln	Pro	Arg	Pro	Gln	Ser	Trp	Leu	Leu	Val	Gly	Ala	Pro
				65					70					75
Gln	Ala	Leu	Ala	Leu	Pro	Gly	Gln	Gln	Ala	Asn	Arg	Thr	Gly	Gly

80										85					90				
Leu	Phe	Ala	Cys	Pro	Leu	Ser	Leu	Glu	Glu	Thr	Asp	Cys	Tyr	Arg					
				95					100					105					
Val	Asp	Ile	Asp	Gln	Gly	Ala	Asp	Met	Gln	Lys	Glu	Ser	Lys	Glu					
				110					115					120					
Asn	Gln	Trp	Leu	Gly	Val	Ser	Val	Arg	Ser	Gln	Gly	Pro	Gly	Gly					
				125					130					135					
Lys	Ile	Val	Thr	Cys	Ala	His	Arg	Tyr	Glu	Ala	Arg	Gln	Arg	Val					
				140					145					150					
Asp	Gln	Ile	Leu	Glu	Thr	Arg	Asp	Met	Ile	Gly	Arg	Cys	Phe	Val					
				155					160					165					
Leu	Ser	Gln	Asp	Leu	Ala	Ile	Arg	Asp	Glu	Leu	Asp	Gly	Gly	Glu					
				170					175					180					
Trp	Lys	Phe	Cys	Glu	Gly	Arg	Pro	Gln	Gly	His	Glu	Gln	Phe	Gly					
				185					190					195					
Phe	Cys	Gln	Gln	Gly	Thr	Ala	Ala	Ala	Phe	Ser	Pro	Asp	Ser	His					
				200					205					210					
Tyr	Leu	Leu	Phe	Gly	Ala	Pro	Gly	Thr	Tyr	Asn	Trp	Lys	Gly	Thr					
				215					220					225					
Ala	Arg	Val	Glu	Leu	Cys	Ala	Gln	Gly	Ser	Ala	Asp	Leu	Ala	His					
				230					235					240					
Leu	Asp	Asp	Gly	Pro	Tyr	Glu	Ala	Gly	Gly	Glu	Lys	Glu	Gln	Asp					
				245					250					255					
Pro	Arg	Leu	Ile	Pro	Val	Pro	Ala	Asn	Ser	Tyr	Phe	Gly	Phe	Ser					
				260					265					270					
Ile	Asp	Ser	Gly	Lys	Gly	Leu	Val	Arg	Ala	Glu	Glu	Leu	Ser	Phe					
				275					280					285					
Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	His	Lys	Gly	Ala	Val	Val	Ile					
				290					295					300					
Leu	Arg	Lys	Asp	Ser	Ala	Ser	Arg	Leu	Val	Pro	Glu	Val	Met	Leu					
				305					310					315					
Ser	Gly	Glu	Arg	Leu	Thr	Ser	Gly	Phe	Gly	Tyr	Ser	Leu	Ala	Val					
				320					325					330					
Ala	Asp	Leu	Asn	Ser	Asp	Gly	Trp	Pro	Asp	Leu	Ile	Val	Gly	Ala					
				335					340					345					
Pro	Tyr	Phe	Phe	Glu	Arg	Gln	Glu	Glu	Leu	Gly	Gly	Ala	Val	Tyr					
				350					355					360					
Val	Tyr	Leu	Asn	Gln	Gly	Gly	His	Trp	Ala	Gly	Ile	Ser	Pro	Leu					
				365					370					375					

Arg	Leu	Cys	Gly	Ser	Pro	Asp	Ser	Met	Phe	Gly	Ile	Ser	Leu	Ala
				380					385					390
Val	Leu	Gly	Asp	Leu	Asn	Gln	Asp	Gly	Phe	Pro	Asp	Ile	Ala	Val
				395					400					405
Gly	Ala	Pro	Phe	Asp	Gly	Asp	Gly	Lys	Val	Phe	Ile	Tyr	His	Gly
				410					415					420
Ser	Ser	Leu	Gly	Val	Val	Ala	Lys	Pro	Ser	Gln	Val	Leu	Glu	Gly
				425					430					435
Glu	Ala	Val	Gly	Ile	Lys	Ser	Phe	Gly	Tyr	Ser	Leu	Ser	Gly	Ser
				440					445					450
Leu	Asp	Met	Asp	Gly	Asn	Gln	Tyr	Pro	Asp	Leu	Leu	Val	Gly	Ser
				455					460					465
Leu	Ala	Asp	Thr	Ala	Val	Leu	Phe	Arg	Ala	Arg	Pro	Ile	Leu	His
				470					475					480
Val	Ser	His	Glu	Val	Ser	Ile	Ala	Pro	Arg	Ser	Ile	Asp	Leu	Glu
				485					490					495
Gln	Pro	Asn	Cys	Ala	Gly	Gly	His	Ser	Val	Cys	Val	Asp	Leu	Arg
				500					505					510
Val	Cys	Phe	Ser	Tyr	Ile	Ala	Val	Pro	Ser	Ser	Tyr	Ser	Pro	Thr
				515					520					525
Val	Ala	Leu	Asp	Tyr	Val	Leu	Asp	Ala	Asp	Thr	Asp	Arg	Arg	Leu
				530					535					540
Arg	Gly	Gln	Val	Pro	Arg	Val	Thr	Phe	Leu	Ser	Arg	Asn	Leu	Glu
				545					550					555
Glu	Pro	Lys	His	Gln	Ala	Ser	Gly	Thr	Val	Trp	Leu	Lys	His	Gln
				560					565					570
His	Asp	Arg	Val	Cys	Gly	Asp	Ala	Met	Phe	Gln	Leu	Gln	Glu	Asn
				575					580					585
Val	Lys	Asp	Lys	Leu	Arg	Ala	Ile	Val	Val	Thr	Leu	Ser	Tyr	Ser
				590					595					600
Leu	Gln	Thr	Pro	Arg	Leu	Arg	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu
				605					610					615
Pro	Pro	Val	Ala	Pro	Ile	Leu	Asn	Ala	His	Gln	Pro	Ser	Thr	Gln
				620					625					630
Arg	Ala	Glu	Ile	His	Phe	Leu	Lys	Gln	Gly	Cys	Gly	Glu	Asp	Lys
				635					640					645
Ile	Cys	Gln	Ser	Asn	Leu	Gln	Leu	Val	His	Ala	Arg	Phe	Cys	Thr
				650					655					660
Arg	Val	Ser	Asp	Thr	Glu	Phe	Gln	Pro	Leu	Pro	Met	Asp	Val	Asp

665					670					675				
Gly	Thr	Thr	Ala	Leu	Phe	Ala	Leu	Ser	Gly	Gln	Pro	Val	Ile	Gly
				680					685					690
Leu	Glu	Leu	Met	Val	Thr	Asn	Leu	Pro	Ser	Asp	Pro	Ala	Gln	Pro
				695					700					705
Gln	Ala	Asp	Gly	Asp	Asp	Ala	His	Glu	Ala	Gln	Leu	Leu	Val	Met
				710					715					720
Leu	Pro	Asp	Ser	Leu	His	Tyr	Ser	Gly	Val	Arg	Ala	Leu	Asp	Pro
				725					730					735
Ala	Glu	Lys	Pro	Leu	Cys	Leu	Ser	Asn	Glu	Asn	Ala	Ser	His	Val
				740					745					750
Glu	Cys	Glu	Leu	Gly	Asn	Pro	Met	Lys	Arg	Gly	Ala	Gln	Val	Thr
				755					760					765
Phe	Tyr	Leu	Ile	Leu	Ser	Thr	Ser	Gly	Ile	Ser	Ile	Glu	Thr	Thr
				770					775					780
Glu	Leu	Glu	Val	Glu	Leu	Leu	Leu	Ala	Thr	Ile	Ser	Glu	Gln	Glu
				785					790					795
Leu	His	Pro	Val	Ser	Ala	Arg	Ala	Arg	Val	Phe	Ile	Glu	Leu	Pro
				800					805					810
Leu	Ser	Ile	Ala	Gly	Met	Ala	Ile	Pro	Gln	Gln	Leu	Phe	Phe	Ser
				815					820					825
Gly	Val	Val	Arg	Gly	Glu	Arg	Ala	Met	Gln	Ser	Glu	Arg	Asp	Val
				830					835					840
Gly	Ser	Lys	Val	Lys	Tyr	Glu	Val	Thr	Val	Ser	Asn	Gln	Gly	Gln
				845					850					855
Ser	Leu	Arg	Thr	Leu	Gly	Ser	Ala	Phe	Leu	Asn	Ile	Met	Trp	Pro
				860					865					870
His	Glu	Ile	Ala	Asn	Gly	Lys	Trp	Leu	Leu	Tyr	Pro	Met	Gln	Val
				875					880					885
Glu	Leu	Glu	Gly	Gly	Gln	Gly	Pro	Gly	Gln	Lys	Gly	Leu	Cys	Ser
				890					895					900
Pro	Arg	Pro	Asn	Ile	Leu	His	Leu	Asp	Val	Asp	Ser	Arg	Asp	Arg
				905					910					915
Arg	Arg	Arg	Glu	Leu	Glu	Pro	Pro	Glu	Gln	Gln	Glu	Pro	Gly	Glu
				920					925					930
Arg	Gln	Glu	Pro	Ser	Met	Ser	Trp	Trp	Pro	Val	Ser	Ser	Ala	Glu
				935					940					945
Lys	Lys	Lys	Asn	Ile	Thr	Leu	Asp	Cys	Ala	Arg	Gly	Thr	Ala	Asn
				950					955					960

Cys Val Val Phe	Ser Cys Pro Leu Tyr	Ser Phe Asp Arg Ala Ala
965	970	975
Val Leu His Val	Trp Gly Arg Leu Trp	Asn Ser Thr Phe Leu Glu
980	985	990
Glu Tyr Ser Ala	Val Lys Ser Leu Glu Val	Ile Val Arg Ala Asn
995	1000	1005
Ile Thr Val Lys	Ser Ser Ile Lys Asn Leu	Met Leu Arg Asp Ala
1010	1015	1020
Ser Thr Val Ile	Pro Val Met Val Tyr Leu	Asp Pro Met Ala Val
1025	1030	1035
Val Ala Glu Gly	Val Pro Trp Trp Val Ile	Leu Leu Ala Val Leu
1040	1045	1050
Ala Gly Leu Leu	Val Leu Ala Leu Leu Val	Leu Leu Leu Trp Lys
1055	1060	1065
Met Gly Phe Phe	Lys Arg Ala Lys His Pro	Glu Ala Thr Val Pro
1070	1075	1080
Gln Tyr His Ala	Val Lys Ile Pro Arg Glu	Asp Arg Gln Gln Phe
1085	1090	1095
Lys Glu Glu Lys	Thr Gly Thr Ile Leu Arg	Asn Asn Trp Gly Ser
1100	1105	1110
Pro Arg Arg Glu	Gly Pro Asp Ala His Pro	Ile Leu Ala Ala Asp
1115	1120	1125
Gly His Pro Glu	Leu Gly Pro Asp Gly His	Pro Gly Pro Gly Thr
1130	1135	1140

Ala

<210> 438

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 438

ggctgacacc gcagtgtctt tcag 24

<210> 439

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

```

<400> 439
gctgctgggg actgcaatgt agct 24

<210> 440
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic oligonucleotide probe

<400> 440
catcctccat gtctcccatg aggtctctat tgctccacga agcatc 46

<210> 441
<211> 1964
<212> DNA
<213> Homo sapiens

<400> 441
cgcgccggggc gcagggagct gagtggacgg ctcgagacgg cggcgcggtgc 50
agcagctcca gaaagcagcg agttggcaga gcagggctgc atttccagca 100
ggagctgcga gcacagtgtt ggctcacaac aagatgotca aggtgtcagc 150
cgtactgtgt gtgtgtgcag ccgcttggtg cagtcagtct ctgcagctg 200
ccgcggcggt ggctgcagcc ggggggcggg cggacggcgg taattttctg 250
gatgataaac aatggctcac cacaatctct cagtatgaca aggaagtcgg 300
acagtggaac aaattccgag acgaagtaga ggatgattat ttccgcactt 350
ggagtccagg aaaacccttc gatcaggctt tagatccagc taaggatcca 400
tgcttaaaga tgaaatgtag tcgccataaa gtatgcattg ctcaagattc 450
tcagactgca gtctgcatta gtcaccggag gtttacacac aggatgaaag 500
aagcaggagt agaccatagg cagtggaggg gtcccatatt atccacctgc 550
aagcagtgcc cagtgggtcta tccagccctt gtttgtggtt cagatggtca 600
tacctactct tttcagtgc aactagaata tcaggcatgt gtcttaggaa 650
aacagatctc agtcaaagt gaaggacatt gcccatgtcc ttcagataag 700
cccaccagta caagcagaaa tgttaagaga gcatgcagtg acctggagtt 750
caggggaagt gcaaacagat tgcgggactg gttcaaggcc cttcatgaaa 800
gtggaagtca aaacaagaag acaaaaacat tgctgaggcc tgagagaagc 850
agattcgata ccagcatctt gccaatgtgc aaggactcac ttggctggat 900
gtttaacaga cttgatacaa actatgacct gctattggac cagtcagagc 950

```

tcagaagcat ttaccttgat aagaatgaac agtgtaccaa ggcattcttc 1000  
aattcttgatg acacatacaa ggacagttta atatctaata atgagtgggtg 1050  
ctactgcttc cagagacagc aagacccacc ttgccagact gagctcagca 1100  
atattcagaa gcggaaggg gtaaagaagc tcctaggaca gtatatcccc 1150  
ctgtgtgatg aagatgggta ctacaagcca acacaatgtc atggcagtgt 1200  
tggacagtgc tgggtgtgtg acagatatgg aaatgaagtc atgggatcca 1250  
gaataaatgg tgttgcatg tgtgctatag attttgagat ctccggagat 1300  
tttgctagtgc gcgattttca tgaatggact gatgatgagg atgatgaaga 1350  
cgatattatg aatgatgaag atgaaattga agatgatgat gaagatgaag 1400  
gggatgatga tgatgggtgt gatgaccatg atgtatacat ttgattgatg 1450  
acagttgaaa tcaataaatt ctacatttct aatatttaca aaaatgatag 1500  
cctattttaa attatcttct tccccataa caaatgatt ctaaacctca 1550  
catatatttt gtataattat ttgaaaaatt gcagctaaag ttatagaact 1600  
ttatgtttaa ataagaatca ttgctttga gtttttatat tccttacaca 1650  
aaaagaaaat acatatgcag tctagtcaga caaaataaag ttttgaagtg 1700  
ctactataat aaatttttca cgagaacaaa ctttgtaaatt cttccataag 1750  
caaatgaca gctagtgtt gggatcgtag atgttaattt tttgaaagat 1800  
aattctaagt gaaattttaa ataaataaat ttttaatgac ctgggtctta 1850  
aggatttagg aaaaatatgc atgctttaat tgcatttcca aagtagcatc 1900  
ttgctagacc tagatgagtc aggataacag agagatacca catgactcca 1950  
aaaaaaaaaa aaaa 1964

<210> 442  
<211> 436  
<212> PRT  
<213> Homo sapiens

<400> 442  
Met Leu Lys Val Ser Ala Val Leu Cys Val Cys Ala Ala Ala Trp  
1 5 10 15  
Cys Ser Gln Ser Leu Ala Ala Ala Ala Val Ala Ala Ala Gly  
20 25 30  
Gly Arg Ser Asp Gly Gly Asn Phe Leu Asp Asp Lys Gln Trp Leu  
35 40 45  
Thr Thr Ile Ser Gln Tyr Asp Lys Glu Val Gly Gln Trp Asn Lys

				50						55					60
Phe	Arg	Asp	Glu	Val	Glu	Asp	Asp	Tyr	Phe	Arg	Thr	Trp	Ser	Pro	
				65					70					75	
Gly	Lys	Pro	Phe	Asp	Gln	Ala	Leu	Asp	Pro	Ala	Lys	Asp	Pro	Cys	
				80					85					90	
Leu	Lys	Met	Lys	Cys	Ser	Arg	His	Lys	Val	Cys	Ile	Ala	Gln	Asp	
				95					100					105	
Ser	Gln	Thr	Ala	Val	Cys	Ile	Ser	His	Arg	Arg	Leu	Thr	His	Arg	
				110					115					120	
Met	Lys	Glu	Ala	Gly	Val	Asp	His	Arg	Gln	Trp	Arg	Gly	Pro	Ile	
				125					130					135	
Leu	Ser	Thr	Cys	Lys	Gln	Cys	Pro	Val	Val	Tyr	Pro	Ser	Pro	Val	
				140					145					150	
Cys	Gly	Ser	Asp	Gly	His	Thr	Tyr	Ser	Phe	Gln	Cys	Lys	Leu	Glu	
				155					160					165	
Tyr	Gln	Ala	Cys	Val	Leu	Gly	Lys	Gln	Ile	Ser	Val	Lys	Cys	Glu	
				170					175					180	
Gly	His	Cys	Pro	Cys	Pro	Ser	Asp	Lys	Pro	Thr	Ser	Thr	Ser	Arg	
				185					190					195	
Asn	Val	Lys	Arg	Ala	Cys	Ser	Asp	Leu	Glu	Phe	Arg	Glu	Val	Ala	
				200					205					210	
Asn	Arg	Leu	Arg	Asp	Trp	Phe	Lys	Ala	Leu	His	Glu	Ser	Gly	Ser	
				215					220					225	
Gln	Asn	Lys	Lys	Thr	Lys	Thr	Leu	Leu	Arg	Pro	Glu	Arg	Ser	Arg	
				230					235					240	
Phe	Asp	Thr	Ser	Ile	Leu	Pro	Ile	Cys	Lys	Asp	Ser	Leu	Gly	Trp	
				245					250					255	
Met	Phe	Asn	Arg	Leu	Asp	Thr	Asn	Tyr	Asp	Leu	Leu	Leu	Asp	Gln	
				260					265					270	
Ser	Glu	Leu	Arg	Ser	Ile	Tyr	Leu	Asp	Lys	Asn	Glu	Gln	Cys	Thr	
				275					280					285	
Lys	Ala	Phe	Phe	Asn	Ser	Cys	Asp	Thr	Tyr	Lys	Asp	Ser	Leu	Ile	
				290					295					300	
Ser	Asn	Asn	Glu	Trp	Cys	Tyr	Cys	Phe	Gln	Arg	Gln	Gln	Asp	Pro	
				305					310					315	
Pro	Cys	Gln	Thr	Glu	Leu	Ser	Asn	Ile	Gln	Lys	Arg	Gln	Gly	Val	
				320					325					330	
Lys	Lys	Leu	Leu	Gly	Gln	Tyr	Ile	Pro	Leu	Cys	Asp	Glu	Asp	Gly	
				335					340					345	



Tyr	Tyr	Lys	Pro	Thr	Gln	Cys	His	Gly	Ser	Val	Gly	Gln	Cys	Trp
				350					355					360
Cys	Val	Asp	Arg	Tyr	Gly	Asn	Glu	Val	Met	Gly	Ser	Arg	Ile	Asn
				365					370					375
Gly	Val	Ala	Asp	Cys	Ala	Ile	Asp	Phe	Glu	Ile	Ser	Gly	Asp	Phe
				380					385					390
Ala	Ser	Gly	Asp	Phe	His	Glu	Trp	Thr	Asp	Asp	Glu	Asp	Asp	Glu
				395					400					405
Asp	Asp	Ile	Met	Asn	Asp	Glu	Asp	Glu	Ile	Glu	Asp	Asp	Asp	Glu
				410					415					420
Asp	Glu	Gly	Asp	Asp	Asp	Asp	Gly	Gly	Asp	Asp	His	Asp	Val	Tyr
				425					430					435

Ile

<210> 443  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 443  
 cagcaatatt cagaagcggc aaggg 25

<210> 444  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 444  
 catcatggtc atcaccacca tcatcatc 28

<210> 445  
 <211> 48  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 445  
 gggtactaca agccaacaca atgtcatggc agtggtggac agtgctgg 48

<210> 446  
 <211> 3617  
 <212> DNA  
 <213> Homo sapiens

105101 "267550

<400> 446  
cagactccag atttccctgt caaccacgag gagtccagag aggaaacgcg 50  
gagcggagac aacagtacct gacgcctctt tcagcccggg atcgccccag 100  
cagggatggg cgacaagatc tggctgccct tccccgtgct ccttctggcc 150  
gctctgcctc cggtgctgct gcctggggcg gccggcttca caccttccct 200  
cgatagcgac ttcaccttta cccttcccg cggccagaag gagtgccttct 250  
accagcccat gcccctgaag gcctcgctgg agatcgagta ccaagtttta 300  
gatggagcag gattagatat tgatttccat cttgcctctc cagaaggcaa 350  
aaccttagtt tttgaacaaa gaaaatcaga tggagttcac actgtagaga 400  
ctgaagttag tgattacatg ttctgctttg acaatacatt cagcaccatt 450  
tctgagaagg tgattttctt tgaattaatc ctggataata tgggagaaca 500  
ggcacaagaa caagaagatt ggaagaaata tattactggc acagatatat 550  
tggatatgaa actggaagac atcctggaat ccatcaacag catcaagtcc 600  
agactaagca aaagtgggca catacaaatt ctgcttagag catttgaagc 650  
tcgtgatcga aacatacaag aaagcaactt tgatagagtc aatttctggt 700  
ctatgggttaa tttagtggtc atgggtggtg tgtcagccat tcaagtttat 750  
atgctgaaga gtctgtttga agataagagg aaaagtagaa cttaaaactc 800  
caaactagag tacgtaacat tgaaaaatga ggcataaaaa tgcaataaac 850  
tgttacagtc aagaccatta atggctcttct ccaaaatatt ttgagatata 900  
aaagtaggaa acaggtataa ttttaatgtg aaaattaagt cttcactttc 950  
tgtgcaagta atcctgctga tccagttgta cttaagtgtg taacaggaat 1000  
attttgcaga atatagggtt aactgaatga agccatatta ataactgcat 1050  
tttctaact ttgaaaaatt ttgcaaatgt cttaggtgat ttaaataaat 1100  
gagtattggg cctaattgca acaccagtct gtttttaaca ggttctatta 1150  
cccagaactt ttttgtaa atgcggcagtt caaattaact gtggaagttt 1200  
tcagttttta gttataaatc acctgagaat tacctaataa tggattgaat 1250  
aaatcttttag actacaaaag cccaactttt ctctatttac atatgcatct 1300  
ctcctataat gtaaatagaa taatagcttt gaaatacaat taggtttttg 1350  
agatttttat aaccaaatat atttcagtgt aacatattag cagaaagcat 1400  
tagtctttgt actttgctta cattcccaaa agctgacatt ttcacgattc 1450

ttaaaaacac aaagttacac ttactaaaat taggacatgt tttctctttg 1500  
 aaatgaagaa tatagtttaa aagcttcctc ctccataggg acacattttc 1550  
 tctaaccctt aactaaagt taggatttta aaattaaatg tgaggtaaaa 1600  
 taagtttatt tttaatagta tctgtcaagt taatatctgt caacagttaa 1650  
 taatcatggt atgttaatth taacatgatt gctgacttgg ataattcatt 1700  
 attaccagca gttatgaagg aaatattgct aaaatgatct gggcctacca 1750  
 taaataaata tctccttttc tgagctctaa gaattatcag aaaacaggaa 1800  
 agaatttaga aaaacttgag aaaacctaata ccaaaataaa attcacttaa 1850  
 gtagaactat aaataaatat ctagaatctg actggctcat catgacatcc 1900  
 tactcataac ataaatcaaa ggagatgatt aatttccagt tagctggaag 1950  
 aaactttggc tgtaggtttt tattttctac aagaattctg gtttgaatta 2000  
 tttttgtaag caggtacatt ttataaaatg taagccctac tgtaaggttt 2050  
 agcactgggt gtacatattt attaaaaatt tttattataa caacttttat 2100  
 taaaatggcc tttctgaaca ctttatttat tgatgttgaa gtaaggatta 2150  
 gaaacataga ctcccaagtt ttaaacacct aaatgtgaat aacctatata 2200  
 tacaacaaag tttctgccat ctagcttttt gaagtctatg ggggtcttac 2250  
 tcaagtacta gtaatttaac ttcatcatga atgaactata atttttaagt 2300  
 tatgcccatt tataacgttg tttatgacta cattgtgagt tagaaacaaa 2350  
 cttaaaattt ggggtataga acccctcaac aggttagtaa tgctggaatt 2400  
 cttgatgagc aataatgata accagagagt gatttcattt aactcatag 2450  
 tagtataaaa agagatacat ttccctctta ggccctggg agaagagcag 2500  
 cttagatttc cctactggca aggtttttta aaatgaggta aatgccgtat 2550  
 atgatcaatt accttaattg gccaagaaaa tgcttcaggt gtctaggggt 2600  
 atcctctgca aacttgcag aacaaaggct aataagatcc ttgcctatga 2650  
 ataccctcc cttttgcgct gttaaatttg caatgagaag caaatttaca 2700  
 gtaccataac taataaagca gggtagagat ataaactact gcactttttc 2750  
 tataaaactg tgattaagaa ttctacctct cctgtatggc tgttactgta 2800  
 ctgtactctc tgactcctta cctaacaatg aatttgttac ataactttct 2850  
 acatgtatga tttgtgccac tgatcttaaa cctatgattc agtaacttct 2900

taccatataa aaacgataat tgctttatctt ggaaaagaat ttaggaatac 2950  
 taaggacaat tatttttata gacaaagtaa aaagacagat atttaagagg 3000  
 cataacccaaa aaagcaaaac ttgtaaacag agtaaaaatc tttaatatctt 3050  
 ctaaagacat actgtttatc tgcttcatat gcttttttta atttcactat 3100  
 tccatttcta aattaaagtt atgctaaatt gagtaagctg tttatcactt 3150  
 aacagctcat tttgtctttt tcaatataca aatttttaaaa atactacaat 3200  
 atttaactaa ggcccaaccg atttcataa tgtagcagtt accgtgttca 3250  
 cctcacacta aggcctagag tttgtcttga tatgcatttg gatgattaat 3300  
 gttatgctgt tctttcatgt gaatgtcaag acatggaggg tgtttgtaat 3350  
 tttatggtaa aattaatcct tcttacacat aatgggtgtct taaaattgac 3400  
 aaaaaatgag cacttacaat tgtatgtctc ctcaaataa gattctttat 3450  
 gtgaaatttt aaaagacatt gattccgcat gtaaggattt ttcacttgaa 3500  
 gtacaataat gcacaatcag tgttgctcaa actgctttat acttataaac 3550  
 agccatctta aataagcaac gtattgtgag tactgatatg tatataataa 3600  
 aaattatcaa aggaaaa 3617

<210> 447

<211> 229

<212> PRT

<213> Homo sapiens

<400> 447

Met	Gly	Asp	Lys	Ile	Trp	Leu	Pro	Phe	Pro	Val	Leu	Leu	Leu	Ala
1				5					10					15
Ala	Leu	Pro	Pro	Val	Leu	Leu	Pro	Gly	Ala	Ala	Gly	Phe	Thr	Pro
				20					25					30
Ser	Leu	Asp	Ser	Asp	Phe	Thr	Phe	Thr	Leu	Pro	Ala	Gly	Gln	Lys
				35					40					45
Glu	Cys	Phe	Tyr	Gln	Pro	Met	Pro	Leu	Lys	Ala	Ser	Leu	Glu	Ile
				50					55					60
Glu	Tyr	Gln	Val	Leu	Asp	Gly	Ala	Gly	Leu	Asp	Ile	Asp	Phe	His
				65					70					75
Leu	Ala	Ser	Pro	Glu	Gly	Lys	Thr	Leu	Val	Phe	Glu	Gln	Arg	Lys
				80					85					90
Ser	Asp	Gly	Val	His	Thr	Val	Glu	Thr	Glu	Val	Gly	Asp	Tyr	Met
				95					100					105
Phe	Cys	Phe	Asp	Asn	Thr	Phe	Ser	Thr	Ile	Ser	Glu	Lys	Val	Ile

	110		115		120
Phe Phe Glu Leu	Ile Leu Asp Asn Met	Gly Glu Gln Ala Gln	Glu		
	125		130		135
Gln Glu Asp Trp	Lys Lys Tyr Ile Thr	Gly Thr Asp Ile Leu	Asp		
	140		145		150
Met Lys Leu Glu	Asp Ile Leu Glu Ser	Ile Asn Ser Ile Lys	Ser		
	155		160		165
Arg Leu Ser Lys	Ser Gly His Ile Gln	Ile Leu Leu Arg Ala	Phe		
	170		175		180
Glu Ala Arg Asp	Arg Asn Ile Gln Glu	Ser Asn Phe Asp Arg	Val		
	185		190		195
Asn Phe Trp Ser	Met Val Asn Leu Val	Val Met Val Val Val	Ser		
	200		205		210
Ala Ile Gln Val	Tyr Met Leu Lys Ser	Leu Phe Glu Asp Lys	Arg		
	215		220		225

Lys Ser Arg Thr

<210> 448  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 448  
 cccagcaggg ctgggcgaca aga 23

<210> 449  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 449  
 gtcttcaggt ttcatatcca ata 23

<210> 450  
 <211> 43  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 450  
 ccagaaggag cacggggaag ggcagccaga tcttgctgcc cat 43

<210> 451  
 <211> 859  
 <212> DNA  
 <213> Homo sapiens

<400> 451  
 ccatccctga gatcttttta taaaaaaccc agtctttgct gaccagacaa 50  
 agcataccag atctcaccag agagtgcag acactatgct gcctcccatg 100  
 gccctgccca gtgtgtcctg gatgctgctt tctgcctca ttctcctgtg 150  
 tcaggttcaa ggtgaagaaa ccagaagga actgccctct ccacggatca 200  
 gctgtcccaa aggcaccaag gcctatggct cccctgcta tgccttgttt 250  
 ttgtcaccaa aatcctggat ggatgcagat ctggcttgcc agaagcggcc 300  
 ctctggaaaa ctggtgtctg tgctcagtgg ggctgagga tccttcgtgt 350  
 cctccctggt gaggagcatt agtaacagct actcatacat ctggattggg 400  
 ctccatgacc ccacacaggg ctctgagcct gatggagatg gatgggagtg 450  
 gagtagcact gatgtgatga attactttgc atgggagaaa aatccctcca 500  
 ccatcttaaa ccctggccac tgtgggagcc tgtcaagaag cacaggattt 550  
 ctgaagtga aagattataa ctgtgatgca aagttaccct atgtctgcaa 600  
 gttcaaggac tagggcaggt ggaagtcag cagcctcagc ttggcgtgca 650  
 gctcatcatg gacatgagac cagtgtgaag actcaccctg gaagagaata 700  
 ttctcccaa actgccctac ctgactacct tgtcatgac ctcttcttt 750  
 ttcttttttc ttcaccttca tttcaggctt ttctctgtct tccatgtctt 800  
 gagatctcag agaataataa taaaaatgtt actttataaa aaaaaaaaaa 850  
 aaaaaaaaaa 859

<210> 452  
 <211> 175  
 <212> PRT  
 <213> Homo sapiens

<400> 452  
 Met Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu  
 1 5 10 15  
 Ser Cys Leu Ile Leu Leu Cys Gln Val Gln Gly Glu Glu Thr Gln  
 20 25 30  
 Lys Glu Leu Pro Ser Pro Arg Ile Ser Cys Pro Lys Gly Ser Lys  
 35 40 45  
 Ala Tyr Gly Ser Pro Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser

	50		55		60
Trp Met Asp Ala Asp	Leu Ala Cys Gln Lys	Arg Pro Ser Gly Lys			
	65	70			75
Leu Val Ser Val Leu	Ser Gly Ala Glu Gly	Ser Phe Val Ser Ser			
	80	85			90
Leu Val Arg Ser Ile	Ser Asn Ser Tyr Ser	Tyr Ile Trp Ile Gly			
	95	100			105
Leu His Asp Pro Thr	Gln Gly Ser Glu Pro	Asp Gly Asp Gly Trp			
	110	115			120
Glu Trp Ser Ser Thr	Asp Val Met Asn Tyr	Phe Ala Trp Glu Lys			
	125	130			135
Asn Pro Ser Thr Ile	Leu Asn Pro Gly His	Cys Gly Ser Leu Ser			
	140	145			150
Arg Ser Thr Gly Phe	Leu Lys Trp Lys Asp	Tyr Asn Cys Asp Ala			
	155	160			165
Lys Leu Pro Tyr Val	Cys Lys Phe Lys Asp				
	170	175			

<210> 453  
 <211> 550  
 <212> DNA  
 <213> Homo sapiens

<400> 453  
 ccagtctgtc gccacctcac ttggtgtctg ctgtccccgc caggcaagcc 50  
 tgggggtgaga gcacagagga gtgggcccggg accatgcggg ggacgcggct 100  
 ggcgtcctctg gcgctgggtgc tggctgcctg cggagagctg gcgccggccc 150  
 tgcgctgcta cgtctgtccg gagccacag gagtgtcgga ctgtgtcacc 200  
 atcgccacct gcaccaccaa cgaaaccatg tgcaagacca cactctactc 250  
 ccgggagata gtgtaccct tccaggggga ctccacggtg accaagtcct 300  
 gtgccagcaa gtgtaagccc tcggatgtgg atggcatcgg ccagaccctg 350  
 cccgtgtcct gctgcaatac tgagctgtgc aatgtagacg gggcgcccgc 400  
 tctgaacagc ctccactgcg gggccctcac gtcctccca ctcttgagcc 450  
 tccgactgta gagtccccgc ccacccccat ggccctatgc ggcccagccc 500  
 cgaatgcctt gaagaagtgc cccctgcacc aggaaaaaaa aaaaaaaaaa 550

<210> 454  
 <211> 125  
 <212> PRT  
 <213> Homo sapiens

<400> 454

```

Met Arg Gly Thr Arg Leu Ala Leu Leu Ala Leu Val Leu Ala Ala
 1           5           10           15

Cys Gly Glu Leu Ala Pro Ala Leu Arg Cys Tyr Val Cys Pro Glu
          20           25           30

Pro Thr Gly Val Ser Asp Cys Val Thr Ile Ala Thr Cys Thr Thr
          35           40           45

Asn Glu Thr Met Cys Lys Thr Thr Leu Tyr Ser Arg Glu Ile Val
          50           55           60

Tyr Pro Phe Gln Gly Asp Ser Thr Val Thr Lys Ser Cys Ala Ser
          65           70           75

Lys Cys Lys Pro Ser Asp Val Asp Gly Ile Gly Gln Thr Leu Pro
          80           85           90

Val Ser Cys Cys Asn Thr Glu Leu Cys Asn Val Asp Gly Ala Pro
          95          100          105

Ala Leu Asn Ser Leu His Cys Gly Ala Leu Thr Leu Leu Pro Leu
          110          115          120

Leu Ser Leu Arg Leu
          125

```

<210> 455

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 455

```

ctgcagtcag gactctggga ccgcaggggg ctcccgacc ctgactctgc 50

agccgaaccg gcacggtttc gtggggaccc aggcttgcaa agtgacggtc 100

attttctctt tctttctccc tcttgagtcc ttctgagatg atggctctgg 150

gcgcagcggg agctaccggg gtctttgtcg cgatggtagc ggcggctctc 200

ggcggccacc ctctgctggg agtgagcgcc accttgaact cggttctcaa 250

ttccaacgct atcaagaacc tgccccacc gctgggcggc gctgcggggc 300

accagggctc tgcagtcagc gccgcgccg gaattcctgta cccgggcggg 350

aataagtacc agaccattga caactaccag ccgtaccgt gcgcagagga 400

cgaggagtgc ggactgatg agtactgcgc tagtcccacc cgcggagggg 450

acgcaggcgt gcaaattctgt ctgcctgca ggaagcgccg aaaacgctgc 500

atgcgtcacg ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550

tgtgtcttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600

```



ctgaaagctt tggtaatgat catagcacct tggatgggta ttccagaaga 650  
 accaccttgt cttcaaaaat gtatcacacc aaaggacaag aaggttctgt 700  
 ttgtctccgg tcatcagact gtgcctcagg attgtgttgt gctagacact 750  
 tctggtccaa gatctgtaaa cctgtcctga aagaagggtca agtgtgtacc 800  
 aagcatagga gaaaaggctc tcatggacta gaaatattcc agcgttggtta 850  
 ctgtggagaa ggtctgtctt gccggatata gaaagatcac catcaagcca 900  
 gtaattcttc taggcttcac acttgtcaga gacactaaac cagctatcca 950  
 aatgcagtga actcctttta tataatagat gctatgaaaa ccttttatga 1000  
 ccttcatcaa ctcaatccta aggatataca agttctgtgg tttcagttaa 1050  
 gcattccaat aacaccttcc aaaaacctgg agtgtaagag ctttgtttct 1100  
 ttatggaact cccctgtgat tgcagtaaata tactgtattg taaattotca 1150  
 gtgtggcact tacctgtaaa tgcaatgaaa cttttaatta tttttctaaa 1200  
 ggtgtgtcac tgccattttt tcctcttggt atgtaaattt ttgtacacat 1250  
 tgattgttat cttgactgac aaatattcta tattgaactg aagtaaataca 1300  
 tttcagctta tagttcttaa aagcataacc ctttaccoca ttttaattcta 1350  
 gagtctagaa cgcaaggatc tcttggaatg acaaatagata ggtacctaata 1400  
 atgtaacatg aaaatactag cttattttct gaaatgtact atcttaatgc 1450  
 ttaaattata tttcccttta ggctgtgata gtttttgaaa taaaatttaa 1500  
 catttaaaaa aaaaaaaaa 1518

<210> 456  
 <211> 266  
 <212> PRT  
 <213> Homo sapiens

<400> 456  
 Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala  
 1 5 10 15  
 Met Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser  
 20 25 30  
 Ala Thr Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu  
 35 40 45  
 Pro Pro Pro Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val  
 50 55 60  
 Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln  
 65 70 75

Thr	Ile	Asp	Asn	Tyr	Gln	Pro	Tyr	Pro	Cys	Ala	Glu	Asp	Glu	Glu	80	85	90
Cys	Gly	Thr	Asp	Glu	Tyr	Cys	Ala	Ser	Pro	Thr	Arg	Gly	Gly	Asp	95	100	105
Ala	Gly	Val	Gln	Ile	Cys	Leu	Ala	Cys	Arg	Lys	Arg	Arg	Lys	Arg	110	115	120
Cys	Met	Arg	His	Ala	Met	Cys	Cys	Pro	Gly	Asn	Tyr	Cys	Lys	Asn	125	130	135
Gly	Ile	Cys	Val	Ser	Ser	Asp	Gln	Asn	His	Phe	Arg	Gly	Glu	Ile	140	145	150
Glu	Glu	Thr	Ile	Thr	Glu	Ser	Phe	Gly	Asn	Asp	His	Ser	Thr	Leu	155	160	165
Asp	Gly	Tyr	Ser	Arg	Arg	Thr	Thr	Leu	Ser	Ser	Lys	Met	Tyr	His	170	175	180
Thr	Lys	Gly	Gln	Glu	Gly	Ser	Val	Cys	Leu	Arg	Ser	Ser	Asp	Cys	185	190	195
Ala	Ser	Gly	Leu	Cys	Cys	Ala	Arg	His	Phe	Trp	Ser	Lys	Ile	Cys	200	205	210
Lys	Pro	Val	Leu	Lys	Glu	Gly	Gln	Val	Cys	Thr	Lys	His	Arg	Arg	215	220	225
Lys	Gly	Ser	His	Gly	Leu	Glu	Ile	Phe	Gln	Arg	Cys	Tyr	Cys	Gly	230	235	240
Glu	Gly	Leu	Ser	Cys	Arg	Ile	Gln	Lys	Asp	His	His	Gln	Ala	Ser	245	250	255
Asn	Ser	Ser	Arg	Leu	His	Thr	Cys	Gln	Arg	His					260	265	

<210> 457  
 <211> 638  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <221> unsure  
 <222> 30, 123, 133, 139, 180, 214, 259, 282, 308, 452, 467, 471, 473,  
 509, 556  
 <223> unknown base  
  
 <400> 457  
 tgtgtttccc tgcagtcaga atttgggacn gcaggggttc ccggacctga 50  
  
 ttttgcagcg gaacgggaag gttttgtggg acccaggttg aaatgacggt 100  
 catttttttt tctttctcct tcnggagtcc ttntgagang atggtttttg 150  
 gcgcagcggg agctaaccgc gttttttgtn gcgatggtag cggcgggttt 200

cggcggccac cttntgctgg gagtgagcgc caccttgaat cggttttcaa 250  
 ttccaacgnt atcaagaacc tgccccacc gntggcgggc gctgcggggc 300  
 acccaggntt tgcagtcagc gccgcgccgg gaatcctgta cccgggcggg 350  
 aataagtacc agaccattga caattaccag ccgtaccctg gcgcagagga 400  
 cgaggagtgc ggcactgatg agtactgcgc tagtcccacc cgcggagggg 450  
 angcggggcg gcaaanttgt ntngcctgca ggaagcgccg aaaacgctgc 500  
 atgcgtcang ctatgtgctg ccccggaat tactgcaaaa atggaatatg 550  
 tgtgtnttct gatcaaaatc atttccgagg agaaattgag gaaaccatca 600  
 ctgaaagctt tggtaatgat catagcacct tggatggg 638

<210> 458  
 <211> 4040  
 <212> DNA  
 <213> Homo sapiens

<400> 458  
 gaggaaccta ccggtaccgg ccgcgcgctg gtagtcgcg gtgtggctgc 50  
 acctcaccaa tcccgtgcgc cgcggctggg ccgtcggaga gtgcgtgtgc 100  
 ttctctcctg caccggtgc ttgggctcgg ccaggcgggg tccgccgcca 150  
 gggtttgagg atgggggagt agctacagga agcgaccccg cgatggcaag 200  
 gtatatTTTT gtggaatgaa aaggaagtat tagaaatgag ctgaagacca 250  
 ttcacagatt aatatTTTT gggacagatt tgtgatgctt gattcacct 300  
 tgaagtaatg tagacagaag ttctcaaatt tgcatattac atcaactgga 350  
 accagcagtg aatcttaatg ttacttaaa tcagaacttg cataagaaag 400  
 agaatgggag tctgggttaa taaagatgac tatatcagag acttgaaaag 450  
 gatcattctc tgttttctga tagtgtatat ggccatttta gtgggcacag 500  
 atcaggattt ttacagttta cttggagtgt ccaaaactgc aagcagtaga 550  
 gaaataagac aagctttcaa gaaattggca ttgaagtac atcctgataa 600  
 aaacccgaat aacccaaatg cacatggcga ttttttaaaa ataaatagag 650  
 catatgaagt actcaaagat gaagatctac ggaaaaagta tgacaaatat 700  
 ggagaaaagg gacttgagga taatcaaggt ggccagtatg aaagctggaa 750  
 ctattatcgt tatgattttg gtatttatga tgatgatcct gaaatcataa 800  
 cattggaaag aagagaattt gatgctgctg ttaattctgg agaactgtgg 850

tttgtaaatt tttactcccc aggctgttca cactgccatg atttagctcc 900  
 cacatggaga gactttgcta aagaagtgga tgggttactt cgaattggag 950  
 ctgttaactg tggatgatgat agaattgcttt gccgaatgaa aggagtcaac 1000  
 agctatccca gtctcttcat ttttcggtct ggaatggccc cagtgaata 1050  
 tcatggagac agatcaaagg agagttagt gagttttgca atgcagcatg 1100  
 ttagaagtac agtgacagaa ctttgacag gaaattttgt caactccata 1150  
 caaactgctt ttgctgctgg tattggctgg ctgatcactt tttgttcaaa 1200  
 aggaggagat tgtttgactt cacagacacg actcaggctt agtggcatgt 1250  
 tgtttctcaa ctcatggat gctaaagaaa tatatttgga agtaatacat 1300  
 aatcttccag attttgaact actttcggca aacacactag aggatcgttt 1350  
 ggctcatcat cgggtggctgt tattttttca ttttgaaaaa aatgaaaatt 1400  
 caaatgatcc tgagctgaaa aaactaaaaa ctctacttaa aaatgatcat 1450  
 attcaagttg gcagggttga ctgttctct gcaccagaca tctgtagtaa 1500  
 tctgtatgtt tttcagccgt ctctagcagt atttaaagga caaggaacca 1550  
 aagaatatga aattcatcat ggaaagaaga ttctatatga tatacttgcc 1600  
 tttgccaaag aaagtgtgaa ttctcatgtt accacgcttg gacctcaaaa 1650  
 ttttctgcc aatgacaaag aaccatggct tgttgatttc tttgccccct 1700  
 ggtgtccacc atgtcgagct ttactaccag agttacgaag agcatcaaat 1750  
 cttctttatg gtcagcttaa gtttggtaca ctagattgta cagttcatga 1800  
 gggactctgt aacatgtata acattcaggc ttatccaaca acagtggat 1850  
 tcaaccagtc caacattcat gagtatgaag gacatcactc tgctgaacaa 1900  
 atottggagt tcatagagga tottatgaat ccttcagtgg tctcccttac 1950  
 acccaccacc ttcaacgaac tagttacaca aagaaaacac aacgaagtct 2000  
 ggatggttga tttctattct ccgtgggtgtc atccttgcca agtcttaatg 2050  
 ccagaatgga aaagaatggc ccggacatta actggactga tcaacgtggg 2100  
 cagtatagat tgccaacagt atcattcttt ttgtgcccag gaaaacgttc 2150  
 aaagataccc tgagataaga ttttttcccc caaatcaaa taaagcttat 2200  
 cagtatcaca gttacaatgg ttggaatagg gatgcttatt ccctgagaat 2250  
 ctgggggtcta ggatttttac ctcaagtatc cacagatcta acacctcaga 2300

ctttcagtga aaaagttcta caagggaaaa atcattgggt gattgatttc 2350  
tatgctcctt ggtgtggacc ttgccagaat tttgctccag aatttgagct 2400  
cttggctagg atgattaaag gaaaagtga agctggaaaa gtagactgtc 2450  
aggcttatgc tcagacatgc cagaaagctg ggatcagggc ctatccaact 2500  
gttaagtttt atttctacga aagagcaaag agaaattttc aagaagagca 2550  
gataaatacc agagatgcaa aagcaatcgc tgccttaata agtgaaaaat 2600  
tggaaactct ccgaaatcaa ggcaagagga ataaggatga actttgataa 2650  
tgttgaagat gaagaaaaag tttaaaagaa attctgacag atgacatcag 2700  
aagacaccta tttagaatgt tacatttatg atgggaatga atgaacatta 2750  
tcttagactt gcagttgtac tgccagaatt atctacagca ctggtgtaaa 2800  
agaagggctc gcaaactttt tctgtaaagg gccggtttat aaatatttta 2850  
gactttgcag gctataatat atggttcaca catgagaaca agaataagagt 2900  
catcatgtat tctttgttat ttgcttttaa caaccttaa aaaatattaa 2950  
aacgattcct agctcagagc catacaaaag taggctggat tcagtccatg 3000  
gaccatagat tgctgtcccc ctgcacggac ttataatggt tcaggtggct 3050  
ggcttgaaca tgagtctgct gtgctatcta cataaatgtc taagttgtat 3100  
aaagtccact ttcccttcac gttttttggc tgacctgaaa agaggtaact 3150  
tagtttttgg tcaattgttc tctaaaaaat gctatcccta accatatatt 3200  
tatatttcgt tttaaaaaca cccatgatgt ggcacagtaa acaaaccctg 3250  
ttatgctgta ttattatgag gagattcttc attgttttct ttccttctca 3300  
aaggttgaaa aaatgctttt aatttttcac agccgagaaa cagtgcagca 3350  
gtatatgtgc acacagtaag tacacaaatt tgagcaacag taagtgcaca 3400  
aattctgtag tttgctgtat catccaggaa aacctgaggg aaaaaatta 3450  
tagcaattaa ctgggcattg tagagtatcc taaatgatgt atcaagtatt 3500  
tagagttcta tattttaaag atatatgtgt tcatgtattt tctgaaattg 3550  
ctttcataga aattttccca ctgatagttg atttttgagg catctaatat 3600  
ttacatatatt gccttctgaa ctttgttttg acctgtatcc tttatttaca 3650  
ttgggttttt ctttcatagt tttgggtttt cactcctgtc cagtctatatt 3700  
attattcaaa taggaaaaat tactttacag gttgttttac tgtagcttat 3750

aatgatactg tagttattcc agttactagt ttactgtcag agggctgcct 3800  
 ttttcagata aatattgaca taataactga agttattttt ataagaaaat 3850  
 caagtatata aatctaggaa agggatcttc tagtttctgt gttgtttaga 3900  
 ctcaaagaat cacaatttg tcagtaacat gtagttgttt agttataatt 3950  
 cagagtgtac agaatggtaa aaattccaat cagtcaaaag aggtcaatga 4000  
 attaaaaggc ttgcaacttt ttcaaaaaaa aaaaaaaaaa 4040

<210> 459

<211> 747

<212> PRT

<213> Homo sapiens

<400> 459

Met	Gly	Val	Trp	Leu	Asn	Lys	Asp	Asp	Tyr	Ile	Arg	Asp	Leu	Lys	1	5	10	15
Arg	Ile	Ile	Leu	Cys	Phe	Leu	Ile	Val	Tyr	Met	Ala	Ile	Leu	Val	20	25	30	
Gly	Thr	Asp	Gln	Asp	Phe	Tyr	Ser	Leu	Leu	Gly	Val	Ser	Lys	Thr	35	40	45	
Ala	Ser	Ser	Arg	Glu	Ile	Arg	Gln	Ala	Phe	Lys	Lys	Leu	Ala	Leu	50	55	60	
Lys	Leu	His	Pro	Asp	Lys	Asn	Pro	Asn	Asn	Pro	Asn	Ala	His	Gly	65	70	75	
Asp	Phe	Leu	Lys	Ile	Asn	Arg	Ala	Tyr	Glu	Val	Leu	Lys	Asp	Glu	80	85	90	
Asp	Leu	Arg	Lys	Lys	Tyr	Asp	Lys	Tyr	Gly	Glu	Lys	Gly	Leu	Glu	95	100	105	
Asp	Asn	Gln	Gly	Gly	Gln	Tyr	Glu	Ser	Trp	Asn	Tyr	Tyr	Arg	Tyr	110	115	120	
Asp	Phe	Gly	Ile	Tyr	Asp	Asp	Asp	Pro	Glu	Ile	Ile	Thr	Leu	Glu	125	130	135	
Arg	Arg	Glu	Phe	Asp	Ala	Ala	Val	Asn	Ser	Gly	Glu	Leu	Trp	Phe	140	145	150	
Val	Asn	Phe	Tyr	Ser	Pro	Gly	Cys	Ser	His	Cys	His	Asp	Leu	Ala	155	160	165	
Pro	Thr	Trp	Arg	Asp	Phe	Ala	Lys	Glu	Val	Asp	Gly	Leu	Leu	Arg	170	175	180	
Ile	Gly	Ala	Val	Asn	Cys	Gly	Asp	Asp	Arg	Met	Leu	Cys	Arg	Met	185	190	195	
Lys	Gly	Val	Asn	Ser	Tyr	Pro	Ser	Leu	Phe	Ile	Phe	Arg	Ser	Gly				

09978192 "101501

	200	205	210
Met Ala Pro Val	Lys Tyr His Gly Asp	Arg Ser Lys Glu Ser	Leu
	215	220	225
Val Ser Phe Ala	Met Gln His Val Arg	Ser Thr Val Thr Glu	Leu
	230	235	240
Trp Thr Gly Asn	Phe Val Asn Ser Ile	Gln Thr Ala Phe Ala	Ala
	245	250	255
Gly Ile Gly Trp	Leu Ile Thr Phe Cys	Ser Lys Gly Gly Asp	Cys
	260	265	270
Leu Thr Ser Gln	Thr Arg Leu Arg Leu	Ser Gly Met Leu Phe	Leu
	275	280	285
Asn Ser Leu Asp	Ala Lys Glu Ile Tyr	Leu Glu Val Ile His	Asn
	290	295	300
Leu Pro Asp Phe	Glu Leu Leu Ser Ala	Asn Thr Leu Glu Asp	Arg
	305	310	315
Leu Ala His His	Arg Trp Leu Leu Phe	Phe His Phe Gly Lys	Asn
	320	325	330
Glu Asn Ser Asn	Asp Pro Glu Leu Lys	Lys Leu Lys Thr Leu	Leu
	335	340	345
Lys Asn Asp His	Ile Gln Val Gly Arg	Phe Asp Cys Ser Ser	Ala
	350	355	360
Pro Asp Ile Cys	Ser Asn Leu Tyr Val	Phe Gln Pro Ser Leu	Ala
	365	370	375
Val Phe Lys Gly	Gln Gly Thr Lys Glu	Tyr Glu Ile His His	Gly
	380	385	390
Lys Lys Ile Leu	Tyr Asp Ile Leu Ala	Phe Ala Lys Glu Ser	Val
	395	400	405
Asn Ser His Val	Thr Thr Leu Gly Pro	Gln Asn Phe Pro Ala	Asn
	410	415	420
Asp Lys Glu Pro	Trp Leu Val Asp Phe	Phe Ala Pro Trp Cys	Pro
	425	430	435
Pro Cys Arg Ala	Leu Leu Pro Glu Leu	Arg Arg Ala Ser Asn	Leu
	440	445	450
Leu Tyr Gly Gln	Leu Lys Phe Gly Thr	Leu Asp Cys Thr Val	His
	455	460	465
Glu Gly Leu Cys	Asn Met Tyr Asn Ile	Gln Ala Tyr Pro Thr	Thr
	470	475	480
Val Val Phe Asn	Gln Ser Asn Ile His	Glu Tyr Glu Gly His	His
	485	490	495

Ser	Ala	Glu	Gln	Ile	Leu	Glu	Phe	Ile	Glu	Asp	Leu	Met	Asn	Pro	500	505	510
Ser	Val	Val	Ser	Leu	Thr	Pro	Thr	Thr	Phe	Asn	Glu	Leu	Val	Thr	515	520	525
Gln	Arg	Lys	His	Asn	Glu	Val	Trp	Met	Val	Asp	Phe	Tyr	Ser	Pro	530	535	540
Trp	Cys	His	Pro	Cys	Gln	Val	Leu	Met	Pro	Glu	Trp	Lys	Arg	Met	545	550	555
Ala	Arg	Thr	Leu	Thr	Gly	Leu	Ile	Asn	Val	Gly	Ser	Ile	Asp	Cys	560	565	570
Gln	Gln	Tyr	His	Ser	Phe	Cys	Ala	Gln	Glu	Asn	Val	Gln	Arg	Tyr	575	580	585
Pro	Glu	Ile	Arg	Phe	Phe	Pro	Pro	Lys	Ser	Asn	Lys	Ala	Tyr	Gln	590	595	600
Tyr	His	Ser	Tyr	Asn	Gly	Trp	Asn	Arg	Asp	Ala	Tyr	Ser	Leu	Arg	605	610	615
Ile	Trp	Gly	Leu	Gly	Phe	Leu	Pro	Gln	Val	Ser	Thr	Asp	Leu	Thr	620	625	630
Pro	Gln	Thr	Phe	Ser	Glu	Lys	Val	Leu	Gln	Gly	Lys	Asn	His	Trp	635	640	645
Val	Ile	Asp	Phe	Tyr	Ala	Pro	Trp	Cys	Gly	Pro	Cys	Gln	Asn	Phe	650	655	660
Ala	Pro	Glu	Phe	Glu	Leu	Leu	Ala	Arg	Met	Ile	Lys	Gly	Lys	Val	665	670	675
Lys	Ala	Gly	Lys	Val	Asp	Cys	Gln	Ala	Tyr	Ala	Gln	Thr	Cys	Gln	680	685	690
Lys	Ala	Gly	Ile	Arg	Ala	Tyr	Pro	Thr	Val	Lys	Phe	Tyr	Phe	Tyr	695	700	705
Glu	Arg	Ala	Lys	Arg	Asn	Phe	Gln	Glu	Glu	Gln	Ile	Asn	Thr	Arg	710	715	720
Asp	Ala	Lys	Ala	Ile	Ala	Ala	Leu	Ile	Ser	Glu	Lys	Leu	Glu	Thr	725	730	735
Leu	Arg	Asn	Gln	Gly	Lys	Arg	Asn	Lys	Asp	Glu	Leu				740	745	

<210> 460

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe



<400> 460  
actccccagg ctgttcacac tgcc 24

<210> 461  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 461  
gatcagccag ccaataccag cagc 24

<210> 462  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 462  
gtggtgatga tagaatgctt tgccgaatga aaggagtcaa cagctatccc 50

<210> 463  
<211> 1818  
<212> DNA  
<213> Homo sapiens

<400> 463  
agacagtacc tcctccctag gactacacaa ggactgaacc agaaggaaga 50  
ggacagagca aagccatgaa catcatccta gaaatccttc tgctttctgat 100  
caccatcatc tactcctact tggagtcgtt ggtgaagttt ttcattcctc 150  
agaggagaaa atctgtggct ggggagattg ttctcattac tggagctggg 200  
catggaatag gcaggcagac tacttatgaa tttgcaaaac gacagagcat 250  
attggttctg tgggatatta ataagcgcg tgtggaggaa actgcagctg 300  
agtgccgaaa actaggcgctc actgcgcgatg cgtatgtggt agactgcagc 350  
aacagagaag agatctatcg ctctctaaat caggtgaaga aagaagtggg 400  
tgatgtaaca atcgtggtga ataatgctgg gacagtatat ccagccgatc 450  
ttctcagcac caaggatgaa gagattacca agacatttga ggtcaacatc 500  
ctaggacatt tttggatcac aaaagcactt cttccatcga tgatggagag 550  
aaatcatggc cacatcgtca cagtggcttc agtgtgcggc cacgaaggga 600  
ttccttacct catcccatat tgttcagca aatttgccgc tgttggtttt 650  
cacagaggtc tgacatcaga acttcaggcc ttgggaaaaa ctggtatcaa 700

aacctcatgt ctctgcccag tttttgtgaa tactggggttc accaaaaatc 750  
 caagcacaag attatggcct gtattggaga cagatgaagt cgtaagaagt 800  
 ctgatagatg gaatacttac caataagaaa atgatttttg ttccatcgta 850  
 tatcaatatc tttctgagac tacagaagtt tcttcctgaa cgcgcctcag 900  
 cgatttttaa tcgtatgcag aatattcaat ttgaagcagt gggtggccac 950  
 aaaatcaaaa tgaaatgaat aaataagctc cagccagaga tgtatgcatg 1000  
 ataatgatat gaatagtttc gaatcaatgc tgcaaagctt tatttcacat 1050  
 tttttcagtc ctgataatat taaaaacatt gggttggcac tagcagcagt 1100  
 caaacgaaca agattaatta cctgtcttcc tgtttctcaa gaatatattac 1150  
 gtagtttttc ataggtctgt ttttcctttc atgcctctta aaaacttctg 1200  
 tgcttacata aacatactta aaagggtttc ttttaagatat tttatttttc 1250  
 catttaaagg tggacaaaag ctacctccct aaaagtaa atacaagagaa 1300  
 cttatttaca cagggaaggt ttaagactgt tcaagtagca ttccaatctg 1350  
 tagccatgcc acagaatatc aacaagaaca cagaatgagt gcacagctaa 1400  
 gagatcaagt ttcagcaggc agctttatct caacctggac atattttaag 1450  
 attcagcatt tgaaagattt ccctagcctc ttcctttttc attagcccaa 1500  
 aacggtgcaa ctctattctg gactttatta cttgattctg tcttctgtat 1550  
 aactctgaag tccacaaaa gtggaccctc tatatttctc ccctttttat 1600  
 agtcttataa gatacattat gaaagggtgac cgactctatt ttaaattctca 1650  
 gaattttaag ttctagcccc atgataacct ttttctttgt aatttatgct 1700  
 ttcatatatc cttggtccca gagatgttta gacaatttta ggctcaaaaa 1750  
 ttaaagctaa cacaggaaaa ggaactgtac tggtatttac ataagaaaca 1800  
 atggacccaa gagaagaa 1818

<210> 464  
 <211> 300  
 <212> PRT  
 <213> Homo sapiens

<400> 464  
 Met Asn Ile Ile Leu Glu Ile Leu Leu Leu Leu Ile Thr Ile Ile  
 1 5 10 15  
 Tyr Ser Tyr Leu Glu Ser Leu Val Lys Phe Phe Ile Pro Gln Arg  
 20 25 30

Arg	Lys	Ser	Val	Ala	Gly	Glu	Ile	Val	Leu	Ile	Thr	Gly	Ala	Gly	
				35					40					45	
His	Gly	Ile	Gly	Arg	Gln	Thr	Thr	Tyr	Glu	Phe	Ala	Lys	Arg	Gln	
				50					55					60	
Ser	Ile	Leu	Val	Leu	Trp	Asp	Ile	Asn	Lys	Arg	Gly	Val	Glu	Glu	
				65					70					75	
Thr	Ala	Ala	Glu	Cys	Arg	Lys	Leu	Gly	Val	Thr	Ala	His	Ala	Tyr	
				80					85					90	
Val	Val	Asp	Cys	Ser	Asn	Arg	Glu	Glu	Ile	Tyr	Arg	Ser	Leu	Asn	
				95					100					105	
Gln	Val	Lys	Lys	Glu	Val	Gly	Asp	Val	Thr	Ile	Val	Val	Asn	Asn	
				110					115					120	
Ala	Gly	Thr	Val	Tyr	Pro	Ala	Asp	Leu	Leu	Ser	Thr	Lys	Asp	Glu	
				125					130					135	
Glu	Ile	Thr	Lys	Thr	Phe	Glu	Val	Asn	Ile	Leu	Gly	His	Phe	Trp	
				140					145					150	
Ile	Thr	Lys	Ala	Leu	Leu	Pro	Ser	Met	Met	Glu	Arg	Asn	His	Gly	
				155					160					165	
His	Ile	Val	Thr	Val	Ala	Ser	Val	Cys	Gly	His	Glu	Gly	Ile	Pro	
				170					175					180	
Tyr	Leu	Ile	Pro	Tyr	Cys	Ser	Ser	Lys	Phe	Ala	Ala	Val	Gly	Phe	
				185					190					195	
His	Arg	Gly	Leu	Thr	Ser	Glu	Leu	Gln	Ala	Leu	Gly	Lys	Thr	Gly	
				200					205					210	
Ile	Lys	Thr	Ser	Cys	Leu	Cys	Pro	Val	Phe	Val	Asn	Thr	Gly	Phe	
				215					220					225	
Thr	Lys	Asn	Pro	Ser	Thr	Arg	Leu	Trp	Pro	Val	Leu	Glu	Thr	Asp	
				230					235					240	
Glu	Val	Val	Arg	Ser	Leu	Ile	Asp	Gly	Ile	Leu	Thr	Asn	Lys	Lys	
				245					250					255	
Met	Ile	Phe	Val	Pro	Ser	Tyr	Ile	Asn	Ile	Phe	Leu	Arg	Leu	Gln	
				260					265					270	
Lys	Phe	Leu	Pro	Glu	Arg	Ala	Ser	Ala	Ile	Leu	Asn	Arg	Met	Gln	
				275					280					285	
Asn	Ile	Gln	Phe	Glu	Ala	Val	Val	Gly	His	Lys	Ile	Lys	Met	Lys	
				290					295					300	

<210> 465  
 <211> 1547  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 465

cggcggcgcg tgcggggcgcg aggtgagggg cgcgaggtga ggggcgcgag 50  
 gttcccagca ggatgccccg gctctgcagg aagctgaagt gagaggcccc 100  
 gagaggggccc agcccggccc gggcaggatg accaaggccc ggctgttccg 150  
 gctgtggctg gtgctggggg cgggtgttcat gacctgctg atcatcgtgt 200  
 actgggacag cgcaggcgcc gcgcacttct acttgcacac gtccttctct 250  
 agggcgcaca cggggccgcc gctgcccacg cccgggcccgg acagggacag 300  
 ggagctcacg gccgactccg atgtcgacga gtttctggac aagtttctca 350  
 gtgctggcgt gaagcagagc gaccttccca gaaaggagac ggagcagccg 400  
 cctgcgccgg ggagcatgga ggagagcgtg agaggctacg actggtcccc 450  
 gcgcgacgcc cggcgcgacc cagaccaggg ccggcagcag gcggagcgga 500  
 ggagcgtgct gcggggcttc tgcgccaact ccagcctggc cttccccacc 550  
 aaggagcgcg cattcgacga catccccaac tcggagctga gccacctgat 600  
 cgtggacgac cggcacgggg ccatctactg ctacgtgccc aagggtggcct 650  
 gcaccaactg gaagcgcggtg atgatcgtgc tgagcggaag cctgctgcac 700  
 cgcggtgcmc cctaccgcmg cccgctgcmc atcccgcgcm agcacgtgca 750  
 caacgccagc gcgcacctga ccttcaacaa gttctggcmc cgctacggga 800  
 agctctcccc ccacctcatg aagggtcaagc tcaagaagta caccaagttc 850  
 ctcttcgtgc gcgacctt ctgtgcgctg atctccgcct tccgcagcaa 900  
 gttcgagctg gagaacgagg agttctaccg caagttcgcc gtgcccattc 950  
 tgcggctgta cgccaaccac accagcctgc ccgcctcggc gcgcgaggcc 1000  
 ttccgcgctg gcctcaaggt gtccttcgcc aacttcatcc agtacctgct 1050  
 ggacctgcac acggagaagc tggcgccctt caacgagcac tggcggcagg 1100  
 tgtaccgcct ctgccacctg tgccagatcg actacgactt cgtggggaag 1150  
 ctggagactc tggacgagga cgccgcgcag ctgctgcagc tactccaggt 1200  
 ggaccggcag ctccgcttcc ccccagcta ccggaacagg accgccagca 1250  
 gctgggagga ggactggttc gccaaagatcc ccctggcctg gaggcagcag 1300  
 ctgtataaac tctacgaggc cgactttggt ctcttcggct accccaagcc 1350  
 cgaaaacctc ctccgagact gaaagctttc gcgttgcttt ttctcgcgtg 1400  
 cctggaacct gacgcacgcg cactccagtt tttttatgac ctacgatttt 1450

gcaatctggg cttcttggtc actccactgc ctctatccat tgagtactgt 1500

atcgatattg ttttttaaga ttaatatatt tcaggtatatt aatacga 1547

<210> 466

<211> 414

<212> PRT

<213> Homo sapiens

<400> 466

Met	Thr	Lys	Ala	Arg	Leu	Phe	Arg	Leu	Trp	Leu	Val	Leu	Gly	Ser
1				5					10					15

Val	Phe	Met	Ile	Leu	Leu	Ile	Ile	Val	Tyr	Trp	Asp	Ser	Ala	Gly
				20					25					30

Ala	Ala	His	Phe	Tyr	Leu	His	Thr	Ser	Phe	Ser	Arg	Pro	His	Thr
				35					40					45

Gly	Pro	Pro	Leu	Pro	Thr	Pro	Gly	Pro	Asp	Arg	Asp	Arg	Glu	Leu
				50					55					60

Thr	Ala	Asp	Ser	Asp	Val	Asp	Glu	Phe	Leu	Asp	Lys	Phe	Leu	Ser
				65					70					75

Ala	Gly	Val	Lys	Gln	Ser	Asp	Leu	Pro	Arg	Lys	Glu	Thr	Glu	Gln
				80					85					90

Pro	Pro	Ala	Pro	Gly	Ser	Met	Glu	Glu	Ser	Val	Arg	Gly	Tyr	Asp
				95					100					105

Trp	Ser	Pro	Arg	Asp	Ala	Arg	Arg	Ser	Pro	Asp	Gln	Gly	Arg	Gln
				110					115					120

Gln	Ala	Glu	Arg	Arg	Ser	Val	Leu	Arg	Gly	Phe	Cys	Ala	Asn	Ser
				125					130					135

Ser	Leu	Ala	Phe	Pro	Thr	Lys	Glu	Arg	Ala	Phe	Asp	Asp	Ile	Pro
				140					145					150

Asn	Ser	Glu	Leu	Ser	His	Leu	Ile	Val	Asp	Asp	Arg	His	Gly	Ala
				155					160					165

Ile	Tyr	Cys	Tyr	Val	Pro	Lys	Val	Ala	Cys	Thr	Asn	Trp	Lys	Arg
				170					175					180

Val	Met	Ile	Val	Leu	Ser	Gly	Ser	Leu	Leu	His	Arg	Gly	Ala	Pro
				185					190					195

Tyr	Arg	Asp	Pro	Leu	Arg	Ile	Pro	Arg	Glu	His	Val	His	Asn	Ala
				200					205					210

Ser	Ala	His	Leu	Thr	Phe	Asn	Lys	Phe	Trp	Arg	Arg	Tyr	Gly	Lys
				215					220					225

Leu	Ser	Arg	His	Leu	Met	Lys	Val	Lys	Leu	Lys	Lys	Tyr	Thr	Lys
				230					235					240

09978192.10501

Phe	Leu	Phe	Val	Arg	Asp	Pro	Phe	Val	Arg	Leu	Ile	Ser	Ala	Phe	
				245					250					255	
Arg	Ser	Lys	Phe	Glu	Leu	Glu	Asn	Glu	Glu	Phe	Tyr	Arg	Lys	Phe	
				260					265					270	
Ala	Val	Pro	Met	Leu	Arg	Leu	Tyr	Ala	Asn	His	Thr	Ser	Leu	Pro	
				275					280					285	
Ala	Ser	Ala	Arg	Glu	Ala	Phe	Arg	Ala	Gly	Leu	Lys	Val	Ser	Phe	
				290					295					300	
Ala	Asn	Phe	Ile	Gln	Tyr	Leu	Leu	Asp	Pro	His	Thr	Glu	Lys	Leu	
				305					310					315	
Ala	Pro	Phe	Asn	Glu	His	Trp	Arg	Gln	Val	Tyr	Arg	Leu	Cys	His	
				320					325					330	
Pro	Cys	Gln	Ile	Asp	Tyr	Asp	Phe	Val	Gly	Lys	Leu	Glu	Thr	Leu	
				335					340					345	
Asp	Glu	Asp	Ala	Ala	Gln	Leu	Leu	Gln	Leu	Leu	Gln	Val	Asp	Arg	
				350					355					360	
Gln	Leu	Arg	Phe	Pro	Pro	Ser	Tyr	Arg	Asn	Arg	Thr	Ala	Ser	Ser	
				365					370					375	
Trp	Glu	Glu	Asp	Trp	Phe	Ala	Lys	Ile	Pro	Leu	Ala	Trp	Arg	Gln	
				380					385					390	
Gln	Leu	Tyr	Lys	Leu	Tyr	Glu	Ala	Asp	Phe	Val	Leu	Phe	Gly	Tyr	
				395					400					405	
Pro	Lys	Pro	Glu	Asn	Leu	Leu	Arg	Asp							
				410											

<210> 467  
 <211> 1071  
 <212> DNA  
 <213> Homo sapiens

<400> 467  
 tcgggccaga attcggcacg aggcggcacg agggcgacgg cctcacgggg 50  
 ctttgagagt gaaagaggcc cagagtagag agagagagag accgacgtac 100  
 acgggatggc tacgggaacg cgctatgccg ggaaggtggt ggtcgtgacc 150  
 gggggcgggc gcggcatcgg agctgggatc gtgcgcgcct tcgtgaacag 200  
 cgggggccga gtggttatct gcgacaagga tgagtctggg ggccggggccc 250  
 tggagcagga gctccctgga gctgtcttta tcctctgtga tgtgactcag 300  
 gaagatgatg tgaagaccct ggtttctgag accatccgcc gatttggccg 350  
 cctggattgt gttgtcaaca acgctggcca ccaccaccc ccacagaggc 400

ctgaggagac ctctgccag ggattccgcc agctgctgga gctgaaccta 450  
 ctggggacgt acaocttgac caagctcgcc ctcccctacc tgcggaagag 500  
 tcaaggggaat gtcatacaaca tctccagcct ggtgggggca atcggccagg 550  
 cccaggcagt tccctatgtg gccaccaagg gggcagtaac agccatgacc 600  
 aaagctttgg ccctggatga aagtccatat ggtgtccgag tcaactgtat 650  
 ctccccagga aacatctgga ccccgctgtg ggaggagctg gcagccttaa 700  
 tgccagaccc tagggccaca atccgagagg gcatgctggc ccagccactg 750  
 ggccgcatgg gccagcccgc tgaggtcggg gctgcggcag tgttcctggc 800  
 ctccgaagcc aacttctgca cgggcattga actgctcgtg acgggggggtg 850  
 cagagctggg gtacgggtgc aaggccagtc ggagcaccgc cgtggacgcc 900  
 cccgatatcc ctctctgatt tctctcattt ctacttgggg ccccttcct 950  
 aggactctcc caccctaaac tccaacctgt atcagatgca gcccctaacg 1000  
 ccttagactc taagcccagt tagcaagggt cggggtcacc ctgcaggttc 1050  
 ccataaaaac gatttgagc c 1071

<210> 468

<211> 270

<212> PRT

<213> Homo sapiens

<400> 468

Met	Ala	Thr	Gly	Thr	Arg	Tyr	Ala	Gly	Lys	Val	Val	Val	Val	Thr
1				5					10					15
Gly	Gly	Gly	Arg	Gly	Ile	Gly	Ala	Gly	Ile	Val	Arg	Ala	Phe	Val
				20					25					30
Asn	Ser	Gly	Ala	Arg	Val	Val	Ile	Cys	Asp	Lys	Asp	Glu	Ser	Gly
				35					40					45
Gly	Arg	Ala	Leu	Glu	Gln	Glu	Leu	Pro	Gly	Ala	Val	Phe	Ile	Leu
				50					55					60
Cys	Asp	Val	Thr	Gln	Glu	Asp	Asp	Val	Lys	Thr	Leu	Val	Ser	Glu
				65					70					75
Thr	Ile	Arg	Arg	Phe	Gly	Arg	Leu	Asp	Cys	Val	Val	Asn	Asn	Ala
				80					85					90
Gly	His	His	Pro	Pro	Pro	Gln	Arg	Pro	Glu	Glu	Thr	Ser	Ala	Gln
				95					100					105
Gly	Phe	Arg	Gln	Leu	Leu	Glu	Leu	Asn	Leu	Leu	Gly	Thr	Tyr	Thr
				110					115					120

Leu Thr Lys Leu Ala Leu Pro Tyr Leu Arg Lys Ser Gln Gly Asn	125	130	135
Val Ile Asn Ile Ser Ser Leu Val Gly Ala Ile Gly Gln Ala Gln	140	145	150
Ala Val Pro Tyr Val Ala Thr Lys Gly Ala Val Thr Ala Met Thr	155	160	165
Lys Ala Leu Ala Leu Asp Glu Ser Pro Tyr Gly Val Arg Val Asn	170	175	180
Cys Ile Ser Pro Gly Asn Ile Trp Thr Pro Leu Trp Glu Glu Leu	185	190	195
Ala Ala Leu Met Pro Asp Pro Arg Ala Thr Ile Arg Glu Gly Met	200	205	210
Leu Ala Gln Pro Leu Gly Arg Met Gly Gln Pro Ala Glu Val Gly	215	220	225
Ala Ala Ala Val Phe Leu Ala Ser Glu Ala Asn Phe Cys Thr Gly	230	235	240
Ile Glu Leu Leu Val Thr Gly Gly Ala Glu Leu Gly Tyr Gly Cys	245	250	255
Lys Ala Ser Arg Ser Thr Pro Val Asp Ala Pro Asp Ile Pro Ser	260	265	270

<210> 469  
 <211> 687  
 <212> DNA  
 <213> Homo sapiens

<400> 469  
 aggcgggcag cagctgcagg ctgaccttgc agcttggcgg aatggactgg 50  
 cctcacaacc tgctgtttct tcttaccatt tccatcttcc tggggctggg 100  
 ccagcccagg agccccaaaa gcaagaggaa ggggcaaggg cggcctgggc 150  
 ccctggcccc tgGCCctcac caggtgccac tggacctggt gtcacggatg 200  
 aaaccgtatg cccgcatgga ggagtatgag aggaacatcg aggagatggt 250  
 ggcccagctg aggaacagct cagagctggc ccagagaaaag tgtgaggtca 300  
 acttgcagct gtggatgtcc aacaagagga gcctgtctcc ctggggctac 350  
 agcatcaacc acgaccccag ccgtatcccc gtggacctgc cggaggcacg 400  
 gtgccttgtg ctgggctgtg tgaaccctt caccatgcag gaggaccgca 450  
 gcatggtgag cgtgccggtg ttcagccagg ttcctgtgcg ccgccgcctc 500  
 tgcccgccac cgccccgcac agggccttgc cgccagcgcg cagtcatgga 550



gaccatcgct gtgggctgca cctgcatctt ctgaatcacc tggcccagaa 600  
gccaggccag cagccccgaga ccatactctt tgcacctttg tgccaagaaa 650  
ggcctatgaa aagtaaacac tgacttttga aagcaag 687

<210> 470  
<211> 180  
<212> PRT  
<213> Homo sapiens

<400> 470  
Met Asp Trp Pro His Asn Leu Leu Phe Leu Leu Thr Ile Ser Ile  
1 5 10 15  
Phe Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys  
20 25 30  
Gly Gln Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val  
35 40 45  
Pro Leu Asp Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu  
50 55 60  
Glu Tyr Glu Arg Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn  
65 70 75  
Ser Ser Glu Leu Ala Gln Arg Lys Cys Glu Val Asn Leu Gln Leu  
80 85 90  
Trp Met Ser Asn Lys Arg Ser Leu Ser Pro Trp Gly Tyr Ser Ile  
95 100 105  
Asn His Asp Pro Ser Arg Ile Pro Val Asp Leu Pro Glu Ala Arg  
110 115 120  
Cys Leu Cys Leu Gly Cys Val Asn Pro Phe Thr Met Gln Glu Asp  
125 130 135  
Arg Ser Met Val Ser Val Pro Val Phe Ser Gln Val Pro Val Arg  
140 145 150  
Arg Arg Leu Cys Pro Pro Pro Pro Arg Thr Gly Pro Cys Arg Gln  
155 160 165  
Arg Ala Val Met Glu Thr Ile Ala Val Gly Cys Thr Cys Ile Phe  
170 175 180

<210> 471  
<211> 2368  
<212> DNA  
<213> Homo sapiens

<400> 471  
gcgcccgcag gcgtaggcgg ggtggccctt gcgtctcccg cttccttgaa 50  
aaaccggcg ggcgagcgag gctgcggggc ggccgctgcc cttccccaca 100

09978192 "101501

ctccccgccg agaagcctcg ctccggcgccc aacatggcgg gtgggcgctg 150  
 cggccccgag ctaacggcgc tcctggccgc ctggatcgcg gctgtggcgg 200  
 cgacggcagg ccccgaggag gccgcgctgc cgccggagca gagccgggtc 250  
 cagcccatga ccgcctcaa ctggacgctg gtgatggagg gcgagtggat 300  
 gctgaaattt tacgccccat ggtgtccatc ctgccagcag actgattcag 350  
 aatgggaggc ttttgcaaag aatggtgaaa tacttcagat cagtgtgggg 400  
 aaggtagatg tcattcaaga accaggtttg agtggccgct tctttgtcac 450  
 cactctccca gcattttttc atgcaaagga tgggatattc cgccgttatt 500  
 gtggcccagg aatcttcgaa gacctgcaga attatatctt agagaagaaa 550  
 tggcaatcag tcgagcctct gactggctgg aaatccccag cttctctaac 600  
 gatgtctgga atggctggtc tttttagcat ctctggcaag atatggcatc 650  
 ttcacaacta tttcacagtg actcttggaa ttctgtcttg gtgttcttat 700  
 gtgtttttcg tcatagccac cttggttttt ggccttttta tgggtctggt 750  
 cttggtggta atatcagaat gtttctatgt gccacttcca aggcatctat 800  
 ctgagcggtc tgagcagaat cggagatcag aggaggctca tagagctgaa 850  
 cagttgcagg atgcggagga ggaaaaagat gattcaaag aagaagaaaa 900  
 caaagacagc cttgtagatg atgaagaaga gaaagaagat cttggcgatg 950  
 aggatgaagc agaggaagaa gaggaggagg acaacttggc tgctgggtgtg 1000  
 gatgaggaga gaagtgaggc caatgatcag gggccccag gagaggacgg 1050  
 tgtgacccgg gaggaagtag agcctgagga ggctgaagaa ggcatctctg 1100  
 agcaaccctg cccagctgac acagagggtg tggaagactc cttgaggcag 1150  
 cgtaaaaagtc agcatgctga caagggactg tagatttaat gatgcgtttt 1200  
 caagaataca caccaaaaaca atatgtcagc ttcccttttg cctgcagttt 1250  
 gtaccaaatc cttaattttt cctgaatgag caagcttctc ttaaaagatg 1300  
 ctctctagtc atttggctc atggcagtaa gcctcatgta tactaaggag 1350  
 agtcttccag gtgtgacaat caggatatag aaaaacaaac gtagtggttg 1400  
 gatctgtttg gagactggga tgggaacaag ttcatttact taggggtcag 1450  
 agagtctcga ccagaggagg ccattcccag tcctaatacag caccttccag 1500  
 agacaaggct gcaggccctg tgaaatgaaa gccaaagcagg agccttggct 1550

cctgagcatc cccaaagtgt aacgtagaag ccttgcaccc ttttcttgtg 1600  
 taaagtatth atthtttgtca aattgcagga aacatcaggc accacagtgc 1650  
 atgaaaaatc tttcacagct agaaattgaa agggccttgg gtatagagag 1700  
 cagctcagaa gtcaccccag ccctctgaat ctctgtgtct atgtttttatt 1750  
 tottaccttt aatttttcca gcattttccac catggggcatt caggctctcc 1800  
 acactcttca ctattatctc ttgggtcagag gactccaata acagccagggt 1850  
 ttacatgaac tgtgtttgtt cattctgacc taaggggttt agataatcag 1900  
 taaccataac ccctgaagct gtgactgcca aacatctcaa atgaaatgtt 1950  
 gtggccatca gagactcaaa aggaagtaag gatttttaca gacagattaa 2000  
 aaaaaaattg ttttgtccaa aatatagttg ttgttgattt ttttttaagt 2050  
 tttctaagca atatttttca agccagaagt cctctaagtc ttgccagtac 2100  
 aaggtagtct tgtgaagaaa agttgaatac tgttttgttt tcatctcaag 2150  
 gggttccctg ggtcttgaac tactttaata ataactaaaa aaccacttct 2200  
 gatttttctt cagtgatgtg cttttgtga aagaattaat gaactccagt 2250  
 acctgaaagt gaaagatttg attttgtttc catcttctgt aatcttccaa 2300  
 agaattatat ctttgtaaatt ctctcaatac tcaatctact gtaagtaccc 2350  
 agggaggcta atttcttt 2368

<210> 472  
 <211> 349  
 <212> PRT  
 <213> Homo sapiens

<400> 472  
 Met Ala Gly Gly Arg Cys Gly Pro Gln Leu Thr Ala Leu Leu Ala  
 1 5 10 15  
 Ala Trp Ile Ala Ala Val Ala Ala Thr Ala Gly Pro Glu Glu Ala  
 20 25 30  
 Ala Leu Pro Pro Glu Gln Ser Arg Val Gln Pro Met Thr Ala Ser  
 35 40 45  
 Asn Trp Thr Leu Val Met Glu Gly Glu Trp Met Leu Lys Phe Tyr  
 50 55 60  
 Ala Pro Trp Cys Pro Ser Cys Gln Gln Thr Asp Ser Glu Trp Glu  
 65 70 75  
 Ala Phe Ala Lys Asn Gly Glu Ile Leu Gln Ile Ser Val Gly Lys  
 80 85 90

Val	Asp	Val	Ile	Gln	Glu	Pro	Gly	Leu	Ser	Gly	Arg	Phe	Phe	Val
				95					100					105
Thr	Thr	Leu	Pro	Ala	Phe	Phe	His	Ala	Lys	Asp	Gly	Ile	Phe	Arg
				110					115					120
Arg	Tyr	Arg	Gly	Pro	Gly	Ile	Phe	Glu	Asp	Leu	Gln	Asn	Tyr	Ile
				125					130					135
Leu	Glu	Lys	Lys	Trp	Gln	Ser	Val	Glu	Pro	Leu	Thr	Gly	Trp	Lys
				140					145					150
Ser	Pro	Ala	Ser	Leu	Thr	Met	Ser	Gly	Met	Ala	Gly	Leu	Phe	Ser
				155					160					165
Ile	Ser	Gly	Lys	Ile	Trp	His	Leu	His	Asn	Tyr	Phe	Thr	Val	Thr
				170					175					180
Leu	Gly	Ile	Pro	Ala	Trp	Cys	Ser	Tyr	Val	Phe	Phe	Val	Ile	Ala
				185					190					195
Thr	Leu	Val	Phe	Gly	Leu	Phe	Met	Gly	Leu	Val	Leu	Val	Val	Ile
				200					205					210
Ser	Glu	Cys	Phe	Tyr	Val	Pro	Leu	Pro	Arg	His	Leu	Ser	Glu	Arg
				215					220					225
Ser	Glu	Gln	Asn	Arg	Arg	Ser	Glu	Glu	Ala	His	Arg	Ala	Glu	Gln
				230					235					240
Leu	Gln	Asp	Ala	Glu	Glu	Glu	Lys	Asp	Asp	Ser	Asn	Glu	Glu	Glu
				245					250					255
Asn	Lys	Asp	Ser	Leu	Val	Asp	Asp	Glu	Glu	Glu	Lys	Glu	Asp	Leu
				260					265					270
Gly	Asp	Glu	Asp	Glu	Ala	Glu	Glu	Glu	Glu	Glu	Glu	Asp	Asn	Leu
				275					280					285
Ala	Ala	Gly	Val	Asp	Glu	Glu	Arg	Ser	Glu	Ala	Asn	Asp	Gln	Gly
				290					295					300
Pro	Pro	Gly	Glu	Asp	Gly	Val	Thr	Arg	Glu	Glu	Val	Glu	Pro	Glu
				305					310					315
Glu	Ala	Glu	Glu	Gly	Ile	Ser	Glu	Gln	Pro	Cys	Pro	Ala	Asp	Thr
				320					325					330
Glu	Val	Val	Glu	Asp	Ser	Leu	Arg	Gln	Arg	Lys	Ser	Gln	His	Ala
				335					340					345

Asp Lys Gly Leu

<210> 473  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 473  
gtccagccca tgaccgcctc caac 24

<210> 474  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 474  
ctctcctcat ccacaccagc agcc 24

<210> 475  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 475  
gtggatgctg aaattttacg ccccatggtg tccatcctgc cagc 44

<210> 476  
<211> 2478  
<212> DNA  
<213> Homo sapiens

<400> 476  
atctggttga actacttaag cttaatttgt taaactccgg taagtaccta 50  
gccacatga tttgactcag agattctctt ttgtccacag acagtcattct 100  
caggggcaga aagaaaagag ctcccaaagt ctatatctat tcaggggctc 150  
tcaagaacaa tggaatatca tcctgattta gaaaatttgg atgaagatgg 200  
atatactcaa ttacacttcg actctcaaag caataccagg atagctgttg 250  
tttcagagaa aggatcgtgt gctgcatctc ctccttggcg cctcattgct 300  
gtaatttttg gaatcctatg cttggtaata ctggtgatag ctgtggtcct 350  
gggtaccatg ggggttcttt ccagcccttg tcctcctaatt tggattatat 400  
atgagaagag ctgttatcta ttcagcatgt cactaaattc ctgggatgga 450  
agtaaaagac aatgctggca actgggctct aatctcctaa agatagacag 500  
ctcaaatgaa ttgggattta tagtaaaaca agtgtcttcc caacctgata 550  
attcattttg gataggcctt tctcggtccc agactgaggt accatggctc 600

tgggaggatg gatcaacatt ctcttctaac ttatttcaga tcagaaccac 650  
 agctacccaa gaaaacccat ctccaaattg tgtatggatt cacgtgtcag 700  
 tcatttatga ccaactgtgt agtgtgccct catatagtat ttgtgagaag 750  
 aagttttcaa tgtaagagga aggggtggaga aggagagaga aatatgtgag 800  
 gtagtaagga ggacagaaaa cagaacagaa aagagtaaca gctgagggtca 850  
 agataaatgc agaaaatggt tagagagctt ggccaactgt aatcttaacc 900  
 aagaaattga agggagaggg tgtgatttct gtatttgtcg acctacaggt 950  
 aggctagtat tatttttcta gttagtagat ccctagacat ggaatcaggg 1000  
 cagccaagct tgagttttta ttttttattt atttattttt ttgagatagg 1050  
 gtctcacttt gttaccagg ctggagtgc gtggcacaat ctcgactcac 1100  
 tgcagctatc tctcgctca gccctcaag tagctgggac tacagggtgca 1150  
 tgccaccatg ccaggctaatt ttttggtgtt tttttagag actgggtttt 1200  
 gccatgttga ccaagctgggt ctctaactcc tgggcttaag tgatctgccc 1250  
 gccttggcct cccaaagtgc tgggattaca gatgtgagcc accacacctg 1300  
 gccccagct tgaattttca ttctgccatt gacttggcat ttaccttggg 1350  
 taagccataa gcgaatctta atttctggct ctatcagagt tgtttcatgc 1400  
 tcaacaatgc cattgaagtg cacggtgtgt tgccacgatt tgaccctcaa 1450  
 cttctagcag tatatcagtt atgaactgag ggtgaaatat atttctgaat 1500  
 agctaaatga agaaatggga aaaaatcttc accacagtca gagcaatttt 1550  
 attattttca tcagtatgat cataattatg attatcatct tagtaaaaag 1600  
 caggaactcc tactttttct ttatcaatta aatagctcag agagtacatc 1650  
 tgccatatct ctaatagaat cttttttttt tttttttttt tttgagacag 1700  
 agtttcgctc ttgttgccca ggctggagtg caacggcacg atctcggctc 1750  
 accgcaacct ccgccccctg ggttcaagca attctcctgc ctcagcctcc 1800  
 caagtagctg ggattacagt caggcaccac cacacccggc taattttgta 1850  
 tttttttagt agagacaggg tttctccatg tcggtcaggg tagtcccgaa 1900  
 ctctgacct caagtatct gcctgcctcg gcctcccaag tgctgggatt 1950  
 acaggcgtga gccactgcac ccagcctaga atcttgtata atatgtaatt 2000  
 gtagggaaac tgctctcata ggaaagtttt ctgcttttta aatacaaaaa 2050

tacataaaaa tacataaaat ctgatgatga atataaaaaa gtaaccaacc 2100  
tcattggaac aagtattaac attttggaat atgttttatt agttttgtga 2150  
tgtactgttt tacaattttt accatttttt tcagtaatta ctgtaaaatg 2200  
gtattattgg aatgaaacta tatttcctca tgtgctgatt tgtcttattt 2250  
ttttcatact ttcccaactgg tgctattttt atttccaatg gatatttctg 2300  
tattactagg gaggcattta cagtcctcta atgttgatta atatgtgaaa 2350  
agaaattgta ccaattttac taaattatgc agtttaaaat ggatgatttt 2400  
atgttatgtg gatttcattt caataaaaaa aaactcttat caaaaaaaaaa 2450  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2478

<210> 477  
<211> 201  
<212> PRT  
<213> Homo sapiens

<400> 477  
Met Glu Tyr His Pro Asp Leu Glu Asn Leu Asp Glu Asp Gly Tyr  
1 5 10 15  
Thr Gln Leu His Phe Asp Ser Gln Ser Asn Thr Arg Ile Ala Val  
20 25 30  
Val Ser Glu Lys Gly Ser Cys Ala Ala Ser Pro Pro Trp Arg Leu  
35 40 45  
Ile Ala Val Ile Leu Gly Ile Leu Cys Leu Val Ile Leu Val Ile  
50 55 60  
Ala Val Val Leu Gly Thr Met Gly Val Leu Ser Ser Pro Cys Pro  
65 70 75  
Pro Asn Trp Ile Ile Tyr Glu Lys Ser Cys Tyr Leu Phe Ser Met  
80 85 90  
Ser Leu Asn Ser Trp Asp Gly Ser Lys Arg Gln Cys Trp Gln Leu  
95 100 105  
Gly Ser Asn Leu Leu Lys Ile Asp Ser Ser Asn Glu Leu Gly Phe  
110 115 120  
Ile Val Lys Gln Val Ser Ser Gln Pro Asp Asn Ser Phe Trp Ile  
125 130 135  
Gly Leu Ser Arg Pro Gln Thr Glu Val Pro Trp Leu Trp Glu Asp  
140 145 150  
Gly Ser Thr Phe Ser Ser Asn Leu Phe Gln Ile Arg Thr Thr Ala  
155 160 165  
Thr Gln Glu Asn Pro Ser Pro Asn Cys Val Trp Ile His Val Ser

09078192.101501  
T05T0T.261B2660

	170		175		180									
Val	Ile	Tyr	Asp	Gln	Leu	Cys	Ser	Val	Pro	Ser	Tyr	Ser	Ile	Cys
				185					190					195
Glu	Lys	Lys	Phe	Ser	Met									
				200										

<210> 478  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 478  
gtccacagac agtcatctca ggagcag 27

<210> 479  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 479  
acaagtgtct tcccaacctg 20

<210> 480  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 480  
atcctcccag agccatggta cctc 24

<210> 481  
<211> 51  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 481  
ccaaggatag ctgttgtttc agagaaagga tcgtgtgctg catctcctcc 50

t 51

<210> 482  
<211> 3819  
<212> DNA  
<213> Homo sapiens



<400> 482

ggaaggggag gagcaggcca cacaggcaca ggccggtgag ggacctgccc 50  
agacctggag ggtctcgctc tgtcacacag gctggagtgc agtgggtgtga 100  
tcttggctca tcgtaacctc cacctcccgg gttcaagtga ttctcatgcc 150  
tcagcctccc gagtagctgg gattacaggt ggtgacttcc aagagtgact 200  
ccgtcggagg aaaatgactc cccagtcgct gctgcagacg aactgttcc 250  
tgctgagtct gctcttcctg gtccaagggtg cccacggcag gggccacagg 300  
gaagactttc gcttctgcag ccagcggaac cagacacaca ggagcagcct 350  
ccactacaaa cccacaccag acctgcgcat ctccatcgag aactccgaag 400  
aggccctcac agtccatgcc cctttccctg cagcccaccc tgcttcccga 450  
tccttccctg accccagggg cctctaccac ttctgcctct actggaaccg 500  
acatgctggg agattacatc ttctctatgg caagcgtgac ttcttgctga 550  
gtgacaaagc ctctagcctc ctctgcttcc agcaccagga ggagagcctg 600  
gctcagggcc ccccgctgtt agccacttct gtcacctcct ggtggagccc 650  
tcagaacatc agcctgcccc gtgccgccag cttcaccttc tccttccaca 700  
gtcctcccca cacggccgct cacaatgcct cgggtggacat gtgcgagctc 750  
aaaagggacc tccagctgct cagccagttc ctgaagcatc cccagaaggc 800  
ctcaaggagg ccctcggctg ccccgccag ccagcagttg cagagcctgg 850  
agtcgaaact gacctctgtg agattcatgg gggacatggt gtccttcgag 900  
gaggaccgga tcaacgccac ggtgtggaag ctccagccca cagccggcct 950  
ccaggacctg cacatccact cccggcagga ggaggagcag agcgagatca 1000  
tggagtactc ggtgctgctg cctcgaacac tcttccagag gacgaaaggc 1050  
cggagcgggg aggtgagaa gagactcctc ctggtggact tcagcagcca 1100  
agccctgttc caggacaaga attccagcca agtcctgggt gagaaggtct 1150  
tggggattgt ggtacagaac accaaagtag ccaacctcac ggagcccgtg 1200  
gtgctcactt tccagacca gctacagccg aagaatgtga ctctgcaatg 1250  
tgtgttctgg gttgaagacc ccacattgag cagcccgggg cattggagca 1300  
gtgctgggtg tgagaccgtc aggagagaaa cccaacatc ctgcttctgc 1350  
aaccacttga cctactttgc agtgctgatg gtctcctcgg tggaggtgga 1400  
cgccgtgcac aagcactacc tgagcctcct ctctacgtg ggctgtgtcg 1450

tctctgccct ggccctgcctt gtcaccattg ccgcctacct ctgctccagg 1500  
gtgcccctgc cgtgcaggag gaaacctcgg gactacacca tcaaggtgca 1550  
catgaacctg ctgctggccg tcttctctgct ggacacgagc ttctgtctca 1600  
gcgagccggg ggccctgaca ggctctgagg ctggctgccg agccagtgcc 1650  
atcttctctgc acttctccct gctcacctgc ctttctctgga tgggcctcga 1700  
ggggtacaac ctctaccgac tcgtgggtgga ggtctttggc acctatgtcc 1750  
ctggctacct actcaagctg agcgccatgg gctggggctt ccccatcttt 1800  
ctgggtgacgc tgggtggccct ggtggatgtg gacaactatg gcccacatcat 1850  
cttggctgtg cataggactc cagagggcgt catctacctt tccatgtgct 1900  
ggatccggga ctccctggtc agctacatca ccaacctggg cctcttcagc 1950  
ctgggtgtttc tgttcaacat ggccatgcta gccaccatgg tgggtgcagat 2000  
cctgcggctg cgtccccaca cccaaaagtg gtcacatgtg ctgacactgc 2050  
tgggcctcag cctgggtcctt ggccctgccct gggccttgat cttcttctcc 2100  
tttgttctg gcaccttcca gcttgctgctc ctctaccttt tcagcatcat 2150  
cacctccttc caaggcttcc tcctcttcat ctggtactgg tccatgcggc 2200  
tgcaggcccg ggggtggccc tccctctga agagcaactc agacagcgcc 2250  
aggctcccca tcagctcggg cagcacctcg tccagccgca tctaggcctc 2300  
cagccacct gccatgtga tgaagcagag atgcggcctc gtgcacact 2350  
gcctgtggcc ccgagccag gccagcccc aggccagtca gccgcagact 2400  
ttggaaagcc caacgaccat ggagagatgg gccgttgcca tgggtggacgg 2450  
actcccgggc tgggcttttg aattggcctt ggggactact cggctctcac 2500  
tcagctccca cgggactcag aagtgcgccg ccatgctgcc tagggtactg 2550  
tccccacatc tgtcccaacc cagctggagg cctgggtctct ccttacaacc 2600  
cctgggcccc gccctcattg ctgggggcca ggcccttgat cttgagggtc 2650  
tggcacatcc ttaatctgt gcccctgcct gggacagaaa tgtggctcca 2700  
gttgctctgt ctctcgtggg caccctgagg gcactctgca tcctctgtca 2750  
ttttaacctc aggtggcacc cagggcgaat gggggccagg gcagaccttc 2800  
agggccagag ccctggcgga ggagaggccc ttgcccagga gcacagcagc 2850  
agctcgcta cctctgagcc caggccccct cctccctca gccccccagt 2900

cctccctcca tcttccctgg ggttctctc ctctcccagg gcctccttgc 2950  
 tcttctgttc acagctgggg gtccccgatt ccaatgctgt tttttgggga 3000  
 gtggtttcca ggagctgcct ggtgtctgct gtaaagtgtt gtctactgca 3050  
 caagcctcgg cctgccccctg agccaggctc ggtaccgatg cgtgggctgg 3100  
 gctaggtccc tctgtccatc tgggcctttg tatgagctgc attgcccttg 3150  
 ctcacctga ccaagcacac gcctcagagg ggccctcagc ctctcctgaa 3200  
 gccctcttgt ggcaagaact gtggaccatg ccagtcccgt ctggtttcca 3250  
 tcccaccact ccaaggactg agactgacct cctctggtga cactggccta 3300  
 gagcctgaca ctctcctaag aggttctctc caagcccca aatagctcca 3350  
 ggcgcctcgg gccgcccac atggttaatt ctgtccaaca aacacacacg 3400  
 ggtagattgc tggcctgttg taggtggtag ggacacagat gaccgacctg 3450  
 gtcactctc ctgccaacat tcagtctggt atgtgaggcg tgcgtgaagc 3500  
 aagaactcct ggagctacag ggacagggag ccatcattcc tgcctgggaa 3550  
 tcttggaaga cttctgcag gagtcagcgt tcaatcttga cttgaagat 3600  
 gggaaggatg ttctttttac gtaccaattc ttttgtctt tgatattaaa 3650  
 aagaagtaca tgttcattgt agagaatttg gaaactgtag aagagaatca 3700  
 agaagaaaaa taaaaatcag ctgttgtaat cgcctagcaa aaaaaaaaaa 3750  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3800  
 aaaaaaaaaa aaaaaaaaaa 3819

<210> 483  
 <211> 693  
 <212> PRT  
 <213> Homo sapiens

<400> 483  
 Met Thr Pro Gln Ser Leu Leu Gln Thr Thr Leu Phe Leu Leu Ser  
 1 5 10 15  
 Leu Leu Phe Leu Val Gln Gly Ala His Gly Arg Gly His Arg Glu  
 20 25 30  
 Asp Phe Arg Phe Cys Ser Gln Arg Asn Gln Thr His Arg Ser Ser  
 35 40 45  
 Leu His Tyr Lys Pro Thr Pro Asp Leu Arg Ile Ser Ile Glu Asn  
 50 55 60  
 Ser Glu Glu Ala Leu Thr Val His Ala Pro Phe Pro Ala Ala His  
 65 70 75

Pro	Ala	Ser	Arg	Ser	Phe	Pro	Asp	Pro	Arg	Gly	Leu	Tyr	His	Phe	
				80					85					90	
Cys	Leu	Tyr	Trp	Asn	Arg	His	Ala	Gly	Arg	Leu	His	Leu	Leu	Tyr	
				95					100					105	
Gly	Lys	Arg	Asp	Phe	Leu	Leu	Ser	Asp	Lys	Ala	Ser	Ser	Leu	Leu	
				110					115					120	
Cys	Phe	Gln	His	Gln	Glu	Glu	Ser	Leu	Ala	Gln	Gly	Pro	Pro	Leu	
				125					130					135	
Leu	Ala	Thr	Ser	Val	Thr	Ser	Trp	Trp	Ser	Pro	Gln	Asn	Ile	Ser	
				140					145					150	
Leu	Pro	Ser	Ala	Ala	Ser	Phe	Thr	Phe	Ser	Phe	His	Ser	Pro	Pro	
				155					160					165	
His	Thr	Ala	Ala	His	Asn	Ala	Ser	Val	Asp	Met	Cys	Glu	Leu	Lys	
				170					175					180	
Arg	Asp	Leu	Gln	Leu	Leu	Ser	Gln	Phe	Leu	Lys	His	Pro	Gln	Lys	
				185					190					195	
Ala	Ser	Arg	Arg	Pro	Ser	Ala	Ala	Pro	Ala	Ser	Gln	Gln	Leu	Gln	
				200					205					210	
Ser	Leu	Glu	Ser	Lys	Leu	Thr	Ser	Val	Arg	Phe	Met	Gly	Asp	Met	
				215					220					225	
Val	Ser	Phe	Glu	Glu	Asp	Arg	Ile	Asn	Ala	Thr	Val	Trp	Lys	Leu	
				230					235					240	
Gln	Pro	Thr	Ala	Gly	Leu	Gln	Asp	Leu	His	Ile	His	Ser	Arg	Gln	
				245					250					255	
Glu	Glu	Glu	Gln	Ser	Glu	Ile	Met	Glu	Tyr	Ser	Val	Leu	Leu	Pro	
				260					265					270	
Arg	Thr	Leu	Phe	Gln	Arg	Thr	Lys	Gly	Arg	Ser	Gly	Glu	Ala	Glu	
				275					280					285	
Lys	Arg	Leu	Leu	Leu	Val	Asp	Phe	Ser	Ser	Gln	Ala	Leu	Phe	Gln	
				290					295					300	
Asp	Lys	Asn	Ser	Ser	Gln	Val	Leu	Gly	Glu	Lys	Val	Leu	Gly	Ile	
				305					310					315	
Val	Val	Gln	Asn	Thr	Lys	Val	Ala	Asn	Leu	Thr	Glu	Pro	Val	Val	
				320					325					330	
Leu	Thr	Phe	Gln	His	Gln	Leu	Gln	Pro	Lys	Asn	Val	Thr	Leu	Gln	
				335					340					345	
Cys	Val	Phe	Trp	Val	Glu	Asp	Pro	Thr	Leu	Ser	Ser	Pro	Gly	His	
				350					355					360	
Trp	Ser	Ser	Ala	Gly	Cys	Glu	Thr	Val	Arg	Arg	Glu	Thr	Gln	Thr	

	365		370		375
Ser Cys Phe Cys	Asn His Leu Thr Tyr	Phe Ala Val Leu Met Val			
	380	385			390
Ser Ser Val Glu	Val Asp Ala Val His	Lys His Tyr Leu Ser Leu			
	395	400			405
Leu Ser Tyr Val	Gly Cys Val Val Ser	Ala Leu Ala Cys Leu Val			
	410	415			420
Thr Ile Ala Ala	Tyr Leu Cys Ser Arg	Val Pro Leu Pro Cys Arg			
	425	430			435
Arg Lys Pro Arg	Asp Tyr Thr Ile Lys	Val His Met Asn Leu Leu			
	440	445			450
Leu Ala Val Phe	Leu Leu Asp Thr Ser	Phe Leu Leu Ser Glu Pro			
	455	460			465
Val Ala Leu Thr	Gly Ser Glu Ala Gly	Cys Arg Ala Ser Ala Ile			
	470	475			480
Phe Leu His Phe	Ser Leu Leu Thr Cys	Leu Ser Trp Met Gly Leu			
	485	490			495
Glu Gly Tyr Asn	Leu Tyr Arg Leu Val	Val Glu Val Phe Gly Thr			
	500	505			510
Tyr Val Pro Gly	Tyr Leu Leu Lys Leu	Ser Ala Met Gly Trp Gly			
	515	520			525
Phe Pro Ile Phe	Leu Val Thr Leu Val	Ala Leu Val Asp Val Asp			
	530	535			540
Asn Tyr Gly Pro	Ile Ile Leu Ala Val	His Arg Thr Pro Glu Gly			
	545	550			555
Val Ile Tyr Pro	Ser Met Cys Trp Ile	Arg Asp Ser Leu Val Ser			
	560	565			570
Tyr Ile Thr Asn	Leu Gly Leu Phe Ser	Leu Val Phe Leu Phe Asn			
	575	580			585
Met Ala Met Leu	Ala Thr Met Val Val	Gln Ile Leu Arg Leu Arg			
	590	595			600
Pro His Thr Gln	Lys Trp Ser His Val	Leu Thr Leu Leu Gly Leu			
	605	610			615
Ser Leu Val Leu	Gly Leu Pro Trp Ala	Leu Ile Phe Phe Ser Phe			
	620	625			630
Ala Ser Gly Thr	Phe Gln Leu Val Val	Leu Tyr Leu Phe Ser Ile			
	635	640			645
Ile Thr Ser Phe	Gln Gly Phe Leu Ile	Phe Ile Trp Tyr Trp Ser			
	650	655			660

Met	Arg	Leu	Gln	Ala	Arg	Gly	Gly	Pro	Ser	Pro	Leu	Lys	Ser	Asn
				665					670					675
Ser	Asp	Ser	Ala	Arg	Leu	Pro	Ile	Ser	Ser	Gly	Ser	Thr	Ser	Ser
				680					685					690

Ser Arg Ile

<210> 484  
 <211> 516  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 68, 70, 84, 147  
 <223> unknown base

<400> 484  
 tgcctggcct gccttgtaa caatgccgt tactctgctt ccaggttgcc 50  
 ctgccttgca gaggaaan cn tcgggactac accntcaagt gcacatgaac 100  
 ctgctgctgg ccgtcttctt gctggacacg agcttcctgc tcagcgnagc 150  
 cgggtggcct gacaggctct gaaggctggc tgccgagcca gtgccatctt 200  
 cctgcacttc tctgctcac ctgcctttcc tggatggggc tcgaggggta 250  
 caacctctac cgactcgtgg tggaggtctt tggcacctat gtccctggct 300  
 acctactcaa gctgagcgcc atgggctggg gcttcccat ctttctgggtg 350  
 acgctggtgg ccctggtgga tgtggacaac tatggcccca tcatcttggc 400  
 tgtgcatagg actccagagg gcgtcatcta cccttccatg tgctggatcc 450  
 gggactccct ggtcagctac atcaccaacc tgggcctctt cagcctgggtg 500  
 tttctgttca acatgg 516

<210> 485  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 485  
 ggcattggag cagtgcctgg tg 22

<210> 486  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

09978192.101501

<220>  
<223> Synthetic oligonucleotide probe

<400> 486  
tggaggccta gatgcggctg gacg 24

<210> 487  
<211> 2849  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2715  
<223> unknown base

<400> 487  
cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggct 50  
ggttcaggctc caggttttgc tttgatcctt ttcaaaaact ggagacacag 100  
aagagggctc taggaaaaag ttttgatgg gattatgtgg aaactaccct 150  
gcgattctct gctgccagag caggctcggc gcttccacc cagtgcagcc 200  
ttcccctggc ggtggtgaaa gagactcggg agtcgctgct tccaaagtgc 250  
ccgccgtgag tgagctctca cccagtcag ccaaagtgc ctcttcgggc 300  
ttctcctgct gacatctgcc ctggccggcc agagacagg gactcaggcg 350  
gaatccaacc tgagtagtaa attccagttt tccagcaaca aggaacagaa 400  
cggagtacaa gatcctcagc atgagagaat tattactgtg tctactaatg 450  
gaagtattca cagcccaagg tttcctcata cttatccaag aaatacggctc 500  
ttggtatgga gattagtagc agtagaggaa aatgtatgga tacaacttac 550  
gtttgatgaa agatttgggc ttgaagacc agaagatgac atatgcaagt 600  
atgattttgt agaagttgag gaaccagtg atggaactat attagggcgc 650  
tggtgtggtt ctggtactgt accaggaaaa cagatttcta aaggaaatca 700  
aattaggata agatttgtat ctgatgaata tttccttct gaaccagggt 750  
tctgcatcca ctacaacatt gtcatgccac aattcacaga agctgtgagt 800  
ccttcagtgc tacccttc agctttgcca ctggacctgc ttaataatgc 850  
tataactgcc tttagtacct tggaagacct tattcgatat cttgaaccag 900  
agagatggca gttggactta gaagatctat ataggccaac ttggcaactt 950  
cttggcaagg cttttgtttt tggaagaaaa tccagagtgg tggatctgaa 1000  
ccttctaaca gaggaggtaa gattatacag ctgcacacct cgtaacttct 1050

cagtgtccat aaggggaagaa ctaaagagaa ccgataccat tttctggcca 1100  
 gggtgtctcc tgggttaaacg ctgtggtggg aactgtgcct gttgtctcca 1150  
 caattgcaat gaatgtcaat gtgtcccaag caaagttact aaaaaatacc 1200  
 acgaggtcct tcagttgaga ccaaagaccg gtgtcagggg attgcacaaa 1250  
 tcactcaccg acgtggccct ggagcaccat gaggagtgtg actgtgtgtg 1300  
 cagaggggagc acaggaggat agccgcatca ccaccagcag ctcttgccca 1350  
 gagctgtgca gtgcagtggc tgattctatt agagaacgta tgcgttatct 1400  
 ccatccttaa tctcagttgt ttgcttcaag gacctttcat cttcaggatt 1450  
 tacagtgcac tctgaaagag gagacatcaa acagaattag gagttgtgca 1500  
 acagctcttt tgagaggagg cctaaaggac aggagaaaag gtcttcaatc 1550  
 gtggaaagaa aattaaatgt tgtattaaat agatcaccag ctagtttcag 1600  
 agttaccatg tacgtattcc actagctggg ttctgtatct cagttctttc 1650  
 gatacggctt agggtaatgt cagtacagga aaaaaactgt gcaagtgagc 1700  
 acctgattcc gttgccttgc ttaactctaa agctccatgt cctgggccta 1750  
 aaatcgtata aaatctggat tttttttttt ttttttgctc atattcacat 1800  
 atgtaaacca gaacattcta tgtactacaa acctggtttt taaaaaggaa 1850  
 ctatgttgct atgaattaaa cttgtgtcat gctgatagga cagactggat 1900  
 ttttcatatt tcttattaaa atttctgcca tttagaagaa gagaactaca 1950  
 ttcattggtt ggaagagata aacctgaaa gaagagtggc cttatcttca 2000  
 ctttatcgat aagtcagttt atttgtttca ttgtgtacat ttttatattc 2050  
 tccttttgac attataactg ttggcttttc taatcttggt aaatatatct 2100  
 atttttacca aaggtaattt atattctttt ttatgacaac ttagatcaac 2150  
 tatttttagc ttggtaaatt tttctaaaca caattgttat agccagagga 2200  
 acaaagatga tataaaatat tgttgctctg acaaaaatac atgtatttca 2250  
 ttctcgtatg gtgctagagt tagattaatc tgcattttta aaaactgaat 2300  
 tggaatagaa ttggtaagtt gcaaagactt tttgaaaata attaaattat 2350  
 catatcttcc attcctgtta ttggagatga aaataaaaag caacttatga 2400  
 aagtagacat tcagatccag ccattactaa cctattcctt ttttggggaa 2450  
 atctgagcct agctcagaaa aacataaagc accttgaaaa agacttgga 2500



gcttcctgat aaagcgtgct gtgctgtgca gtaggaacac atcctattta 2550  
 ttgtgatgtt gtggttttat tatcttaaac tctgttccat acacttgtat 2600  
 aaatacatgg atatttttat gtacagaagt atgtctctta accagttcac 2650  
 ttattgtact ctggcaattht aaaagaaaat cagtaaaata ttttgcttgt 2700  
 aaaatgctta atatngtgcc taggttatgt ggtgactatt tgaatcaaaa 2750  
 atgtattgaa tcatcaata aaagaatgtg gctattttgg ggagaaaatt 2800  
 aaaaaaaaaa aaaaaaaaaa aggttttaggg ataacagggt aatgcggcc 2849

<210> 488

<211> 345

<212> PRT

<213> Homo sapiens

<400> 488

Met	Ser	Leu	Phe	Gly	Leu	Leu	Leu	Leu	Thr	Ser	Ala	Leu	Ala	Gly	1	5	10	15
Gln	Arg	Gln	Gly	Thr	Gln	Ala	Glu	Ser	Asn	Leu	Ser	Ser	Lys	Phe	20	25	30	
Gln	Phe	Ser	Ser	Asn	Lys	Glu	Gln	Asn	Gly	Val	Gln	Asp	Pro	Gln	35	40	45	
His	Glu	Arg	Ile	Ile	Thr	Val	Ser	Thr	Asn	Gly	Ser	Ile	His	Ser	50	55	60	
Pro	Arg	Phe	Pro	His	Thr	Tyr	Pro	Arg	Asn	Thr	Val	Leu	Val	Trp	65	70	75	
Arg	Leu	Val	Ala	Val	Glu	Glu	Asn	Val	Trp	Ile	Gln	Leu	Thr	Phe	80	85	90	
Asp	Glu	Arg	Phe	Gly	Leu	Glu	Asp	Pro	Glu	Asp	Asp	Ile	Cys	Lys	95	100	105	
Tyr	Asp	Phe	Val	Glu	Val	Glu	Glu	Pro	Ser	Asp	Gly	Thr	Ile	Leu	110	115	120	
Gly	Arg	Trp	Cys	Gly	Ser	Gly	Thr	Val	Pro	Gly	Lys	Gln	Ile	Ser	125	130	135	
Lys	Gly	Asn	Gln	Ile	Arg	Ile	Arg	Phe	Val	Ser	Asp	Glu	Tyr	Phe	140	145	150	
Pro	Ser	Glu	Pro	Gly	Phe	Cys	Ile	His	Tyr	Asn	Ile	Val	Met	Pro	155	160	165	
Gln	Phe	Thr	Glu	Ala	Val	Ser	Pro	Ser	Val	Leu	Pro	Pro	Ser	Ala	170	175	180	
Leu	Pro	Leu	Asp	Leu	Leu	Asn	Asn	Ala	Ile	Thr	Ala	Phe	Ser	Thr	185	190	195	

Leu	Glu	Asp	Leu	Ile	Arg	Tyr	Leu	Glu	Pro	Glu	Arg	Trp	Gln	Leu	
				200					205					210	
Asp	Leu	Glu	Asp	Leu	Tyr	Arg	Pro	Thr	Trp	Gln	Leu	Leu	Gly	Lys	
				215					220					225	
Ala	Phe	Val	Phe	Gly	Arg	Lys	Ser	Arg	Val	Val	Asp	Leu	Asn	Leu	
				230					235					240	
Leu	Thr	Glu	Glu	Val	Arg	Leu	Tyr	Ser	Cys	Thr	Pro	Arg	Asn	Phe	
				245					250					255	
Ser	Val	Ser	Ile	Arg	Glu	Glu	Leu	Lys	Arg	Thr	Asp	Thr	Ile	Phe	
				260					265					270	
Trp	Pro	Gly	Cys	Leu	Leu	Val	Lys	Arg	Cys	Gly	Gly	Asn	Cys	Ala	
				275					280					285	
Cys	Cys	Leu	His	Asn	Cys	Asn	Glu	Cys	Gln	Cys	Val	Pro	Ser	Lys	
				290					295					300	
Val	Thr	Lys	Lys	Tyr	His	Glu	Val	Leu	Gln	Leu	Arg	Pro	Lys	Thr	
				305					310					315	
Gly	Val	Arg	Gly	Leu	His	Lys	Ser	Leu	Thr	Asp	Val	Ala	Leu	Glu	
				320					325					330	
His	His	Glu	Glu	Cys	Asp	Cys	Val	Cys	Arg	Gly	Ser	Thr	Gly	Gly	
				335					340					345	

<210> 489

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 489

acttctcagt gtccataagg g 21

<210> 490

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 490

gaactaaaga gaaccgatac cattttctgg ccaggttgtc 40

<210> 491

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 491  
caccacagcg ttttaaccagg 20

<210> 492  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 492  
acaacaggca cagttcccac 20

<210> 493  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 493  
ggcgggaatcc aacctgagta g 21

<210> 494  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 494  
gcggctatcc tcctgtgctc 20

<210> 495  
<211> 3283  
<212> DNA  
<213> Homo sapiens

<400> 495  
cccattctcaa gctgatcttg gcacctctca tgctctgctc tcttcaacca 50  
gacctctaca ttccatcttg gaagaagact aaaaatgggtg tttccaatgt 100  
ggacactgaa gagacaaaatt cttatccttt ttaacataat cctaatttcc 150  
aaactccttg gggctagatg gtttcctaaa actctgccct gtgatgtcac 200  
tctggatgtt ccaaagaacc atgtgatcgt ggactgcaca gacaagcatt 250  
tgacagaaat tcctggaggt attcccacga acaccacgaa cctcaccctc 300  
accattaacc acataaccaga catctcccca gcgtcctttc acagactgga 350

ccatctggta gagatcgatt tcagatgcaa ctgtgtacct attccactgg 400  
 ggtcaaaaaa caacatgtgc atcaagaggc tgcagattaa acccagaagc 450  
 tttagtggac tcacttattt aaaatccctt tacctggatg gaaaccagct 500  
 actagagata ccgcagggcc tcccgcctag cttacagctt ctcagccttg 550  
 aggccaacaa catcttttcc atcagaaaaag agaattctaac agaactggcc 600  
 aacatagaaa tactctacct gggccaaaaac tggtattatc gaaatccttg 650  
 ttatgtttca tattcaatag agaaagatgc cttcctaaac ttgacaaagt 700  
 taaaagtgtc ctccctgaaa gataacaatg tcacagccgt ccctactgtt 750  
 ttgccatcta ctttaacaga actatatctc tacaacaaca tgattgcaaa 800  
 aatccaagaa gatgatttta ataacctcaa ccaattacaa attcttgacc 850  
 taagtggaaa ttgccctcgt tggtataatg ccccathttcc ttgtgcgccg 900  
 tgtaaaaata attctcccct acagatccct gtaaatgctt ttgatgcgct 950  
 gacagaatta aaagtthttac gtctacacag taactctctt cagcatgtgc 1000  
 cccaagatg gtttaagaac atcaacaaac tccaggaact ggatctgtcc 1050  
 caaaacttct tggccaaaga aattggggat gctaaatttc tgcattttct 1100  
 cccagcctc atccaattgg atctgtcttt caattttgaa cttcaggtct 1150  
 atcgtgcac tatgaatcta tcacaagcat tttcttcact gaaaagcctg 1200  
 aaaattctgc ggatcagagg atatgtcttt aaagagttga aaagctttaa 1250  
 cctctcgcca ttacataatc ttcaaaatct tgaagtctt gatcttggca 1300  
 ctaactttat aaaaattgct aacctcagca tgtttaaaca atttaaaaga 1350  
 ctgaaagtca tagatcttcc agtgaataaa atatcacctt caggagattc 1400  
 aagtgaagtt ggcttctgct caaatgccag aacttctgta gaaagttatg 1450  
 aaccccaggt cctggaacaa ttacattatt tcagatatga taagtatgca 1500  
 aggagttgca gattcaaaaa caaagaggct tctttcatgt ctgttaatga 1550  
 aagctgctac aagtatgggc agaccttga tctaagtaaa aatagtatat 1600  
 tttttgtcaa gtcctctgat tttcagcatc tttctttcct caaatgcctg 1650  
 aatctgtcag gaaatctcat tagccaaact cttaatggca gtgaattcca 1700  
 accttagca gagctgagat atttggactt ctccaacaac cggcttgatt 1750  
 tactccattc aacagcattt gaagagcttc acaaactgga agttctggat 1800

ataagcagta atagccatta ttttcaatca gaaggaatta ctcatatgct 1850  
 aaactttacc aagaacctaa aggttctgca gaaactgatg atgaacgaca 1900  
 atgacatctc ttctccacc agcaggacca tggagagtga gtctcttaga 1950  
 actctggaat tcagaggaaa tcaacttagat gttttatgga gagaagggtga 2000  
 taacagatac ttacaattat tcaagaatct gctaaaatta gaggaattag 2050  
 acatctctaa aaattcccta agtttcttgc cttctggagt ttttgatggt 2100  
 atgcctccaa atctaaagaa tctctctttg gccaaaaatg ggctcaaadc 2150  
 tttcagttgg aagaaactcc agtgtctaaa gaacctggaa actttggacc 2200  
 tcagccacaa ccaactgacc actgtccctg agagattatc caactgttcc 2250  
 agaagcctca agaattctgat tcttaagaat aatcaaatca ggagtctgac 2300  
 gaagtatttt ctacaagatg ccttccagtt gcgatatctg gatctcagct 2350  
 caaataaaat ccagatgatc caaaagacca gcttcccaga aaatgtcctc 2400  
 aacaatctga agatgttgct tttgcatcat aatcggtttc tgtgcacctg 2450  
 tgatgctgtg tggtttgtct ggtgggttaa ccatacggag gtgactattc 2500  
 cttacctggc cacagatgtg acttgtgtgg gcccaggagc acacaagggc 2550  
 caaagtgtga tctccctgga tctgtacacc tgtgagttag atctgactaa 2600  
 cctgattctg ttctcacttt ccatactctgt atctctcttt ctcatgggtga 2650  
 tgatgacagc aagtcacctc tattttctggg atgtgtggta tatttaccat 2700  
 ttctgtaagg ccaagataaa ggggtatcag cgtctaatat caccagactg 2750  
 ttgctatgat gcttttattg tgtatgacac taaagacca gctgtgaccg 2800  
 agtgggtttt ggctgagctg gtggccaaac tggaagaccc aagagagaaa 2850  
 cattttaatt tatgtctcga ggaaagggac tggttaccag ggcagccagt 2900  
 tctggaaaac ctttcccaga gcatacagct tagcaaaaag acagtgtttg 2950  
 tgatgacaga caagtatgca aagactgaaa attttaagat agcattttac 3000  
 ttgtcccatc agaggctcat ggatgaaaaa gttgatgtga ttatcttgat 3050  
 atttcttgag aagccctttc agaagtccaa gttcctccag ctccggaaaa 3100  
 ggctctgtgg gagttctgtc cttgagtggc caacaaacc gcaagctcac 3150  
 ccatacttct ggcagtgtct aaagaacgcc ctggccacag acaatcatgt 3200  
 ggcctatagt caggtgttca aggaaacggt ctagcccttc tttgcaaac 3250

acaactgcct agtttaccaa ggagaggcct ggc 3283

<210> 496

<211> 1049

<212> PRT

<213> Homo sapiens

<400> 496

Met	Val	Phe	Pro	Met	Trp	Thr	Leu	Lys	Arg	Gln	Ile	Leu	Ile	Leu
1				5					10					15

Phe	Asn	Ile	Ile	Leu	Ile	Ser	Lys	Leu	Leu	Gly	Ala	Arg	Trp	Phe
				20					25					30

Pro	Lys	Thr	Leu	Pro	Cys	Asp	Val	Thr	Leu	Asp	Val	Pro	Lys	Asn
				35					40					45

His	Val	Ile	Val	Asp	Cys	Thr	Asp	Lys	His	Leu	Thr	Glu	Ile	Pro
				50					55					60

Gly	Gly	Ile	Pro	Thr	Asn	Thr	Thr	Asn	Leu	Thr	Leu	Thr	Ile	Asn
				65					70					75

His	Ile	Pro	Asp	Ile	Ser	Pro	Ala	Ser	Phe	His	Arg	Leu	Asp	His
				80					85					90

Leu	Val	Glu	Ile	Asp	Phe	Arg	Cys	Asn	Cys	Val	Pro	Ile	Pro	Leu
				95					100					105

Gly	Ser	Lys	Asn	Asn	Met	Cys	Ile	Lys	Arg	Leu	Gln	Ile	Lys	Pro
				110					115					120

Arg	Ser	Phe	Ser	Gly	Leu	Thr	Tyr	Leu	Lys	Ser	Leu	Tyr	Leu	Asp
				125					130					135

Gly	Asn	Gln	Leu	Leu	Glu	Ile	Pro	Gln	Gly	Leu	Pro	Pro	Ser	Leu
				140					145					150

Gln	Leu	Leu	Ser	Leu	Glu	Ala	Asn	Asn	Ile	Phe	Ser	Ile	Arg	Lys
				155					160					165

Glu	Asn	Leu	Thr	Glu	Leu	Ala	Asn	Ile	Glu	Ile	Leu	Tyr	Leu	Gly
				170					175					180

Gln	Asn	Cys	Tyr	Tyr	Arg	Asn	Pro	Cys	Tyr	Val	Ser	Tyr	Ser	Ile
				185					190					195

Glu	Lys	Asp	Ala	Phe	Leu	Asn	Leu	Thr	Lys	Leu	Lys	Val	Leu	Ser
				200					205					210

Leu	Lys	Asp	Asn	Asn	Val	Thr	Ala	Val	Pro	Thr	Val	Leu	Pro	Ser
				215					220					225

Thr	Leu	Thr	Glu	Leu	Tyr	Leu	Tyr	Asn	Asn	Met	Ile	Ala	Lys	Ile
				230					235					240

Gln	Glu	Asp	Asp	Phe	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Ile	Leu	Asp
				245					250					255

Leu Ser Gly Asn Cys Pro Arg Cys Tyr Asn Ala Pro Phe Pro Cys	260	265	270
Ala Pro Cys Lys Asn Asn Ser Pro Leu Gln Ile Pro Val Asn Ala	275	280	285
Phe Asp Ala Leu Thr Glu Leu Lys Val Leu Arg Leu His Ser Asn	290	295	300
Ser Leu Gln His Val Pro Pro Arg Trp Phe Lys Asn Ile Asn Lys	305	310	315
Leu Gln Glu Leu Asp Leu Ser Gln Asn Phe Leu Ala Lys Glu Ile	320	325	330
Gly Asp Ala Lys Phe Leu His Phe Leu Pro Ser Leu Ile Gln Leu	335	340	345
Asp Leu Ser Phe Asn Phe Glu Leu Gln Val Tyr Arg Ala Ser Met	350	355	360
Asn Leu Ser Gln Ala Phe Ser Ser Leu Lys Ser Leu Lys Ile Leu	365	370	375
Arg Ile Arg Gly Tyr Val Phe Lys Glu Leu Lys Ser Phe Asn Leu	380	385	390
Ser Pro Leu His Asn Leu Gln Asn Leu Glu Val Leu Asp Leu Gly	395	400	405
Thr Asn Phe Ile Lys Ile Ala Asn Leu Ser Met Phe Lys Gln Phe	410	415	420
Lys Arg Leu Lys Val Ile Asp Leu Ser Val Asn Lys Ile Ser Pro	425	430	435
Ser Gly Asp Ser Ser Glu Val Gly Phe Cys Ser Asn Ala Arg Thr	440	445	450
Ser Val Glu Ser Tyr Glu Pro Gln Val Leu Glu Gln Leu His Tyr	455	460	465
Phe Arg Tyr Asp Lys Tyr Ala Arg Ser Cys Arg Phe Lys Asn Lys	470	475	480
Glu Ala Ser Phe Met Ser Val Asn Glu Ser Cys Tyr Lys Tyr Gly	485	490	495
Gln Thr Leu Asp Leu Ser Lys Asn Ser Ile Phe Phe Val Lys Ser	500	505	510
Ser Asp Phe Gln His Leu Ser Phe Leu Lys Cys Leu Asn Leu Ser	515	520	525
Gly Asn Leu Ile Ser Gln Thr Leu Asn Gly Ser Glu Phe Gln Pro	530	535	540
Leu Ala Glu Leu Arg Tyr Leu Asp Phe Ser Asn Asn Arg Leu Asp			

545	550	555
Leu Leu His Ser Thr Ala Phe Glu Glu	Leu His Lys Leu Glu Val	
560	565	570
Leu Asp Ile Ser Ser Asn Ser His Tyr	Phe Gln Ser Glu Gly Ile	
575	580	585
Thr His Met Leu Asn Phe Thr Lys Asn	Leu Lys Val Leu Gln Lys	
590	595	600
Leu Met Met Asn Asp Asn Asp Ile Ser	Ser Ser Thr Ser Arg Thr	
605	610	615
Met Glu Ser Glu Ser Leu Arg Thr Leu	Glu Phe Arg Gly Asn His	
620	625	630
Leu Asp Val Leu Trp Arg Glu Gly Asp	Asn Arg Tyr Leu Gln Leu	
635	640	645
Phe Lys Asn Leu Leu Lys Leu Glu Glu	Leu Asp Ile Ser Lys Asn	
650	655	660
Ser Leu Ser Phe Leu Pro Ser Gly Val	Phe Asp Gly Met Pro Pro	
665	670	675
Asn Leu Lys Asn Leu Ser Leu Ala Lys	Asn Gly Leu Lys Ser Phe	
680	685	690
Ser Trp Lys Lys Leu Gln Cys Leu Lys	Asn Leu Glu Thr Leu Asp	
695	700	705
Leu Ser His Asn Gln Leu Thr Thr Val	Pro Glu Arg Leu Ser Asn	
710	715	720
Cys Ser Arg Ser Leu Lys Asn Leu Ile	Leu Lys Asn Asn Gln Ile	
725	730	735
Arg Ser Leu Thr Lys Tyr Phe Leu Gln	Asp Ala Phe Gln Leu Arg	
740	745	750
Tyr Leu Asp Leu Ser Ser Asn Lys Ile	Gln Met Ile Gln Lys Thr	
755	760	765
Ser Phe Pro Glu Asn Val Leu Asn Asn	Leu Lys Met Leu Leu Leu	
770	775	780
His His Asn Arg Phe Leu Cys Thr Cys	Asp Ala Val Trp Phe Val	
785	790	795
Trp Trp Val Asn His Thr Glu Val Thr	Ile Pro Tyr Leu Ala Thr	
800	805	810
Asp Val Thr Cys Val Gly Pro Gly Ala	His Lys Gly Gln Ser Val	
815	820	825
Ile Ser Leu Asp Leu Tyr Thr Cys Glu	Leu Asp Leu Thr Asn Leu	
830	835	840



Ile Leu Phe Ser	Leu Ser Ile Ser Val	Ser Leu Phe Leu Met Val
845		855
Met Met Thr Ala	Ser His Leu Tyr Phe	Trp Asp Val Trp Tyr Ile
860		870
Tyr His Phe Cys	Lys Ala Lys Ile Lys	Gly Tyr Gln Arg Leu Ile
875		885
Ser Pro Asp Cys	Cys Tyr Asp Ala Phe	Ile Val Tyr Asp Thr Lys
890		900
Asp Pro Ala Val	Thr Glu Trp Val Leu	Ala Glu Leu Val Ala Lys
905		915
Leu Glu Asp Pro	Arg Glu Lys His Phe	Asn Leu Cys Leu Glu Glu
920		930
Arg Asp Trp Leu	Pro Gly Gln Pro Val	Leu Glu Asn Leu Ser Gln
935		945
Ser Ile Gln Leu	Ser Lys Lys Thr Val	Phe Val Met Thr Asp Lys
950		960
Tyr Ala Lys Thr	Glu Asn Phe Lys Ile	Ala Phe Tyr Leu Ser His
965		975
Gln Arg Leu Met	Asp Glu Lys Val Asp	Val Ile Ile Leu Ile Phe
980		990
Leu Glu Lys Pro	Phe Gln Lys Ser Lys	Phe Leu Gln Leu Arg Lys
995		1005
Arg Leu Cys Gly	Ser Ser Val Leu Glu Trp	Pro Thr Asn Pro Gln
1010		1020
Ala His Pro Tyr	Phe Trp Gln Cys Leu Lys	Asn Ala Leu Ala Thr
1025		1035
Asp Asn His Val	Ala Tyr Ser Gln Val	Phe Lys Glu Thr Val
1040		1045

<210> 497  
 <211> 4199  
 <212> DNA  
 <213> Homo sapiens

<400> 497  
 ggggtaccatt ctgcgctgct gcaagttacg gaatgaaaa ttagaacaac 50  
 agaaacatgg aaaacatggt ccttcagtcg tcaatgctga cctgcatttt 100  
 cctgctaata tctggttcct gtgagttatg cgccgaagaa aatttttcta 150  
 gaagctatcc ttgtgatgag aaaaagcaaa atgactcagt tattgcagag 200  
 tgcagcaatc gtcgactaca ggaagttccc caaacggtgg gcaaatatgt 250

gacagaacta gacctgtctg ataatttcat cacacacata acgaatgaat 300  
 catttcaagg gctgcaaaat ctactataaa taaatctaaa ccacaacccc 350  
 aatgtacagc accagaacgg aaatcccgg atacaatcaa atggcttgaa 400  
 tatcacagac ggggcattcc tcaacctaaa aaacctaagg gagttactgc 450  
 ttgaagacaa ccagttaccc caaataccct ctggtttgcc agagtctttg 500  
 acagaactta gtctaattca aaacaatata tacaacataa ctaaagaggg 550  
 catttcaaga cttataaact tgaaaaatct ctatttggcc tggaactgct 600  
 attttaacaa agtttgcgag aaaactaaca tagaagatgg agtatttgaa 650  
 acgctgacaa atttgaggtt gctatcacta tctttcaatt ctctttcaca 700  
 cgtgccaccc aaactgccaa gctccctacg caaacttttt ctgagcaaca 750  
 ccagatcaa atacattagt gaagaagatt tcaagggatt gataaattta 800  
 acattactag atttaagcgg gaactgtccg aggtgcttca atgccccatt 850  
 tccatgcgtg ccttgtgatg gtggtgcttc aattaatata gatcgttttg 900  
 cttttcaaaa cttgacccaa cttcgatacc taaacctctc tagcacttcc 950  
 ctcaggaaga ttaatgctgc ctggtttaaa aatatgcctc atctgaaggt 1000  
 gctggatctt gaattcaact atttagtggg agaaatagtc tctggggcat 1050  
 ttttaacgat gctgccccgc ttagaaatac ttgacttgtc ttttaactat 1100  
 ataaagggga gttatccaca gcatattaat atttccagaa acttctctaa 1150  
 acttttgtct ctacgggcat tgcatttaag aggttatgtg ttccaggaac 1200  
 tcagagaaga tgatttccag cccctgatgc agcttccaaa cttatcgact 1250  
 atcaacttgg gtattaattt tattaagcaa atcgatttca aacttttcca 1300  
 aaatttctcc aatctggaaa ttatttactt gtcagaaaac agaatatcac 1350  
 cgttggtaaa agatacccg cagagttatg caaatagttc ctcttttcaa 1400  
 cgtcatatcc ggaaacgacg ctcaacagat tttgagtttg acccacattc 1450  
 gaacttttat catttcaccc gtcotttaat aaagccacaa tgtgctgctt 1500  
 atggaaaagc cttagattta agcctcaaca gtattttctt cattgggcca 1550  
 aaccaatttg aaaatcttcc tgacattgcc tgtttaaatc tgtctgcaaa 1600  
 tagcaatgct caagtgttaa gtggaactga attttcagcc attcctcatg 1650  
 tcaaatatth ggatttgaca aacaatagac tagactttga taatgctagt 1700

gctcttactg aattgtccga cttggaagtt ctagatctca gctataattc 1750  
acactatttc agaatagcag gcgtaacaca tcattctagaa tttattcaaa 1800  
atttcacaaa tctaaaagtt ttaaacttga gccacaacaa catttatact 1850  
ttaacagata agtataacct ggaaagcaag tccctggtag aattagtttt 1900  
cagtggcaat cgccttgaca ttttgtggaa tgatgatgac aacaggtata 1950  
tctccatttt caaaggtctc aagaatctga cacgtctgga tttatccctt 2000  
aataggctga agcacatccc aaatgaagca ttccttaatt tgccagcgag 2050  
tctcactgaa ctacatataa atgataatat gttaaagttt tttaactgga 2100  
cattactcca gcagtttctt cgtctcgagt tgcttgactt acgtggaaac 2150  
aaactactct ttttaactga tagcctatct gactttacat cttcccttcg 2200  
gacactgctg ctgagtcata acaggatttc ccacctaccc tctggctttc 2250  
tttctgaagt cagtagtctg aagcacctcg atttaagttc caatctgcta 2300  
aaaacaatca acaaatccgc acttgaaact aagaccacca ccaaattatc 2350  
tatgttgga ctacacggaa acccctttga atgcacctgt gacattggag 2400  
atttccgaag atggatggat gaacatctga atgtcaaaat tcccagactg 2450  
gtagatgtca tttgtgccag tcctggggat caaagaggga agagtattgt 2500  
gagtctggag ctaacaactt gtgtttcaga tgtcactgca gtgatattat 2550  
ttttcttcac gttctttatc accaccatgg ttatgttggc tgccctggct 2600  
caccatttgt tttactggga tgtttggttt atatataatg tgtgttttagc 2650  
taaggtaaaa ggctacaggt ctctttccac atcccaaact ttctatgatg 2700  
cttacatttc ttatgacacc aaagatgcct ctgttactga ctgggtgata 2750  
aatgagctgc gctaccacct tgaagagagc cgagacaaaa acgtttctct 2800  
ttgtctagag gagagggatt gggacccggg attggccatc atcgacaacc 2850  
tcattgcagag catcaaccaa agcaagaaaa cagtatttgt tttaaccaa 2900  
aaatatgcaa aaagctggaa ctttaaaaca gctttttact tggctttgca 2950  
gaggctaatt gatgagaaca tggatgtgat tatatttata ctgctggagc 3000  
cagtgttaca gcattctcag tatttgaggc tacggcagcg gatctgtaag 3050  
agctccatcc tccagtggcc tgacaacccg aaggcagaag gcttgttttg 3100  
gcaaactctg agaaatgtgg tcttgactga aaatgattca cggataaaca 3150

atatgtatgt cgattccatt aagcaatact aactgacggt aagtcattgat 3200  
 ttgcgcgcat aataaagatg caaaggaatg acattttctgt attagttatc 3250  
 tattgctatg taacaaatta tcccaaaact tagtggttta aaacaacaca 3300  
 tttgctggcc cacagttttt gagggtcagg agtccaggcc cagcataact 3350  
 gggtcctctg ctgagggtgt ctgagggt gcaatgtagg tggtcaccag 3400  
 agacataggc atcactgggg tcacactcat gtggttggtt tctggattca 3450  
 attcctcctg ggctattggc caaaggctat actcatgtaa gccatgcgag 3500  
 cctctccac aaggcagctt gcttcattcag agctagcaaa aaagagaggt 3550  
 tgctagcaag atgaagtcac aatcttttgt aatcgaatca aaaaagtgat 3600  
 atctcatcac ttgggccata ttctatttgt tagaagtaaa ccacagggtcc 3650  
 caccagctcc atgggagtgga ccacctcagt ccagggaataa cagctgaaga 3700  
 ccaagatggg gagctctgat tgcttcagtt ggtcatcaac tattttccct 3750  
 tgactgctgt cctgggatgg cctgctatct tgatgataga ttgtgaatat 3800  
 caggaggcag ggatcactgt ggaccatctt agcagttgac ctaacacatc 3850  
 ttcttttcaa tatctaagaa cttttgccac tgtgactaat ggtcctaata 3900  
 ttaagctggt gtttatattt atcatatatac tatggctaca tggttatatt 3950  
 atgctgtggt tgcgttcggt tttatttaca gttgctttta caaatatttg 4000  
 ctgtaacatt tgacttctaa gggttagatg ccatttaaga actgagatgg 4050  
 atagctttta aagcatcttt tacttcttac ctttttttaa aagtatgcag 4100  
 ctaaattcga agcttttggt ctatattggt aattgccatt gctgtaaatc 4150  
 ttaaatgaa tgaataaaaa tgtttcattt tacaaaaaaa aaaaaaaaaa 4199

<210> 498  
 <211> 1041  
 <212> PRT  
 <213> Homo sapiens

<400> 498  
 Met Glu Asn Met Phe Leu Gln Ser Ser Met Leu Thr Cys Ile Phe  
 1 5 10 15  
 Leu Leu Ile Ser Gly Ser Cys Glu Leu Cys Ala Glu Glu Asn Phe  
 20 25 30  
 Ser Arg Ser Tyr Pro Cys Asp Glu Lys Lys Gln Asn Asp Ser Val  
 35 40 45  
 Ile Ala Glu Cys Ser Asn Arg Arg Leu Gln Glu Val Pro Gln Thr

Val Gly Lys Tyr	Val Thr Glu Leu Asp	Leu Ser Asp Asn Phe	Ile
65	70		75
Thr His Ile Thr	Asn Glu Ser Phe Gln	Gly Leu Gln Asn Leu	Thr
80	85		90
Lys Ile Asn Leu	Asn His Asn Pro Asn	Val Gln His Gln Asn	Gly
95	100		105
Asn Pro Gly Ile	Gln Ser Asn Gly Leu	Asn Ile Thr Asp Gly	Ala
110	115		120
Phe Leu Asn Leu	Lys Asn Leu Arg Glu	Leu Leu Leu Glu Asp	Asn
125	130		135
Gln Leu Pro Gln	Ile Pro Ser Gly Leu	Pro Glu Ser Leu Thr	Glu
140	145		150
Leu Ser Leu Ile	Gln Asn Asn Ile Tyr	Asn Ile Thr Lys Glu	Gly
155	160		165
Ile Ser Arg Leu	Ile Asn Leu Lys Asn	Leu Tyr Leu Ala Trp	Asn
170	175		180
Cys Tyr Phe Asn	Lys Val Cys Glu Lys	Thr Asn Ile Glu Asp	Gly
185	190		195
Val Phe Glu Thr	Leu Thr Asn Leu Glu	Leu Leu Ser Leu Ser	Phe
200	205		210
Asn Ser Leu Ser	His Val Pro Pro Lys	Leu Pro Ser Ser Leu	Arg
215	220		225
Lys Leu Phe Leu	Ser Asn Thr Gln Ile	Lys Tyr Ile Ser Glu	Glu
230	235		240
Asp Phe Lys Gly	Leu Ile Asn Leu Thr	Leu Leu Asp Leu Ser	Gly
245	250		255
Asn Cys Pro Arg	Cys Phe Asn Ala Pro	Phe Pro Cys Val Pro	Cys
260	265		270
Asp Gly Gly Ala	Ser Ile Asn Ile Asp	Arg Phe Ala Phe Gln	Asn
275	280		285
Leu Thr Gln Leu	Arg Tyr Leu Asn Leu	Ser Ser Thr Ser Leu	Arg
290	295		300
Lys Ile Asn Ala	Ala Trp Phe Lys Asn	Met Pro His Leu Lys	Val
305	310		315
Leu Asp Leu Glu	Phe Asn Tyr Leu Val	Gly Glu Ile Val Ser	Gly
320	325		330
Ala Phe Leu Thr	Met Leu Pro Arg Leu	Glu Ile Leu Asp Leu	Ser
335	340		345

05978192-101501

Phe Asn Tyr Ile	Lys Gly Ser Tyr Pro	Gln His Ile Asn Ile	Ser
350	355	360	
Arg Asn Phe Ser	Lys Leu Leu Ser Leu	Arg Ala Leu His Leu	Arg
365	370	375	
Gly Tyr Val Phe	Gln Glu Leu Arg Glu	Asp Asp Phe Gln Pro	Leu
380	385	390	
Met Gln Leu Pro	Asn Leu Ser Thr Ile	Asn Leu Gly Ile Asn	Phe
395	400	405	
Ile Lys Gln Ile	Asp Phe Lys Leu Phe	Gln Asn Phe Ser Asn	Leu
410	415	420	
Glu Ile Ile Tyr	Leu Ser Glu Asn Arg	Ile Ser Pro Leu Val	Lys
425	430	435	
Asp Thr Arg Gln	Ser Tyr Ala Asn Ser	Ser Ser Phe Gln Arg	His
440	445	450	
Ile Arg Lys Arg	Arg Ser Thr Asp Phe	Glu Phe Asp Pro His	Ser
455	460	465	
Asn Phe Tyr His	Phe Thr Arg Pro Leu	Ile Lys Pro Gln Cys	Ala
470	475	480	
Ala Tyr Gly Lys	Ala Leu Asp Leu Ser	Leu Asn Ser Ile Phe	Phe
485	490	495	
Ile Gly Pro Asn	Gln Phe Glu Asn Leu	Pro Asp Ile Ala Cys	Leu
500	505	510	
Asn Leu Ser Ala	Asn Ser Asn Ala Gln	Val Leu Ser Gly Thr	Glu
515	520	525	
Phe Ser Ala Ile	Pro His Val Lys Tyr	Leu Asp Leu Thr Asn	Asn
530	535	540	
Arg Leu Asp Phe	Asp Asn Ala Ser Ala	Leu Thr Glu Leu Ser	Asp
545	550	555	
Leu Glu Val Leu	Asp Leu Ser Tyr Asn	Ser His Tyr Phe Arg	Ile
560	565	570	
Ala Gly Val Thr	His His Leu Glu Phe	Ile Gln Asn Phe Thr	Asn
575	580	585	
Leu Lys Val Leu	Asn Leu Ser His Asn	Asn Ile Tyr Thr Leu	Thr
590	595	600	
Asp Lys Tyr Asn	Leu Glu Ser Lys Ser	Leu Val Glu Leu Val	Phe
605	610	615	
Ser Gly Asn Arg	Leu Asp Ile Leu Trp	Asn Asp Asp Asp Asn	Arg
620	625	630	
Tyr Ile Ser Ile	Phe Lys Gly Leu Lys	Asn Leu Thr Arg Leu	Asp

	635		640		645
Leu Ser Leu Asn Arg	Leu Lys His Ile	Pro Asn Glu Ala Phe	Leu		
	650		655		660
Asn Leu Pro Ala Ser	Leu Thr Glu Leu	His Ile Asn Asp Asn	Met		
	665		670		675
Leu Lys Phe Phe Asn	Trp Thr Leu Leu	Gln Gln Phe Pro Arg	Leu		
	680		685		690
Glu Leu Leu Asp Leu	Arg Gly Asn Lys	Leu Leu Phe Leu Thr	Asp		
	695		700		705
Ser Leu Ser Asp Phe	Thr Ser Ser Leu	Arg Thr Leu Leu Leu	Ser		
	710		715		720
His Asn Arg Ile Ser	His Leu Pro Ser	Gly Phe Leu Ser Glu	Val		
	725		730		735
Ser Ser Leu Lys His	Leu Asp Leu Ser	Ser Asn Leu Leu Lys	Thr		
	740		745		750
Ile Asn Lys Ser Ala	Leu Glu Thr Lys	Thr Thr Thr Lys Leu	Ser		
	755		760		765
Met Leu Glu Leu His	Gly Asn Pro Phe	Glu Cys Thr Cys Asp	Ile		
	770		775		780
Gly Asp Phe Arg Arg	Trp Met Asp Glu	His Leu Asn Val Lys	Ile		
	785		790		795
Pro Arg Leu Val Asp	Val Ile Cys Ala	Ser Pro Gly Asp Gln	Arg		
	800		805		810
Gly Lys Ser Ile Val	Ser Leu Glu Leu	Thr Thr Cys Val Ser	Asp		
	815		820		825
Val Thr Ala Val Ile	Leu Phe Phe Phe	Thr Phe Phe Ile Thr	Thr		
	830		835		840
Met Val Met Leu Ala	Ala Leu Ala His	His Leu Phe Tyr Trp	Asp		
	845		850		855
Val Trp Phe Ile Tyr	Asn Val Cys Leu	Ala Lys Val Lys Gly	Tyr		
	860		865		870
Arg Ser Leu Ser Thr	Ser Gln Thr Phe	Tyr Asp Ala Tyr Ile	Ser		
	875		880		885
Tyr Asp Thr Lys Asp	Ala Ser Val Thr	Asp Trp Val Ile Asn	Glu		
	890		895		900
Leu Arg Tyr His Leu	Glu Glu Ser Arg	Asp Lys Asn Val Leu	Leu		
	905		910		915
Cys Leu Glu Glu Arg	Asp Trp Asp Pro	Gly Leu Ala Ile Ile	Asp		
	920		925		930

Asn	Leu	Met	Gln	Ser	Ile	Asn	Gln	Ser	Lys	Lys	Thr	Val	Phe	Val
				935						940				945
Leu	Thr	Lys	Lys	Tyr	Ala	Lys	Ser	Trp	Asn	Phe	Lys	Thr	Ala	Phe
				950						955				960
Tyr	Leu	Ala	Leu	Gln	Arg	Leu	Met	Asp	Glu	Asn	Met	Asp	Val	Ile
				965						970				975
Ile	Phe	Ile	Leu	Leu	Glu	Pro	Val	Leu	Gln	His	Ser	Gln	Tyr	Leu
				980						985				990
Arg	Leu	Arg	Gln	Arg	Ile	Cys	Lys	Ser	Ser	Ile	Leu	Gln	Trp	Pro
				995						1000				1005
Asp	Asn	Pro	Lys	Ala	Glu	Gly	Leu	Phe	Trp	Gln	Thr	Leu	Arg	Asn
				1010						1015				1020
Val	Val	Leu	Thr	Glu	Asn	Asp	Ser	Arg	Tyr	Asn	Asn	Met	Tyr	Val
				1025						1030				1035
Asp	Ser	Ile	Lys	Gln	Tyr									
				1040										

<210> 499  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 499  
 taaagaccca gctgtgaccg 20

<210> 500  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 500  
 atccatgagc ctctgatggg 20

<210> 501  
 <211> 45  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 501  
 atttatgtct cgaggaaagg gactgggttac cagggcagcc agttc 45

<210> 502



<211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 502  
 gccgagacaa aaacgttctc c 21

<210> 503  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 503  
 catccatggt ctcattccatt agcc 24

<210> 504  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 504  
 tcgacaacct catgcagagc atcaacaaaa gcaagaaaac agtatt 46

<210> 505  
 <211> 1738  
 <212> DNA  
 <213> Homo sapiens

<400> 505  
 ccaggtccaa ctgcacctcg gttctatcga ttgaattccc cggggatcct 50  
 ctagagatcc ctcgacctcg acccagcgt cgcgaagct ggccctgcac 100  
 ggctgcaagg gaggtcctg tggacaggcc aggcaggtgg gcctcaggag 150  
 gtgcctccag gcggccagt ggctgaggg cccagcaagg gctaggggtcc 200  
 atctccagtc ccaggacaca gcagcggcca ccatggccac gcctggggtc 250  
 cagcagcatc agcagcccc aggaccggg aggcacaggt ggccccacc 300  
 acccgaggga gcagctcctg cccctgtccg ggggatgact gattctctc 350  
 cgccaggcca cccagaggag aaggccacc cgcctggagg cacaggccat 400  
 gaggggctct caggaggtgc tgctgatgtg gcttctggtg ttggcagtg 450  
 gcggcacaga gcagcctac cggcccggcc gtaggggtgtg tgctgtccg 500

gctcacgggg accctgtctc cgagtcgttc gtgcagcgtg tgtaccagcc 550  
cttcctcacc acctgcgacg ggcaccgggc ctgcagcacc taccgaacca 600  
tctataggac cgcctaccgc cgcagccctg ggctggcccc tgccaggcct 650  
cgctacgcgt gctgccccgg ctggaagagg accagcgggc ttcctggggc 700  
ctgtggagca gcaatatgcc agccgccatg ccggaacgga gggagctgtg 750  
tccagcctgg ccgctgccgc tgccctgcag gatggcgggg tgacacttgc 800  
cagtcagatg tggatgaatg cagtgcctagg aggggcggct gtccccagcg 850  
ctgcatcaac accgccggca gttactggtg ccagtgttgg gaggggcaca 900  
gcctgtctgc agacggtaca ctctgtgtgc ccaagggagg gccccccagg 950  
gtggccccca acccgacagg agtggacagt gcaatgaagg aagaagtgca 1000  
gaggctgcag tccagggtgg acctgctgga ggagaagctg cagctggtgc 1050  
tgggccccact gcacagcctg gcctcgcagg cactggagca tgggctcccg 1100  
gaccccgga gcctcctggt gcaactcctc cagcagctcg gccgcatcga 1150  
ctccctgagc gagcagattt ccttcctgga ggagcagctg gggctcctgct 1200  
cctgcaagaa agactcgtga ctgccagcg cccagggctg gactgagccc 1250  
ctcacgccgc cctgcagccc ccatgcccct gcccaacatg ctgggggtcc 1300  
agaagccacc tcggggtgac tgagcggaag gccaggcagg gccttcctcc 1350  
tcttcctcct ccccttcctc gggaggctcc ccagaccctg gcatgggatg 1400  
ggctgggata ttctctgtga atccaccct ggctaccccc acctggcta 1450  
ccccaacggc atcccaaggc cagggtgggcc ctcagctgag ggaagggtacg 1500  
agctccctgc tggagcctgg gacccatggc acaggccagg cagcccgag 1550  
gctgggtggg gcctcagtgg gggctgctgc ctgaccccca gcacaataaa 1600  
aatgaaacgt gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgcatg 1700  
gccaacttg tttattgcag cttataatgg ttacaaat 1738

<210> 506

<211> 273

<212> PRT

<213> Homo sapiens

<400> 506

Met	Arg	Gly	Ser	Gln	Glu	Val	Leu	Leu	Met	Trp	Leu	Leu	Val	Leu
1					5				10					15

Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val	20	25	30
Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val	35	40	45
Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg	50	55	60
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg	65	70	75
Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro	80	85	90
Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala	95	100	105
Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro	110	115	120
Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln	125	130	135
Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln	140	145	150
Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu	155	160	165
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly	170	175	180
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala	185	190	195
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu	200	205	210
Glu Glu Lys Leu Gln Leu Val Leu Ala Pro Leu His Ser Leu Ala	215	220	225
Ser Gln Ala Leu Glu His Gly Leu Pro Asp Pro Gly Ser Leu Leu	230	235	240
Val His Ser Phe Gln Gln Leu Gly Arg Ile Asp Ser Leu Ser Glu	245	250	255
Gln Ile Ser Phe Leu Glu Glu Gln Leu Gly Ser Cys Ser Cys Lys	260	265	270

Lys Asp Ser

<210> 507  
 <211> 1700  
 <212> DNA  
 <213> Homo sapiens

<400> 507

gccaggcagg tgggcctcag gaggtgcctc caggcggcca gtgggcctga 50  
ggccccagca agggctaggg tccatctcca gtcccaggac acagcagcgg 100  
ccaccatggc cagcctggg ctccagcagc atcagagcag cccctgtggt 150  
tggcagcaaa gttcagcttg gctgggcccg ctgtgagggg cttcgcgcta 200  
cgccctgcgg tgtcccagg gctgaggtct cctcatcttc tccctagcag 250  
tggatgagca acccaacggg ggcccgggga ggggaactgg ccccgaggga 300  
gaggaacccc aaagccacat ctgtagccag gatgagcagt gtgaatccag 350  
gcagccccca ggaccgggga ggcacagggtg gccccacca cccggaggag 400  
cagctcctgc cctgtccgg gggatgactg attctcctcc gccaggccac 450  
ccagaggaga agggcacccc gcctggaggc acaggccatg aggggctctc 500  
aggaggtgct gctgatgtgg cttctggtgt tggcagtggg cggcacagag 550  
cacgcctacc ggcccggccg tagggtgtgt gctgtccggg ctcacgggga 600  
ccctgtctcc gagtcgttcg tgcagcgtgt gtaccagccc ttcctcacca 650  
cctgcgacgg gcaccgggcc tgcagcacct accgaaccat ctataggacc 700  
gcctaccgcc gcagccctgg gctggcccct gccaggcctc gctacgcgtg 750  
ctgccccggc tggaagagga ccagcgggct tcctggggcc tgtggagcag 800  
caatatgcca gccgccatgc cggaacggag ggagctgtgt ccagcctggc 850  
cgctgccgct gccctgcagg atggcggggg gacacttgcc agtcagatgt 900  
ggatgaatgc agtgctagga ggggcggctg tcccagcgc tgcataaca 950  
ccgccggcag ttactggtgc cagtgttggg aggggcacag cctgtctgca 1000  
gacggtacac tctgtgtgcc caaggagggg cccccaggg tggcccccaa 1050  
cccagacagga gtggacagtg caatgaagga agaagtgcag aggctgcagt 1100  
ccagggtgga cctgctggag gagaagctgc agctggtgct ggccccactg 1150  
cacagcctgg cctcgcaggc actggagcat gggctcccgg accccggcag 1200  
cctcctggtg cactccttcc agcagctcgg ccgcatcgac tccctgagcg 1250  
agcagatttc cttcctggag gagcagctgg ggtcctgctc ctgcaagaaa 1300  
gactcgtgac tgcccagcgc tccaggctgg actgagcccc tcacgccgcc 1350  
ctgcagcccc catgccctg cccaacatgc tgggggtcca gaagccacct 1400  
cggggtgact gagcggaagg ccaggcaggg ccttcctcct cttcctcctc 1450

cccttcctcg ggaggctccc cagaccctgg catgggatgg gctgggatct 1500  
tctctgtgaa tccacccctg gctaccccca ccttggctac cccaacggca 1550  
tccaaggcc aggtggaccc tcagctgagg gaaggtacga gctccctgct 1600  
ggagcctggg acccatggca caggccaggc agcccgagg ctgggtgggg 1650  
cctcagtggg ggctgctgcc tgacccccag cacaataaaa atgaaacgtg 1700

<210> 508  
<211> 273  
<212> PRT  
<213> Homo sapiens

<400> 508  
Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu  
1 5 10 15  
Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
20 25 30  
Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
35 40 45  
Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
50 55 60  
Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
65 70 75  
Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
80 85 90  
Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
95 100 105  
Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
110 115 120  
Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
125 130 135  
Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln  
140 145 150  
Arg Cys Ile Asn Thr Ala Gly Ser Tyr Trp Cys Gln Cys Trp Glu  
155 160 165  
Gly His Ser Leu Ser Ala Asp Gly Thr Leu Cys Val Pro Lys Gly  
170 175 180  
Gly Pro Pro Arg Val Ala Pro Asn Pro Thr Gly Val Asp Ser Ala  
185 190 195  
Met Lys Glu Glu Val Gln Arg Leu Gln Ser Arg Val Asp Leu Leu  
200 205 210

0997819E-101501

Glu	Glu	Lys	Leu	Gln	Leu	Val	Leu	Ala	Pro	Leu	His	Ser	Leu	Ala
				215					220					225
Ser	Gln	Ala	Leu	Glu	His	Gly	Leu	Pro	Asp	Pro	Gly	Ser	Leu	Leu
				230					235					240
Val	His	Ser	Phe	Gln	Gln	Leu	Gly	Arg	Ile	Asp	Ser	Leu	Ser	Glu
				245					250					255
Gln	Ile	Ser	Phe	Leu	Glu	Glu	Gln	Leu	Gly	Ser	Cys	Ser	Cys	Lys
				260					265					270

Lys Asp Ser

<210> 509  
 <211> 1538  
 <212> DNA  
 <213> Homo sapiens

<400> 509  
 cccacgcgtc cgaagctggc cctgcacggc tgcaagggag gctcctgtgg 50  
 acaggccagg caggtgggcc tcaggaggtg cctccaggcg gccagtgggc 100  
 ctgaggcccc agcaagggct agggctccatc tccagtccca ggacacagca 150  
 gcggccacca tggccaogcc tgggctccag cagcatcagc agccccagg 200  
 accggggagg cacaggtggc cccaccacc cggaggagca gctcctgcc 250  
 ctgtccgggg gatgactgat tctcctccgc caggccaacc agaggagaag 300  
 gccaccccg ctaggagcac aggccatgag gggctctcag gaggtgctgc 350  
 tgatgtggct tctggtgttg gcagtgggcg gcacagagca cgcctaccgg 400  
 cccggccgta ggggtgtgtg tgtccgggct cacggggacc ctgtctccga 450  
 gtcgttcgtg cagcgtgtgt accagccctt cctcaccacc tgcgacgggc 500  
 accgggcctg cagcacctac cgaaccatct ataggaccgc ctaccgccgc 550  
 agccctgggc tggcccctgc caggcctcgc tacgcgtgct gcccgggctg 600  
 gaagaggacc agcgggcttc ctggggcctg tggagcagca atatgccagc 650  
 cgccatgccg gaacggaggg agctgtgtcc agcctggccg ctgccgctgc 700  
 cctgcaggat ggcggggtga cacttgccag tcagatgtgg atgaatgcag 750  
 tgctaggagg ggcggctgtc cccagcgtg cgtcaacacc gccggcagtt 800  
 actggtgcca gtgttgggag gggcacagcc tgtctgcaga cggtacactc 850  
 tgtgtgcccc agggagggcc cccagggtg gcccacaacc cgacaggagt 900  
 ggacagtgca atgaaggaag aagtgcagag gctgcagtcc agggtgagacc 950

tgctggagga gaagctgcag ctggtgctgg cccactgca cagcctggcc 1000  
 tcgcaggcac tggagcatgg gctcccggac cccggcagcc tcttggtgca 1050  
 ctccttccag cagctcggcc gcatcgactc cctgagcgag cagatttcct 1100  
 tcttgaggga gcagctgggg tcttgctcct gcaagaaaga ctctgactg 1150  
 cccagcgccc caggctggac tgagcccctc acgcccgcct gcagccccca 1200  
 tgcccctgcc caacatgctg ggggtccaga agccacctcg gggtgactga 1250  
 gcggaaggcc aggcagggcc ttctctctct tctctctccc cttctctggg 1300  
 aggctcccca gaccctggca tgggatgggc tgggatcttc tctgtgaatc 1350  
 caccctggc tacccccacc ctggctaccc caacggcatc ccaaggccag 1400  
 gtggggccctc agctgaggga aggtacgagc tccctgctgg agcctgggac 1450  
 ccatggcaca ggccaggcag cccggaggct ggggtggggc tcagtggggg 1500  
 ctgctgcctg acccccagca caataaaaat gaaacgtg 1538

<210> 510  
 <211> 273  
 <212> PRT  
 <213> Homo sapiens

<400> 510  
 Met Arg Gly Ser Gln Glu Val Leu Leu Met Trp Leu Leu Val Leu  
 1 5 10 15  
 Ala Val Gly Gly Thr Glu His Ala Tyr Arg Pro Gly Arg Arg Val  
 20 25 30  
 Cys Ala Val Arg Ala His Gly Asp Pro Val Ser Glu Ser Phe Val  
 35 40 45  
 Gln Arg Val Tyr Gln Pro Phe Leu Thr Thr Cys Asp Gly His Arg  
 50 55 60  
 Ala Cys Ser Thr Tyr Arg Thr Ile Tyr Arg Thr Ala Tyr Arg Arg  
 65 70 75  
 Ser Pro Gly Leu Ala Pro Ala Arg Pro Arg Tyr Ala Cys Cys Pro  
 80 85 90  
 Gly Trp Lys Arg Thr Ser Gly Leu Pro Gly Ala Cys Gly Ala Ala  
 95 100 105  
 Ile Cys Gln Pro Pro Cys Arg Asn Gly Gly Ser Cys Val Gln Pro  
 110 115 120  
 Gly Arg Cys Arg Cys Pro Ala Gly Trp Arg Gly Asp Thr Cys Gln  
 125 130 135  
 Ser Asp Val Asp Glu Cys Ser Ala Arg Arg Gly Gly Cys Pro Gln

	140		145		150
Arg Cys Val Asn	Thr Ala Gly Ser Tyr	Trp Cys Gln Cys Trp	Glu		
	155		160		165
Gly His Ser Leu	Ser Ala Asp Gly Thr	Leu Cys Val Pro Lys	Gly		
	170		175		180
Gly Pro Pro Arg	Val Ala Pro Asn Pro	Thr Gly Val Asp Ser	Ala		
	185		190		195
Met Lys Glu Glu	Val Gln Arg Leu Gln	Ser Arg Val Asp Leu	Leu		
	200		205		210
Glu Glu Lys Leu	Gln Leu Val Leu Ala	Pro Leu His Ser Leu	Ala		
	215		220		225
Ser Gln Ala Leu	Glu His Gly Leu Pro	Asp Pro Gly Ser Leu	Leu		
	230		235		240
Val His Ser Phe	Gln Gln Leu Gly Arg	Ile Asp Ser Leu Ser	Glu		
	245		250		255
Gln Ile Ser Phe	Leu Glu Glu Gln Leu	Gly Ser Cys Ser Cys	Lys		
	260		265		270

Lys Asp Ser

<210> 511  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 511  
 tggagcagca atatgccagc c 21

<210> 512  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 512  
 ttttcactc ctgtcgggtt gg 22

<210> 513  
 <211> 46  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe



<400> 513  
ggtgacactt gccagtcaga tgtggatgaa tgcagtgcta ggaggg 46

<210> 514  
<211> 2690  
<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> 2039-2065  
<223> unknown base

<400> 514  
ggttgccaca gctggtttag ggccccgacc actggggccc cttgtcagga 50  
ggagacagcc tcccggcccc gggaggacaa gtcgctgcca cctttggctg 100  
ccgacgtgat tccctgggac ggtccgtttc ctgccgtcag ctgccggccg 150  
agttgggtct ccgtgtttca ggccggctcc cccttctctg tctcccttct 200  
cccgtgggc cggtttatcg ggaggagatt gtcttccagg gctagcaatt 250  
ggacttttga tgatgtttga ccagcggca ggaatagcag gcaacgtgat 300  
ttcaaagctg ggctcagcct ctgtttcttc tctcgtgtaa tcgcaaaacc 350  
cattttggag caggaattcc aatcatgtct gtgatggtgg tgagaaagaa 400  
ggtgacacgg aaatgggaga aactcccagg caggaacacc ttttgctgtg 450  
atggccgcgt catgatggcc cggcaaaagg gcattttcta cctgaccctt 500  
ttcctcatcc tggggacatg tacactcttc ttgcctttg agtgccgcta 550  
cctggctgtt cagctgtctc ctgccatccc tgtatttget gccatgctct 600  
tccttttctc catggctaca ctgttgagga ccagcttcag tgaccctgga 650  
gtgattcctc gggcgctacc agatgaagca gctttcatag aaatggagat 700  
agaagctacc aatggtgcgg tgccccaggg ccagcgacca ccgcctcgta 750  
tcaagaattt ccagataaac aaccagattg tgaaactgaa atactgttac 800  
acatgcaaga tcttccggcc tcccggggcc tccattgca gcattctgtga 850  
caactgtgtg gagcgcttcg accatcactg cccctgggtg gggaattgtg 900  
ttggaaagag gaactaccgc tacttctacc tcttcatcct ttctctctcc 950  
ctcctcacia tctatgtctt cgccttcaac atcgtctatg tggccctcaa 1000  
atctttgaaa attggcttct tggagacatt gaaagaaact cctggaactg 1050  
ttctagaagt cctcatttgc ttctttacac tctggtccgt cgtgggactg 1100

09978192.101501

actggatttc atacttttct cgtggctctc aaccagacaa ccaatgaaga 1150  
catcaaagga tcatggacag ggaagaatcg cgtccagaat ccctacagcc 1200  
atggcaatat tgtgaagaac tgctgtgaag tgctgtgtgg ccccttgccc 1250  
cccagtgtgc tggatcgaag gggatatttg cactggagg aaagtggaag 1300  
tcgacctccc agtactcaag agaccagtag cagcctcttg ccacagagcc 1350  
cagccccac agaacacctg aactcaaag agatgccgga ggacagcagc 1400  
actcccgaag agatgccacc tccagagccc ccagagccac cacaggaggc 1450  
agctgaagct gagaagtagc ctatctatgg aagagacttt tgtttgtgtt 1500  
taattagggc tatgagagat ttcaggtag aagttaaacc tgagacagag 1550  
agcaagtaag ctgtcccttt taactgtttt tcttttgtct ttagtcaccc 1600  
agttgcacac tggcattttc ttgctgcaag cttttttaaa tttctgaact 1650  
caaggcagtg gcagaagatg tcagtcacct ctgataactg gaaaaatggg 1700  
tctcttgggc cctggcactg gttctccatg gcctcagcca cagggctccc 1750  
ttggaccccc tctcttccct ccagatccca gccctcctgc ttgggggtcac 1800  
tggtctcatt ctggggctaa aagtttttga gactggctca aatcctccca 1850  
agctgctgca cgtgctgagt ccagaggcag tcacagagac ctctggccag 1900  
gggatcctaa ctgggttctt ggggtcttca ggactgaaga ggaggagag 1950  
tggggtcaga agattctcct ggccaccaag tgccagcatt gccacaaat 2000  
ccttttagga atgggacagg taccttcac ttgttgann nnnnnnnnn 2050  
nnnnnnnnnn nnnnnttgtt tttccttttg actcctgctc ccattaggag 2100  
caggaatggc agtaataaaa gtctgcactt tggtcatttc ttttctcag 2150  
aggaagccc agtgctcact taaacactat cccctcagac tccctgtgtg 2200  
aggcctgcag aggcctgaa tgcacaaatg ggaaaccaag gcacagagag 2250  
gctctcctct cctctcctct ccccgatgt accctcaaaa aaaaaaaat 2300  
gctaaccagt tcttccatta agcctcggt gagtgaggga aagcccagca 2350  
ctgctgcct ctgggtaac tcaccctaag gcctcgccc acctctggct 2400  
atggtaacca cactgggggc ttctccaag ccccgctctt ccagcacttc 2450  
caccggcaga gtccagagc cacttcaccc tgggggtggg ctgtggcccc 2500  
cagtcagctc tgctcaggac ctgctctatt tcagggaaga agatttatgt 2550

attatatgtg gctatatattc ctagagcacc tgtgttttcc tctttctaag 2600  
ccagggtcct gtctggatga cttatgcggt gggggagtgt aaaccggaac 2650  
ttttcatcta tttgaaggcg attaaactgt gtctaatagca 2690

<210> 515  
<211> 364  
<212> PRT  
<213> Homo sapiens

<400> 515  
Met Ser Val Met Val Val Arg Lys Lys Val Thr Arg Lys Trp Glu  
1 5 10 15  
Lys Leu Pro Gly Arg Asn Thr Phe Cys Cys Asp Gly Arg Val Met  
20 25 30  
Met Ala Arg Gln Lys Gly Ile Phe Tyr Leu Thr Leu Phe Leu Ile  
35 40 45  
Leu Gly Thr Cys Thr Leu Phe Phe Ala Phe Glu Cys Arg Tyr Leu  
50 55 60  
Ala Val Gln Leu Ser Pro Ala Ile Pro Val Phe Ala Ala Met Leu  
65 70 75  
Phe Leu Phe Ser Met Ala Thr Leu Leu Arg Thr Ser Phe Ser Asp  
80 85 90  
Pro Gly Val Ile Pro Arg Ala Leu Pro Asp Glu Ala Ala Phe Ile  
95 100 105  
Glu Met Glu Ile Glu Ala Thr Asn Gly Ala Val Pro Gln Gly Gln  
110 115 120  
Arg Pro Pro Pro Arg Ile Lys Asn Phe Gln Ile Asn Asn Gln Ile  
125 130 135  
Val Lys Leu Lys Tyr Cys Tyr Thr Cys Lys Ile Phe Arg Pro Pro  
140 145 150  
Arg Ala Ser His Cys Ser Ile Cys Asp Asn Cys Val Glu Arg Phe  
155 160 165  
Asp His His Cys Pro Trp Val Gly Asn Cys Val Gly Lys Arg Asn  
170 175 180  
Tyr Arg Tyr Phe Tyr Leu Phe Ile Leu Ser Leu Ser Leu Leu Thr  
185 190 195  
Ile Tyr Val Phe Ala Phe Asn Ile Val Tyr Val Ala Leu Lys Ser  
200 205 210  
Leu Lys Ile Gly Phe Leu Glu Thr Leu Lys Glu Thr Pro Gly Thr  
215 220 225  
Val Leu Glu Val Leu Ile Cys Phe Phe Thr Leu Trp Ser Val Val

00978192.101501

230	235	240
Gly Leu Thr Gly Phe His Thr Phe Leu Val Ala Leu Asn Gln Thr		
245	250	255
Thr Asn Glu Asp Ile Lys Gly Ser Trp Thr Gly Lys Asn Arg Val		
260	265	270
Gln Asn Pro Tyr Ser His Gly Asn Ile Val Lys Asn Cys Cys Glu		
275	280	285
Val Leu Cys Gly Pro Leu Pro Pro Ser Val Leu Asp Arg Arg Gly		
290	295	300
Ile Leu Pro Leu Glu Glu Ser Gly Ser Arg Pro Pro Ser Thr Gln		
305	310	315
Glu Thr Ser Ser Ser Leu Leu Pro Gln Ser Pro Ala Pro Thr Glu		
320	325	330
His Leu Asn Ser Asn Glu Met Pro Glu Asp Ser Ser Thr Pro Glu		
335	340	345
Glu Met Pro Pro Pro Glu Pro Pro Glu Pro Pro Gln Glu Ala Ala		
350	355	360

Glu Ala Glu Lys

<210> 516  
 <211> 255  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 36, 38, 88, 118, 135, 193, 213, 222  
 <223> unknown base

<400> 516  
 aaaaccctgt attttttaca atgcaaatac acaatnancc tggagggttt 50  
 tgaattaggt attataggga tgggtgggggtt gatttttntt cctggagggt 100  
 tttggctttg gactctcnct ttctcccaca gagcncttcg accatcaactg 150  
 cccctgggtg gggaattgtg ttggaaagag gaactaccgc tanttctacc 200  
 tcttcatcct ttntctctcc cncctcaciaa tctatgtctt cgccttcaac 250  
 atcgt 255

<210> 517  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 517

caacgtgatt tcaaagctgg gctc 24

<210> 518

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 518

gcctcgatc aagaatttcc 20

<210> 519

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 519

agtggaagtc gacctccc 18

<210> 520

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 520

ctcacctgaa atctctcata gcc 24

<210> 521

<211> 50

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 521

cgcaaaaccc attttgggag caggaattcc aatcatgtct gtgatggtgg 50

<210> 522

<211> 1679

<212> DNA

<213> Homo sapiens

<400> 522

gttgtgtcct tcagcaaac agtggattta aatctccttg cacaagcttg 50

agagcaacac aatctatcag gaaagaaaga aagaaaaaaa ccgaacctga 100

caaaaaagaa gaaaaagaag aagaaaaaaa atcatgaaaa ccatccagcc 150  
 aaaaatgcac aattctatct cttgggcaat cttcacgggg ctggctgctc 200  
 tgtgtctctt ccaaggagtg cccgtgcgca gcggagatgc caccttcccc 250  
 aaagctatgg acaacgtgac ggtccggcag ggggagagcg ccaccctcag 300  
 gtgcactatt gacaaccggg tcacccgggt ggcctggcta aaccgcagca 350  
 ccacctctta tgctgggaat gacaagtggg gcctggatcc tcgctgggtc 400  
 cttctgagca acacccaaac gcagtacagc atcgagatcc agaacgtgga 450  
 tgtgtatgac gagggccctt acacctgctc ggtgcagaca gacaaccacc 500  
 caaagacctc taggggccac ctcatgtgac aagtatctcc caaaattgta 550  
 gagatttctt cagatatctc cattaatgaa gggaacaata ttagcctcac 600  
 ctgcatagca actggtagac cagagcctac ggttacttgg agacacatct 650  
 ctcccaaagc ggttggcttt gtgagtgaag acgaatactt ggaaattcag 700  
 ggcatcaccg gggagcagtc aggggactac gagtgcagtg cctccaatga 750  
 cgtggccgcg cccgtggtag ggagagtaaa ggtcaccgtg aactatccac 800  
 catacatttc agaagccaag ggtacagggtg tccccgtggg acaaaagggg 850  
 aactgcagtg gtgaagcctc agcagtcacc tcagcagaat tccagtggta 900  
 caaggatgac aaaagactga ttgaaggaaa gaaaggggtg aaagtggaaa 950  
 acagaccttt cctctcaaaa ctcatcttct tcaatgtctc tgaacatgac 1000  
 tatgggaact aacttgcgt ggctccaac aagctgggcc acaccaatgc 1050  
 cagcatcatg ctatttggtc caggcgccgt cagcgagggtg agcaacggca 1100  
 cgtcgaggag ggcaggctgc gtctggctgc tgcctcttct ggtcttgca 1150  
 ctgcttctca aattttgatg tgagtgcac ttccccaccc gggaaaggct 1200  
 gccgccacca ccaccacca cacaacagca atggcaacac cgacagcaac 1250  
 caatcagata tatacaaatg aaattagaag aaacacagcc tcatgggaca 1300  
 gaaatttgag ggaggggaac aaagaatact ttggggggaa aagagtttta 1350  
 aaaaagaaat tgaaaattgc cttgcagata tttaggtaca atggagtttt 1400  
 cttttcccaa acgggaagaa cacagcacac ccggcttgga cccactgcaa 1450  
 gctgcatcgt gcaacctctt tgggtgccagt gtgggcaagg gctcagcctc 1500  
 tctgcccaca gagtgcacct acgtggaaca ttctggagct ggccatccca 1550

aattcaatca gtccatagag acgaacagaa tgagaccttc cggcccaagc 1600  
 gtggcgctgc gggcactttg gtagactgtg ccaccacggc gtgtgttgtg 1650  
 aaacgtgaaa taaaaagagc aaaaaaaaaa 1679

<210> 523  
 <211> 344  
 <212> PRT  
 <213> Homo sapiens

<400> 523  
 Met Lys Thr Ile Gln Pro Lys Met His Asn Ser Ile Ser Trp Ala  
 1 5 10 15  
 Ile Phe Thr Gly Leu Ala Ala Leu Cys Leu Phe Gln Gly Val Pro  
 20 25 30  
 Val Arg Ser Gly Asp Ala Thr Phe Pro Lys Ala Met Asp Asn Val  
 35 40 45  
 Thr Val Arg Gln Gly Glu Ser Ala Thr Leu Arg Cys Thr Ile Asp  
 50 55 60  
 Asn Arg Val Thr Arg Val Ala Trp Leu Asn Arg Ser Thr Ile Leu  
 65 70 75  
 Tyr Ala Gly Asn Asp Lys Trp Cys Leu Asp Pro Arg Val Val Leu  
 80 85 90  
 Leu Ser Asn Thr Gln Thr Gln Tyr Ser Ile Glu Ile Gln Asn Val  
 95 100 105  
 Asp Val Tyr Asp Glu Gly Pro Tyr Thr Cys Ser Val Gln Thr Asp  
 110 115 120  
 Asn His Pro Lys Thr Ser Arg Val His Leu Ile Val Gln Val Ser  
 125 130 135  
 Pro Lys Ile Val Glu Ile Ser Ser Asp Ile Ser Ile Asn Glu Gly  
 140 145 150  
 Asn Asn Ile Ser Leu Thr Cys Ile Ala Thr Gly Arg Pro Glu Pro  
 155 160 165  
 Thr Val Thr Trp Arg His Ile Ser Pro Lys Ala Val Gly Phe Val  
 170 175 180  
 Ser Glu Asp Glu Tyr Leu Glu Ile Gln Gly Ile Thr Arg Glu Gln  
 185 190 195  
 Ser Gly Asp Tyr Glu Cys Ser Ala Ser Asn Asp Val Ala Ala Pro  
 200 205 210  
 Val Val Arg Arg Val Lys Val Thr Val Asn Tyr Pro Pro Tyr Ile  
 215 220 225  
 Ser Glu Ala Lys Gly Thr Gly Val Pro Val Gly Gln Lys Gly Thr

09978192 101501

230	235	240
Leu Gln Cys Glu Ala Ser Ala Val Pro Ser Ala Glu Phe Gln Trp		
245	250	255
Tyr Lys Asp Asp Lys Arg Leu Ile Glu Gly Lys Lys Gly Val Lys		
260	265	270
Val Glu Asn Arg Pro Phe Leu Ser Lys Leu Ile Phe Phe Asn Val		
275	280	285
Ser Glu His Asp Tyr Gly Asn Tyr Thr Cys Val Ala Ser Asn Lys		
290	295	300
Leu Gly His Thr Asn Ala Ser Ile Met Leu Phe Gly Pro Gly Ala		
305	310	315
Val Ser Glu Val Ser Asn Gly Thr Ser Arg Arg Ala Gly Cys Val		
320	325	330
Trp Leu Leu Pro Leu Leu Val Leu His Leu Leu Leu Lys Phe		
335	340	

<210> 524  
 <211> 503  
 <212> DNA  
 <213> Homo sapiens

<400> 524  
 gaaaaaaaaat catgaaaacc atccagccaa aaatgcacaa ttctatctct 50  
 tgggcaatct tcacggggct ggctgctctg tgtctcttcc aaggagtgcc 100  
 cgtgcgacgc ggagatgcc ccttcccca agctatggac aacgtgacgg 150  
 tccggcaggg ggagagcgcc accctcaggt gcactattga caaccgggtc 200  
 acccgggtgg cctggctaaa ccgcagcacc atcctctatg ctgggaatga 250  
 caagtgggtgc ctggatcctc gcgtgggtcct tctgagcaac acccaaacgc 300  
 agtacagcat cgagatccag aacgtggatg tgtatgacga gggcccttac 350  
 acctgctcgg tgcagacaga caaccaccca aagacctcta gggccacct 400  
 cattgtgcaa gtatctccca aaattgtaga gatttcttca gatatctcca 450  
 ttaatgaagg gaacaatatt agcctcacct gcatagcaac tggtagacca 500  
 gag 503

<210> 525  
 <211> 2602  
 <212> DNA  
 <213> Homo sapiens

<400> 525  
 atggctggtg acggcggggc cgggcagggg accggggccg cggcccggga 50



gcggggccagc tgccgggagc cctgaatcac cgcctggccc gactccacca 100  
tgaacgtcgc gctgcaggag ctgggagctg gcagcaacgt gggattccag 150  
aaggggacaa gacagctgtt aggctcacgc acgcagctgg agctggtctt 200  
agcaggtgcc tctctactgc tggctgcaact gcttctgggc tgccttgtgg 250  
ccctaggggt ccagtaccac agagacccat cccacagcac ctgccttaca 300  
gaggcctgca ttcgagtggc tggaaaaatc ctggagtccc tggaccgagg 350  
ggtgagcccc tgtgaggact tttaccagtt ctctgtggg ggctggattc 400  
ggaggaaccc cctgcccgat gggcgttctc gctggaacac cttcaacagc 450  
ctctgggacc aaaaccaggc catactgaag cacctgcttg aaaacaccac 500  
cttcaactcc agcagtgaag ctgagcagaa gacacagcgc ttctacctat 550  
cttgcctaca ggtggagcgc attgaggagc tgggagccca gccactgaga 600  
gacctcattg agaagattgg tggttggaac attacggggc cctgggacca 650  
ggacaacttt atggaggtgt tgaaggcagt agcagggacc tacagggcca 700  
ccccattctt caccgtctac atcagtgccg actctaagag ttccaacagc 750  
aatgttatcc aggtggacca gtctgggctc tttctgccct ctggggatta 800  
ctacttaaac agaactgcca atgagaaagt gctcactgcc tatctggatt 850  
acatggagga actggggatg ctgctgggtg ggcggccac ctccacgagg 900  
gagcagatgc agcaggtgct ggagttggag atacagctgg ccaacatcac 950  
agtgccccag gaccagcggc gcgacgagga gaagatctac cacaagatga 1000  
gcatttcgga gctgcaggct ctggcgccct ccatggactg gcttgagttc 1050  
ctgtctttct tgctgtcacc attggagttg agtgactctg agcctgtggt 1100  
ggtgtatggg atggattatt tgcagcaggt gtcagagctc atcaaccgca 1150  
cggaaccaag catcctgaac aattacctga tctggaacct ggtgcaaaaag 1200  
acaacctcaa gcctggaccg acgctttgag tctgcacaag agaagctgct 1250  
ggagaccctc tatggcacta agaagtcctg tgtgccgagg tggcagacct 1300  
gcatctccaa cacggatgac gcccttggct ttgctttggg gtcactcttc 1350  
gtgaaggcca cgtttgaccg gcaaagcaaa gaaattgcag aggggatgat 1400  
cagcgaaatc cggaccgcat ttgaggaggc cctgggacag ctggtttgga 1450  
tggatgagaa gacccgccag gcagccaagg agaaagcaga tgccatctat 1500

gatatgattg gtttcccaga ctttatcctg gagcccaaag agctggatga 1550  
 tgtttatgac ggggtacgaaa tttctgaaga ttctttcttc caaaacatgt 1600  
 tgaatttgta caacttctct gccaaagtta tggctgacca gctccgcaag 1650  
 cctccagacc gagaccagtg gagcatgacc ccccagacag tgaatgccta 1700  
 ctaccttcca actaagaatg agatcgtctt ccccgctggc atcctgcagg 1750  
 ccccttcta tgcccgcaac caccccaagg ccttgaactt cgggtggcatc 1800  
 ggtgtggtca tgggcatga gttgacgcat gcctttgatg accaagggcg 1850  
 cgagtatgac aaagaaggga acctgcggcc ctggtggcag aatgagtccc 1900  
 tggcagcctt ccggaaccac acggcctgca tggaggaaca gtacaatcaa 1950  
 taccaggtca atggggagag gctcaacggc cggcagacgc tgggggagaa 2000  
 cattactgac aacggggggc tgaaggctgc ctacaatgct taaaaagcat 2050  
 ggctgagaaa gcatggggag gagcagcaac tgccagccgt ggggctcacc 2100  
 aaccaccagc tcttcttcgt gggatttgcc cagggtgtgt gctcgggtccg 2150  
 cacaccagag agctctcacg aggggctggt gaccgacccc cacagccctg 2200  
 cccgcttccg cgtgctgggc actctctcca actcccgtga ctctctgcgg 2250  
 cacttcggct gccctgtcgg ctcccccatg aaccagggc agctgtgtga 2300  
 ggtgtggtag acctggatca ggggagaaat ggccagctgt caccagacct 2350  
 ggggcagctc tcttgacaaa gctgtttgct cttgggttgg gaggaagcaa 2400  
 atgcaagctg ggctgggtct agtccctccc cccacaggt gacatgagta 2450  
 cagaccctcc tcaatcacca cattgtgect ctgctttggg ggtgcccctg 2500  
 cctccagcag agccccacc attcactgtg acatctttcc gtgtcaccct 2550  
 gcctggaaga ggtctgggtg gggaggccag ttcccatagg aaggagtctg 2600  
 cc 2602

<210> 526  
 <211> 736  
 <212> PRT  
 <213> Homo sapiens

<400> 526  
 Met Asn Val Ala Leu Gln Glu Leu Gly Ala Gly Ser Asn Val Gly  
 1 5 10 15  
 Phe Gln Lys Gly Thr Arg Gln Leu Leu Gly Ser Arg Thr Gln Leu  
 20 25 30

Glu	Leu	Val	Leu	Ala	Gly	Ala	Ser	Leu	Leu	Leu	Ala	Ala	Leu	Leu		35	40	45
Leu	Gly	Cys	Leu	Val	Ala	Leu	Gly	Val	Gln	Tyr	His	Arg	Asp	Pro		50	55	60
Ser	His	Ser	Thr	Cys	Leu	Thr	Glu	Ala	Cys	Ile	Arg	Val	Ala	Gly		65	70	75
Lys	Ile	Leu	Glu	Ser	Leu	Asp	Arg	Gly	Val	Ser	Pro	Cys	Glu	Asp		80	85	90
Phe	Tyr	Gln	Phe	Ser	Cys	Gly	Gly	Trp	Ile	Arg	Arg	Asn	Pro	Leu		95	100	105
Pro	Asp	Gly	Arg	Ser	Arg	Trp	Asn	Thr	Phe	Asn	Ser	Leu	Trp	Asp		110	115	120
Gln	Asn	Gln	Ala	Ile	Leu	Lys	His	Leu	Leu	Glu	Asn	Thr	Thr	Phe		125	130	135
Asn	Ser	Ser	Ser	Glu	Ala	Glu	Gln	Lys	Thr	Gln	Arg	Phe	Tyr	Leu		140	145	150
Ser	Cys	Leu	Gln	Val	Glu	Arg	Ile	Glu	Glu	Leu	Gly	Ala	Gln	Pro		155	160	165
Leu	Arg	Asp	Leu	Ile	Glu	Lys	Ile	Gly	Gly	Trp	Asn	Ile	Thr	Gly		170	175	180
Pro	Trp	Asp	Gln	Asp	Asn	Phe	Met	Glu	Val	Leu	Lys	Ala	Val	Ala		185	190	195
Gly	Thr	Tyr	Arg	Ala	Thr	Pro	Phe	Phe	Thr	Val	Tyr	Ile	Ser	Ala		200	205	210
Asp	Ser	Lys	Ser	Ser	Asn	Ser	Asn	Val	Ile	Gln	Val	Asp	Gln	Ser		215	220	225
Gly	Leu	Phe	Leu	Pro	Ser	Arg	Asp	Tyr	Tyr	Leu	Asn	Arg	Thr	Ala		230	235	240
Asn	Glu	Lys	Val	Leu	Thr	Ala	Tyr	Leu	Asp	Tyr	Met	Glu	Glu	Leu		245	250	255
Gly	Met	Leu	Leu	Gly	Gly	Arg	Pro	Thr	Ser	Thr	Arg	Glu	Gln	Met		260	265	270
Gln	Gln	Val	Leu	Glu	Leu	Glu	Ile	Gln	Leu	Ala	Asn	Ile	Thr	Val		275	280	285
Pro	Gln	Asp	Gln	Arg	Arg	Asp	Glu	Glu	Lys	Ile	Tyr	His	Lys	Met		290	295	300
Ser	Ile	Ser	Glu	Leu	Gln	Ala	Leu	Ala	Pro	Ser	Met	Asp	Trp	Leu		305	310	315
Glu	Phe	Leu	Ser	Phe	Leu	Leu	Ser	Pro	Leu	Glu	Leu	Ser	Asp	Ser				

	320		325		330
Glu Pro Val Val	Val Tyr Gly Met Asp	Tyr Leu Gln Gln Val	Ser		
	335		340		345
Glu Leu Ile Asn	Arg Thr Glu Pro Ser	Ile Leu Asn Asn Tyr	Leu		
	350		355		360
Ile Trp Asn Leu	Val Gln Lys Thr Thr	Ser Ser Leu Asp Arg	Arg		
	365		370		375
Phe Glu Ser Ala	Gln Glu Lys Leu Leu	Glu Thr Leu Tyr Gly	Thr		
	380		385		390
Lys Lys Ser Cys	Val Pro Arg Trp Gln	Thr Cys Ile Ser Asn	Thr		
	395		400		405
Asp Asp Ala Leu	Gly Phe Ala Leu Gly	Ser Leu Phe Val Lys	Ala		
	410		415		420
Thr Phe Asp Arg	Gln Ser Lys Glu Ile	Ala Glu Gly Met Ile	Ser		
	425		430		435
Glu Ile Arg Thr	Ala Phe Glu Glu Ala	Leu Gly Gln Leu Val	Trp		
	440		445		450
Met Asp Glu Lys	Thr Arg Gln Ala Ala	Lys Glu Lys Ala Asp	Ala		
	455		460		465
Ile Tyr Asp Met	Ile Gly Phe Pro Asp	Phe Ile Leu Glu Pro	Lys		
	470		475		480
Glu Leu Asp Asp	Val Tyr Asp Gly Tyr	Glu Ile Ser Glu Asp	Ser		
	485		490		495
Phe Phe Gln Asn	Met Leu Asn Leu Tyr	Asn Phe Ser Ala Lys	Val		
	500		505		510
Met Ala Asp Gln	Leu Arg Lys Pro Pro	Ser Arg Asp Gln Trp	Ser		
	515		520		525
Met Thr Pro Gln	Thr Val Asn Ala Tyr	Tyr Leu Pro Thr Lys	Asn		
	530		535		540
Glu Ile Val Phe	Pro Ala Gly Ile Leu	Gln Ala Pro Phe Tyr	Ala		
	545		550		555
Arg Asn His Pro	Lys Ala Leu Asn Phe	Gly Gly Ile Gly Val	Val		
	560		565		570
Met Gly His Glu	Leu Thr His Ala Phe	Asp Asp Gln Gly Arg	Glu		
	575		580		585
Tyr Asp Lys Glu	Gly Asn Leu Arg Pro	Trp Trp Gln Asn Glu	Ser		
	590		595		600
Leu Ala Ala Phe	Arg Asn His Thr Ala	Cys Met Glu Glu Gln	Tyr		
	605		610		615

Asn	Gln	Tyr	Gln	Val	Asn	Gly	Glu	Arg	Leu	Asn	Gly	Arg	Gln	Thr
				620					625					630
Leu	Gly	Glu	Asn	Ile	Thr	Asp	Asn	Gly	Gly	Leu	Lys	Ala	Ala	Tyr
				635					640					645
Asn	Ala	Tyr	Lys	Ala	Trp	Leu	Arg	Lys	His	Gly	Glu	Glu	Gln	Gln
				650					655					660
Leu	Pro	Ala	Val	Gly	Leu	Thr	Asn	His	Gln	Leu	Phe	Phe	Val	Gly
				665					670					675
Phe	Ala	Gln	Val	Trp	Cys	Ser	Val	Arg	Thr	Pro	Glu	Ser	Ser	His
				680					685					690
Glu	Gly	Leu	Val	Thr	Asp	Pro	His	Ser	Pro	Ala	Arg	Phe	Arg	Val
				695					700					705
Leu	Gly	Thr	Leu	Ser	Asn	Ser	Arg	Asp	Phe	Leu	Arg	His	Phe	Gly
				710					715					720
Cys	Pro	Val	Gly	Ser	Pro	Met	Asn	Pro	Gly	Gln	Leu	Cys	Glu	Val
				725					730					735

Trp

<210> 527  
 <211> 4308  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 1478, 3978, 4057-4058, 4070  
 <223> unknown base

<400> 527  
 gcccgccct ccgcccctccg cactcccgcc tccctccctc cggccgctcc 50  
 cgcgcctcc tccctccctc ctcccagct gtcccgctcg cgtcatgcgc 100  
 agcctcccg ccccgccggc cccgctgctg ctctcgggc tgcctgctgct 150  
 cggctcccg cggcccgcg gcgcccggcc agagccccc gtgctgccc 200  
 tccgttctga gaaggagcgc ctgcccgttc ggggagcggc aggtaggtgg 250  
 gcgcccgggg gaggcgcggg cggggagtcg ggctcggggc gagtcagcgc 300  
 cagcccggag ggggcgcggg gcgcaggtgg ctcggcgcgg cgggcggccc 350  
 ggaggggtgg cgggggcaga agggcgcggt gcctgggacc cgggacccgc 400  
 gggcagcccc cggggcggca cacggcgoga gctgggcagc ggcctccagc 450  
 caagcccgtc cccgcaggct gcaccttcgg cgggaaggtc tatgccttgg 500

acgagacgtg gcacccggac ctaggggagc cattcggggt gatgcgctgc 550  
 gtgctgtgcg cctgcgaggc gcagtgggt cgccgtacca ggggccctgg 600  
 cagggtcagc tgcaagaaca tcaaaccaga gtgccaacc ccggcctgtg 650  
 ggcagccgcg ccagctgccg ggacactgct gccagacctg ccccaggac 700  
 ttctgtggcg tgctgacagg gccgaggtcg caggcgggtg caccagcccg 750  
 agtctcgctg ctgcgctcta gcctccgctt ctctatctcc tacaggcggc 800  
 tggaccgcc taccaggatc cgcttctcag actccaatgg cagtgtcctg 850  
 tttgagcacc ctgcagcccc caccgaagat ggcttggctt gtgggggtgtg 900  
 gcgggcagtg cctcggttgt ctctgcggct ccttagggca gaacagctgc 950  
 atgtggcact tgtgacactc actcaccctt caggggaggt ctgggggcct 1000  
 ctcatccggc accgggccct gtcccagag accttcagt ccatacctgac 1050  
 tctagaaggc ccccaccagc agggcgtagg gggcatcacc ctgctcactc 1100  
 tcagtgcac agaggactcc ttgcattttt tgctgctctt ccgaggcctt 1150  
 gcaggactaa ccaggttcc cttagagctc cagattctac accaggggca 1200  
 gctactgcga gaacttcagg ccaatgtctc agcccaggaa ccaggctttg 1250  
 ctgaggtgct gcccaacctg acagtccagg agatggactg gctggtgctg 1300  
 ggggagctgc agatggccct ggagtgggca ggcaggccag ggctgcgcat 1350  
 cagtggacac attgctgcc ggaagagctg cgacgtcctg caaagtgtcc 1400  
 tttgtggggc taatgcctg atcccagtc aaacgggtgc tgccggctca 1450  
 gccagcctca ctctgctagg aaatggcncc ctgatcctcc aggtgcaatt 1500  
 ggtagggaca accagtgagg tgggtggccat gacactggaa accaagcctc 1550  
 agcggagggg tcagcccaact gtctgtgcc acatggctgg cctatcctcc 1600  
 cctgccccca ggccgtgggt atctgccctg ggctgggggt cccgaggggc 1650  
 tcatatgctg ctgcagaatg agctcttct gaacgtgggc accaaggact 1700  
 tcccagacgg agagcttcgg gggcaacgtg gctgccctgc cctactgtgg 1750  
 ggcatagcgc ccgccctgcc cgtgcccta gcaggagccc tgggtgctacc 1800  
 ccctgtgaag agccaagcag cagggcacgc ctggctttcc ttggataccc 1850  
 actgtcacct gcactatgaa gtgctgctgg ctgggcttgg tggctcagaa 1900  
 caaggcactg tcaactgcca cctccttggg cctcctggaa cgccagggcc 1950

tcggcggctg ctgaaggat tctatggctc agaggcccag ggtgtggtga 2000  
aggacctgga gccggaactg ctgcggcacc tggcaaaagg catggcttcc 2050  
ctgatgatca ccaccaaggt agccccagag gggagctccg agggcagcct 2100  
ctcctcccag gtgcacatag ccaaccaatg tgaggttggc ggactgcgcc 2150  
tggaggcggc cggggccgag ggggtgcggg cgctgggggc tccggataca 2200  
gcctctgctg cgccgcctgt ggtgcctggt ctcccggccc tagcgcccg 2250  
caaacctggt ggtcctgggc ggccccgaga cccaacaca tgcttcttcg 2300  
aggggcagca gcgccccac ggggtcgct gggcgcccaa ctacgaccg 2350  
ctctgctcac tctgcacctg ccagagacga acggtgatct gtgaccgggt 2400  
ggtgtgcca ccgcccagct gccacaccc ggtgcaggct cccgaccagt 2450  
gctgccctgt ttgccctggc tgctattttg atggtgaccg gagctggcgg 2500  
gcagcgggta cgcggtggca ccccgttgtg cccccctttg gcttaattaa 2550  
gtgtgctgtc tgcacctgca agcagggggg cactggagag gtgactgtg 2600  
agaaggtgca gtgtccccg ctggcctgtg ccagcctgt gcgtgtcaac 2650  
cccaccgact gctgcaaaca gtgtccagggt gagggccacc ccagctggg 2700  
ggaccccatg caggctgatg ggccccggg ctgccgtttt gctgggcagt 2750  
ggttcccaga gagtcaagc tggcaccct cagtgcccc gtttgagag 2800  
atgagctgta tcacctgcag atgtggggta agtggggagc agaggcttgt 2850  
gtgaggtggg tactgggagc ctggtctgga gtagggagac cttcccaggg 2900  
aggtccctga agaagctgaa ggtcactgtg tcccagtgcc tctgggggac 2950  
actcagtgtc tgctctgtct tgtaccaggc aggggtgcct cactgtgagc 3000  
gggatgactg ttactgcca ctgtcctgtg gctcggggaa ggagagtcga 3050  
tgctgttccc gctgcacggc ccaccggcg cgtaagtga ggagtccagg 3100  
gtcagcagct gtgagtggag ggctcacctg cctgtgggac tcctgatcag 3150  
ggaaggagc actcactgtg tgcaggaaca gtgcagcctg cctcacaagt 3200  
gccattccaa tccaccctca cagcaacctg gtggaattgt tatttatgac 3250  
cttttcttta caaatgagat ttctgaagct cagagaaatt aagcaacgag 3300  
atgaaggtca ccagctgtg tgcactgacc tgtttagaaa atactggcct 3350  
ttctgggacc aaggcaggga tgctttgcc tgccctctat gcctctctgt 3400

gcctctccac tccctctccc ctctccaac attccctccc ttctgtctcc 3450  
 agcagcccca gagaccagaa ctgatccaga gctggagaaa gaagccgaag 3500  
 gctcttaggg agcagccaga gggccaagtg accaagagga tggggcctga 3550  
 gctggggaag ggggtggcatc gaggaccttc ttgcattctc ctgtgggaag 3600  
 cccagtgcct ttgtctctct gtcctgcctc tactcccacc cccactacct 3650  
 ctgggaacca cagctccaca agggggagag gcagctgggc cagaccgagg 3700  
 tcacagccac tccaagtcct gccctgccac cctcggcctc tgcctggaa 3750  
 gccccacccc tttcttctg tacataatgt cactggcttg ttgggatttt 3800  
 taatttatct tcaactcagca ccaagggccc cggacactcc actcctgctg 3850  
 cccctgagct gagcagagtc attattggag agttttgtat ttattaaaac 3900  
 atttcttttt cagtcttttg gcatgagggt ggctctttgt ggccaggaac 3950  
 ctgagtgggg cctggtggag aaggggcnga gagtaggagg tgagagagag 4000  
 gagctctgac acttggggag ctgaaagaga cctggagagg cagaggatag 4050  
 cgtggcnntt ggctggcatn cctgggttcc gcagaggggc tggggatggt 4100  
 tcttgagatg gtctagagac tcaagaattt agggaaagtag aagcaggatt 4150  
 ttgactcaag tttagtttcc cacatcgctg gcctgtttgc tgacttcattg 4200  
 tttgaagttg ctccagagag agaatcaaag gtgtcaccag cccctctctc 4250  
 cctccttccc ttcccttccc tttctttccc tcccctcccc tcccctcccc 4300  
 tcccctcc 4308

<210> 528  
 <211> 1285  
 <212> DNA  
 <213> Homo sapiens

<400> 528  
 ggccgagcgg ggggtgctgcg cggcgccgt gatggctggt gacggcggg 50  
 ccgggcaggg gaccggggcc gcggcccggg agcgggccag ctgccgggag 100  
 ccctgaatca ccgcctggcc cgactccacc atgaacgtcg cgctgcagga 150  
 gctgggagct ggcagcaacg tgggattcca gaaggggaca agacagctgt 200  
 taggctcacg cacgcagctg gagctggtct tagcaggtgc ctctctactg 250  
 ctggctgcac tgcttctggg ctgccttgtg gccctagggg tccagtacca 300  
 cagagacca tcccacagca cctgccttac agaggcctgc attcgagtgg 350



ctggaaaaat cctggagtcc ctggaccgag gggtagagccc ctgtgaggac 400  
 ttttaccagt tctcctgtgg gggctggatt cggaggaacc ccctgcccga 450  
 tgggcgttct cgctggaaca ccttcaacag cctctgggac caaaaccagg 500  
 ccatactgaa gcacctgctt gaaaacacca ccttcaactc cagcagttaa 550  
 gctgagcaga agacacagcg cttctaccta tcttgccctac aggtggagcg 600  
 cattgaggag ctgggagccc agccactgag agacctcatt gagaagattg 650  
 gtggttgaa cattacgggg ccctgggacc aggacaactt tatggaggtg 700  
 ttgaaggcag tagcaggagc ctacagggcc accccattct tcaccgtcta 750  
 catcagtgcc gactctaaga gttccaacag caatgttatc caggtggacc 800  
 agtctgggct ctttctgccc tctcgggatt actacttaaa cagaactgcc 850  
 aatgagaaag taaggaacat cttccgaacc cccatcccta cccctggctg 900  
 agctgggctg atccctgttg acttttccct ttgccaaggg tcagagcagg 950  
 gaaggtgagc ctatcctgtc acctagttaa caaactgccc ctcccttctt 1000  
 tcttcttttc ttctccctc cctcccttct tctccctttt ccttccctcc 1050  
 ttctctttat tcttctagta ggtttcatag acacctactg tgtgccaggt 1100  
 ccagtggggg aattcggaga tataagtttc cgagccattg ccacaggaag 1150  
 cgttcagtgt cgatgggttc atggacctag ataggctgat aacaaagctc 1200  
 acaagagggt cctgaggatt caggagagac ttatggagcc agcaaagtct 1250  
 tctgaagag attgcatttg agccaggctc tgtag 1285

<210> 529  
 <211> 1380  
 <212> DNA  
 <213> Homo sapiens

<400> 529  
 atgcctacta ccttccaact aagaatgaga tcgtcttccc cgctggcatc 50  
 ctgcaggccc ccttctatgc ccgcaaccac cccaaggccc tgaacttcgg 100  
 tggcatcggg gtggtcatgg gccatgagtt gacgcatgcc tttgatgacc 150  
 aagggcgcca gtatgacaaa gaagggaacc tgcggccctg gtggcagaat 200  
 gagtccctgg cagccttccg gaaccacacg gcctgcatgg aggaacagta 250  
 caatcaatac caggtaaatg gggagaggct caacggccgc cagacgctgg 300  
 gggagaacat tgctgacaac ggggggctga aggctgccta caatgcttac 350

aaagcatggc tgagaaagca tggggaggag cagcaactgc cagccgtggg 400  
gctcaccaac caccagctct tcttcgtggg atttgcccag gtgtggtgct 450  
cggtccgcac accagagagc tctcacgagg ggctggtgac cgacccccac 500  
agccctgccc gcttccgcgt gctgggcaact ctctccaact cccgtgactt 550  
cctgoggcac ttcggctgcc ctgtcggctc ccccatgaac ccagggcagc 600  
tgtgtgaggt gtggtagacc tggatcaggg gagaaatggc cagctgtcac 650  
cagacctggg gcagctctcc tgacaaagct gtttgcctt gggttgggag 700  
gaagcaaagc caagctgggc tgggtctagt cctcccccc cacaggtgac 750  
atgagtacag accctcctca atcaccacat tgtgcctctg ctttgggggt 800  
gccctgcct ccagcagagc cccaccatt cactgtgaca tctttccgtg 850  
tcacctgcc tggaagaggt ctgggtgggg aggccagttc ccataggaag 900  
gagtctgcct cttctgtccc caggctcact cagcctggcg gccatggggc 950  
ctgccgtgcc tgcccactg tgaccacag gcctgggtgg tgtacctcct 1000  
ggacttctcc ccaggctcac tcagtgcga cttaggggtg gactcagctc 1050  
tgtctggctc accctcacgg gctaccccca cctcaccctg tgctccttgt 1100  
gccactgctc ccagtgtgc tgctgacct cactgacagc tcctagtggg 1150  
agcccaaggc cctctgaaag cctcctgctg cccactgttt ccctgggctg 1200  
agaggggaag tgcatatgtg tagcgggtac tggttcctgt gtcttagggc 1250  
acaagcctta gcaaatgatt gattctccct ggacaaagca ggaaagcaga 1300  
tagagcaggg aaaaggaaga acagagttta tttttacaga aaagagggtg 1350  
ggagggtgtg gtcttgccc ttataggacc 1380

<210> 530

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 530

gaagcagtgc agccagcagt agagaggcac ctgctaaga 39

<210> 531

<211> 24

<212> DNA

<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 531  
acgcagctgg agctggtctt agca 24

<210> 532  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 532  
ggtactggac ccctagggcc acaa 24

<210> 533  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 533  
cctcccagcc gagaccagtg g 21

<210> 534  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 534  
ggtcctataa gggccaagac c 21

<210> 535  
<211> 44  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 535  
gactagttct agatcgcgag cggccgccct tttttttttt tttt 44

<210> 536  
<211> 16  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 536  
cggacgcgtg ggtcga 16

<210> 537  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 537  
cggccgtgat ggctggtgac g 21

<210> 538  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 538  
ggcagactcc ttcttatggg 20

<210> 539  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 539  
ggcacttcat ggtccttgaa a 21

<210> 540  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 540  
cggatgtgtg tgaggccatg cc 22

<210> 541  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 541  
gaaagtaacc acggaggtca agat 24

<210> 542  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 542  
 cctcctccga gactgaaagc t 21  
  
 <210> 543  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 543  
 tcgcggttgct ttttctcgcg tg 22  
  
 <210> 544  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 544  
 gcgtgcgtca ggttcca 17  
  
 <210> 545  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 545  
 cgttcgtgca gcgtgtgta 19  
  
 <210> 546  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 546  
 cttcctcacc acctgcgacg gg 22  
  
 <210> 547  
 <211> 23  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 547  
ggtaggcggg cctatagatg gtt 23

<210> 548  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 548  
agatgtggat gaatgcagtg cta 23

<210> 549  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 549  
atcaacaccg ccggcagtta ctgg 24

<210> 550  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 550  
acagagtgta ccgtctgcag aca 23

<210> 551  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 551  
agcctcctgg tgcactcct 19

<210> 552  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 552  
cgactccctg agcgagcaga tttcc 25

<210> 553  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 553  
gctgggcagt cacgagtctt 20

<210> 554  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 554  
aatcctccat ctcagatctt ccag 24

<210> 555  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 555  
cctcagcggc aacagccggc c 21

<210> 556  
<211> 15  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 556  
tgggccaagg gctgc 15

<210> 557  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 557

tggtggataa ccaacaagat gg 22

<210> 558

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 558

gagtctgcat ccacaccact cttaaagttc tcaa 34

<210> 559

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 559

caggtgctct tttcagtcac gttt 24

<210> 560

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 560

tggccattct caggacaaga g 21

<210> 561

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetic oligonucleotide probe

<400> 561

cagtaatgcc atttgctgc ctgcat 26

<210> 562

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 562

tgcttggaat cacatgaca 19

<210> 563



<211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> synthetic oligonucleotide probe  
  
 <400> 563  
 tgtggcacag acccaatcct 20  
  
 <210> 564  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 564  
 gaccctgaag gcctccggcc t 21  
  
 <210> 565  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 565  
 gagagaggga aggcagctat gtc 23  
  
 <210> 566  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 566  
 cagcccctct ctttcacctg t 21  
  
 <210> 567  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 567  
 ccatcctgtg cagctgacac acagc 25  
  
 <210> 568  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 568  
gccaggctat gaggtcctt 20

<210> 569  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 569  
ttcaagttcc tgaagccgat tat 23

<210> 570  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 570  
ccaacttccc tccccagtgc cct 23

<210> 571  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 571  
ttggggaagg tagaatttcc ttgtat 26

<210> 572  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 572  
cccttctgcc tccaattct 20

<210> 573  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 573  
tctcctccgt ccccttctc cact 24

<210> 574  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 574  
tgagccactg ccttgatta 20

<210> 575  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 575  
tctgcagacg cgatggataa 20

<210> 576  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 576  
ccgaaaataa aacatgccc cttctg 26

<210> 577  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 577  
cacgtggcct ttcacactga 20

<210> 578  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 578  
acttgatgaca gcagtatgct gtctt 25

<210> 579  
 <211> 26  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 579  
 aagcttctgt tcaatcccag cggtcc 26  
  
 <210> 580  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 580  
 atgcacaggc tttttctggt aa 22  
  
 <210> 581  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 581  
 gcaggaaacc ttcgaatctg ag 22  
  
 <210> 582  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 582  
 acacctgagg cacctgagag aggaactct 29  
  
 <210> 583  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 583  
 gacagcccag tacacctgca a 21  
  
 <210> 584  
 <211> 21  
 <212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 584

gacggctgga tctgtgagaa a 21

<210> 585

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 585

cacaactgct gaccccgccc a 21

<210> 586

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 586

ccaggatacg acatgctgca 20

<210> 587

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 587

aaactccaac ctgtatcaga tgca 24

<210> 588

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 588

ccccaagcc cttagactct aagcc 25

<210> 589

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 589  
gacccggcac cttgctaac 19

<210> 590  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 590  
ggacggtcag tcaggatgac a 21

<210> 591  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 591  
ttcggcatca tctcttccct ctccc 25

<210> 592  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 592  
acaaaaaaaaa gggaacaaaa tacga 25

<210> 593  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 593  
ctttgaatag aagacttctg gacaattt 28

<210> 594  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 594

ttgcaactgg gaatatacca cgacatgaga 30

<210> 595

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 595

tagggtgcta atttgtgcta taacct 26

<210> 596

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 596

ggctctgagt ctctgcttga 20

<210> 597

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 597

tccaacaacc attttcctct ggtcc 25

<210> 598

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 598

aagcagtagc cattaacaag tca 23

<210> 599

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 599

caagcgtcca gggtttattga 20

<210> 600

<211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 600  
     gactacaagg cgctcagcta 20  
  
 <210> 601  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 601  
     ccggctgggt ctcaactctc c 21  
  
 <210> 602  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 602  
     cgttcgtgca gcgtgtgta 19  
  
 <210> 603  
 <211> 22  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 603  
     cttcctcacc acctgacgacg gg 22  
  
 <210> 604  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 604  
     ggtaggcggt cctatagatg gtt 23  
  
 <210> 605  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence



<220>  
<223> Synthetic oligonucleotide probe

<400> 605  
agatgtggat gaatgcagtg cta 23

<210> 606  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 606  
atcaacaccg ccggcagtta ctgg 24

<210> 607  
<211> 23  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 607  
acagagtgta ccgtctgcag aca 23

<210> 608  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 608  
agcctcctgg tgcactcct 19

<210> 609  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 609  
cgactccctg agcgagcaga tttcc 25

<210> 610  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 610  
gctgggcagt cacgagtctt 20

<210> 611  
<211> 2840  
<212> DNA  
<213> Homo Sapien

<400> 611  
cccacgcgtc cgagccgccc gagaattaga cacactccgg acgcggccaa 50  
aagcaaccga gaggagggga ggcaaaaaca ccgaaaaaca aaaagagaga 100  
aacaacaccc aacaactggg gtgggggggaa gaaagaaaga aaagaaaccc 150  
accacccac caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaatc 200  
ctgtggcgcg ccgcctgggt cccgggaaga ctgccagca ccagggggtg 250  
ggggagtgcg agctgaaagc tgctggagag tgagcagccc tagcagggat 300  
ggacatgatg ctgttggtgc aggggtgcttg ttgctcgaac cagtggctgg 350  
cggcgggtgct cctcagcctg tgctgcctgc taccctcctg cctcccggct 400  
ggacagagtg tggacttccc ctgggcggcc gtggacaaca tgatggtcag 450  
aaaaggggac acggcgggtgc ttaggtgtta tttggaagat ggagcttcaa 500  
aggggtgcctg gctgaaccgg tcaagtatta tttttgcggg aggtgataag 550  
tggtcagtgg atcctcgagt ttcaatttca acattgaata aaagggacta 600  
cagcctccag atacagaatg tagatgtgac agatgatggc ccatacacgt 650  
gttctgttca gactcaacat acaccagaa caatgcaggt gcatctaact 700  
gtgcaagttc ctctaagat atatgacatc tcaaatgata tgaccgtcaa 750  
tgaaggaacc aacgtcactc ttacttgttt ggccactggg aaaccagagc 800  
cttcatttcc ttggcgacac atctcccat cagcaaaacc atttgaaaat 850  
ggacaatatt tggacattta tggaattaca agggaccagg ctggggaata 900  
tgaatgcagt gcggaaaatg ctgtgtcatt ccagatgtg aggaaagtaa 950  
aagttgttgt caactttgct cctactattc aggaaattaa atctggcacc 1000  
gtgacccccg gacgcagtgg cctgataaga tgtgaaggtg caggtgtgcc 1050  
gcctccagcc tttgaatggt acaaaggaga gaagaagctc ttcaatggcc 1100  
aacaaggaat tattattcaa aatttttagca caagatccat tctactgtt 1150  
accaacgtga cacaggagca cttcggcaat tatacctgtg tggctgcaa 1200  
caagctaggc acaaccaatg cgagcctgcc tottaaccct ccaagtacag 1250

0997819101501

cccagtatgg aattaccggg agcgcctgatg ttcttttctc ctgctggtac 1300  
 cttgtgttga cactgtcctc tttcaccagc atattctacc tgaagaatgc 1350  
 cattctacaa taaattcaaa gaccataaa aggccttttaa ggattctctg 1400  
 aaagtgctga tggctggatc caatctggta cagtttggtta aaagcagcgt 1450  
 gggatataat cagcagtgc tcatgggga tgatcgccctt ctgtagaatt 1500  
 gctcattatg taaatacttt aattctactc ttttttgatt agctacatta 1550  
 ccttgtgaag cagtacacat tgcctttttt ttaagacgtg aaagctctga 1600  
 aattactttt agaggatatt aattgtgatt tcatgtttgt aatctacaac 1650  
 ttttcaaaag cattcagtca tggctctgcta gggtgcaggc tgtagtttac 1700  
 aaaaacgaat attgcagtga atatgtgatt ctttaaggct gcaatacaag 1750  
 cattcagttc cctgtttcaa taagagtcaa tccacattta caaagatgca 1800  
 tttttttctt ttttgataaa aaagcaaata atattgcctt cagattattt 1850  
 cttcaaaata taacacatat ctagattttt ctgcttgcat gatattcagg 1900  
 tttcaggaat gagccttgta atataactgg ctgtgcagct ctgcttctct 1950  
 ttctgtgaag ttcagcatgg gtgtgccttc atacaataat atttttctct 2000  
 ttgtctccaa ctaatatata atgttttgct aaatcttaca atttgaaagt 2050  
 aaaaataaac cagagtgatc aagttaaacc atacactatc tctaagtaac 2100  
 gaaggagcta ttggactgta aaaatctctt cctgcactga caatgggggtt 2150  
 tgagaatttt gccccacact aactcagttc ttgtgatgag agacaattta 2200  
 ataacagtat agtaaataata ccatatgatt tcttttagttg tagctaaatg 2250  
 ttagatccac cgtgggaaat cattcccttt aaaatgacag cacagtccac 2300  
 tcaaaggatt gcctagcaat acagcatctt ttcttttcac tagtccaagc 2350  
 caaaaatttt aagatgattt gtcagaaagg gcacaaagtc ctatcaccta 2400  
 atattacaag agttggtaag cgctcatcat taattttatt ttgtggcagg 2450  
 tattatgaca gtgcacctgg agggatatga tatggatatg gacgttccag 2500  
 agactataat ggcagaaacc aggggtggtta tgaccgctac tcaggaggaa 2550  
 attacagaga caattatgac aactgaaatg agacatgcac ataatataga 2600  
 tacacaagga ataatttctg atccaggatc gtccttccaa atggctgtat 2650  
 ttataaagggt ttttggagct gcaactgaagc atcttatatt atagtatatc 2700

aaccttttgt ttttaaattg acctgccaag gtagctgaag acctttttaga 2750  
 cagttccatc ttttttttta aattttttct gcctatttaa agacaaatta 2800  
 tgggacgttt gtcaaaaaaa aaaaaaaaaa aaaaaaaaaa 2840

<210> 612  
 <211> 352  
 <212> PRT  
 <213> Homo Sapien

<400> 612  
 Met Met Leu Leu Val Gln Gly Ala Cys Cys Ser Asn Gln Trp Leu  
 1 5 10 15  
 Ala Ala Val Leu Leu Ser Leu Cys Cys Leu Leu Pro Ser Cys Leu  
 20 25 30  
 Pro Ala Gly Gln Ser Val Asp Phe Pro Trp Ala Ala Val Asp Asn  
 35 40 45  
 Met Met Val Arg Lys Gly Asp Thr Ala Val Leu Arg Cys Tyr Leu  
 50 55 60  
 Glu Asp Gly Ala Ser Lys Gly Ala Trp Leu Asn Arg Ser Ser Ile  
 65 70 75  
 Ile Phe Ala Gly Gly Asp Lys Trp Ser Val Asp Pro Arg Val Ser  
 80 85 90  
 Ile Ser Thr Leu Asn Lys Arg Asp Tyr Ser Leu Gln Ile Gln Asn  
 95 100 105  
 Val Asp Val Thr Asp Asp Gly Pro Tyr Thr Cys Ser Val Gln Thr  
 110 115 120  
 Gln His Thr Pro Arg Thr Met Gln Val His Leu Thr Val Gln Val  
 125 130 135  
 Pro Pro Lys Ile Tyr Asp Ile Ser Asn Asp Met Thr Val Asn Glu  
 140 145 150  
 Gly Thr Asn Val Thr Leu Thr Cys Leu Ala Thr Gly Lys Pro Glu  
 155 160 165  
 Pro Ser Ile Ser Trp Arg His Ile Ser Pro Ser Ala Lys Pro Phe  
 170 175 180  
 Glu Asn Gly Gln Tyr Leu Asp Ile Tyr Gly Ile Thr Arg Asp Gln  
 185 190 195  
 Ala Gly Glu Tyr Glu Cys Ser Ala Glu Asn Ala Val Ser Phe Pro  
 200 205 210  
 Asp Val Arg Lys Val Lys Val Val Val Asn Phe Ala Pro Thr Ile  
 215 220 225  
 Gln Glu Ile Lys Ser Gly Thr Val Thr Pro Gly Arg Ser Gly Leu

00978192-101501

	230	235	240
Ile Arg Cys Glu	Gly Ala Gly Val Pro	Pro Pro Ala Phe Glu	Trp
	245	250	255
Tyr Lys Gly Glu	Lys Lys Leu Phe Asn	Gly Gln Gln Gly Ile	Ile
	260	265	270
Ile Gln Asn Phe	Ser Thr Arg Ser Ile	Leu Thr Val Thr Asn	Val
	275	280	285
Thr Gln Glu His	Phe Gly Asn Tyr Thr	Cys Val Ala Ala Asn	Lys
	290	295	300
Leu Gly Thr Thr	Asn Ala Ser Leu Pro	Leu Asn Pro Pro Ser	Thr
	305	310	315
Ala Gln Tyr Gly	Ile Thr Gly Ser Ala	Asp Val Leu Phe Ser	Cys
	320	325	330
Trp Tyr Leu Val	Leu Thr Leu Ser Ser	Phe Thr Ser Ile Phe	Tyr
	335	340	345
Leu Lys Asn Ala	Ile Leu Gln		
	350		

<210> 613  
 <211> 1797  
 <212> DNA  
 <213> Homo Sapien

<400> 613  
 agtgggttcga tgggaaggat ctttctccaa gtggttcctc ttgaggggag 50  
 cattttctgct ggctccagga ctttggccat ctataaagct tggcaatgag 100  
 aaataagaaa atttctcaagg aggacgagct cttgagttag acccaacaag 150  
 ctgctttttca ccaaattgca atggagcctt tcgaaatcaa tgttccaaag 200  
 cccaagagga gaaatggggt gaacttctcc ctagctgtgg tggatcatcta 250  
 cctgatcctg ctcaccgctg gcgctgggct gctgggtggc caagttctga 300  
 atctgcaggc gcggctccgg gtctctggaga tgtattttcct caatgacact 350  
 ctggcgggctg aggacagccc gtccttctcc ttgctgcagt cagcacaccc 400  
 tggagaacac ctggctcagg gtgcatcgag gctgcaagtc ctgcaggccc 450  
 aactcacctg ggtccgctc agccatgagc acttgctgca gcgggtagac 500  
 aacttcactc agaaccagg gatgttcaga atcaaagggtg aacaaggcgc 550  
 cccaggtctt caaggtcaca agggggccat gggcatgcct ggtgcccctg 600  
 gcccgccggg accacctgct gagaaggag ccaagggggc tatgggacga 650

gatggagcaa caggccccctc gggaccccaa gggccaccgg gagtcaagg 700  
agaggcgggc ctccaaggac cccaggggtgc tccagggaag caaggagcca 750  
ctggcacccc aggaccccaa ggagagaagg gcagcaaagg cgatgggggt 800  
ctcattggcc caaaagggga aactggaact aaggagaga aaggagacct 850  
gggtctccca ggaagcaaag gggacagggg catgaaagga gatgcaggg 900  
tcatggggcc tcctggagcc caggggagta aaggtgactt cgggaggcca 950  
ggcccaccag gtttggttg ttttcctgga gctaaaggag atcaaggaca 1000  
acctggactg caggggtgtt cgggccctcc tgggtgcagt ggacaccag 1050  
gtgccaaggg tgagcctggc agtgcctggc cccctgggag agcaggactt 1100  
ccagggagcc ccgggagtc aggagccaca ggcctgaaag gaagcaaagg 1150  
ggacacagga cttcaaggac agcaaggaag aaaaggagaa tcaggagttc 1200  
caggccctgc aggtgtgaag ggagaacagg ggagcccagg gctggcaggt 1250  
cccaagggag cccctggaca agctggccag aaggagagacc agggagtga 1300  
aggatcttct ggggagcaag gagtaaggg agaaaaagg gaaagaggtg 1350  
aaaactcagt gtccgtcagg attgtcggca gtagtaaccg aggccgggct 1400  
gaagtttact acagtggtag ctgggggaca atttgcgatg acgagtggca 1450  
aaattctgat gccattgtct tctgccgat gctgggttac tccaaaggaa 1500  
gggccctgta caaagtggga gctggcactg ggcagatctg gctggataat 1550  
gttcagtgtc ggggcacgga gtagacctg tggagctgca ccaagaatag 1600  
ctggggccat catgactgca gccacgagga ggacgcaggc gtggagtgca 1650  
gcgtctgacc cggaaaccct ttcacttctc tgctcccgag gtgtcctcgg 1700  
gctcatatgt gggaaggcag aggatctctg aggagttccc tggggacaac 1750  
tgagcagcct ctggagaggg gccattaata aagctcaaca tcattga 1797

<210> 614  
<211> 520  
<212> PRT  
<213> Homo Sapien

<400> 614  
Met Arg Asn Lys Lys Ile Leu Lys Glu Asp Glu Leu Leu Ser Glu  
1 5 10 15  
Thr Gln Gln Ala Ala Phe His Gln Ile Ala Met Glu Pro Phe Glu  
20 25 30

Ile	Asn	Val	Pro	Lys	Pro	Lys	Arg	Arg	Asn	Gly	Val	Asn	Phe	Ser	35	40	45
Leu	Ala	Val	Val	Val	Ile	Tyr	Leu	Ile	Leu	Leu	Thr	Ala	Gly	Ala	50	55	60
Gly	Leu	Leu	Val	Val	Gln	Val	Leu	Asn	Leu	Gln	Ala	Arg	Leu	Arg	65	70	75
Val	Leu	Glu	Met	Tyr	Phe	Leu	Asn	Asp	Thr	Leu	Ala	Ala	Glu	Asp	80	85	90
Ser	Pro	Ser	Phe	Ser	Leu	Leu	Gln	Ser	Ala	His	Pro	Gly	Glu	His	95	100	105
Leu	Ala	Gln	Gly	Ala	Ser	Arg	Leu	Gln	Val	Leu	Gln	Ala	Gln	Leu	110	115	120
Thr	Trp	Val	Arg	Val	Ser	His	Glu	His	Leu	Leu	Gln	Arg	Val	Asp	125	130	135
Asn	Phe	Thr	Gln	Asn	Pro	Gly	Met	Phe	Arg	Ile	Lys	Gly	Glu	Gln	140	145	150
Gly	Ala	Pro	Gly	Leu	Gln	Gly	His	Lys	Gly	Ala	Met	Gly	Met	Pro	155	160	165
Gly	Ala	Pro	Gly	Pro	Pro	Gly	Pro	Pro	Ala	Glu	Lys	Gly	Ala	Lys	170	175	180
Gly	Ala	Met	Gly	Arg	Asp	Gly	Ala	Thr	Gly	Pro	Ser	Gly	Pro	Gln	185	190	195
Gly	Pro	Pro	Gly	Val	Lys	Gly	Glu	Ala	Gly	Leu	Gln	Gly	Pro	Gln	200	205	210
Gly	Ala	Pro	Gly	Lys	Gln	Gly	Ala	Thr	Gly	Thr	Pro	Gly	Pro	Gln	215	220	225
Gly	Glu	Lys	Gly	Ser	Lys	Gly	Asp	Gly	Gly	Leu	Ile	Gly	Pro	Lys	230	235	240
Gly	Glu	Thr	Gly	Thr	Lys	Gly	Glu	Lys	Gly	Asp	Leu	Gly	Leu	Pro	245	250	255
Gly	Ser	Lys	Gly	Asp	Arg	Gly	Met	Lys	Gly	Asp	Ala	Gly	Val	Met	260	265	270
Gly	Pro	Pro	Gly	Ala	Gln	Gly	Ser	Lys	Gly	Asp	Phe	Gly	Arg	Pro	275	280	285
Gly	Pro	Pro	Gly	Leu	Ala	Gly	Phe	Pro	Gly	Ala	Lys	Gly	Asp	Gln	290	295	300
Gly	Gln	Pro	Gly	Leu	Gln	Gly	Val	Pro	Gly	Pro	Pro	Gly	Ala	Val	305	310	315
Gly	His	Pro	Gly	Ala	Lys	Gly	Glu	Pro	Gly	Ser	Ala	Gly	Ser	Pro			

320	325	330
Gly Arg Ala Gly Leu Pro Gly Ser Pro	Gly Ser Pro Gly Ala Thr	
335	340	345
Gly Leu Lys Gly Ser Lys Gly Asp Thr	Gly Leu Gln Gly Gln Gln	
350	355	360
Gly Arg Lys Gly Glu Ser Gly Val Pro	Gly Pro Ala Gly Val Lys	
365	370	375
Gly Glu Gln Gly Ser Pro Gly Leu Ala	Gly Pro Lys Gly Ala Pro	
380	385	390
Gly Gln Ala Gly Gln Lys Gly Asp Gln	Gly Val Lys Gly Ser Ser	
395	400	405
Gly Glu Gln Gly Val Lys Gly Glu Lys	Gly Glu Arg Gly Glu Asn	
410	415	420
Ser Val Ser Val Arg Ile Val Gly Ser	Ser Asn Arg Gly Arg Ala	
425	430	435
Glu Val Tyr Tyr Ser Gly Thr Trp Gly	Thr Ile Cys Asp Asp Glu	
440	445	450
Trp Gln Asn Ser Asp Ala Ile Val Phe	Cys Arg Met Leu Gly Tyr	
455	460	465
Ser Lys Gly Arg Ala Leu Tyr Lys Val	Gly Ala Gly Thr Gly Gln	
470	475	480
Ile Trp Leu Asp Asn Val Gln Cys Arg	Gly Thr Glu Ser Thr Leu	
485	490	495
Trp Ser Cys Thr Lys Asn Ser Trp Gly	His His Asp Cys Ser His	
500	505	510
Glu Glu Asp Ala Gly Val Glu Cys Ser	Val	
515	520	

<210> 615  
 <211> 647  
 <212> DNA  
 <213> Homo Sapien

<400> 615  
 cccacgcgtc cgaaggcaga caaaggttca tttgtaaaga agtccttcc 50  
 agcacctcct ctctttctcct tttgccc aaa ctcacccagt gagtgtgagc 100  
 atttaagaag catcctctgc caagaccaa aggaaagaag aaaaagggcc 150  
 aaaagccaaa atgaaactga tggtaacttgt tttcaccatt gggctaactt 200  
 tgctgctagg agttcaagcc atgcctgcaa atgcctctc ttgctacaga 250  
 aagatactaa aagatcacia ctgtcacaac cttccggaag gagtagctga 300



cctgacacag attgatgtca atgtccagga tcatttctgg gatgggaagg 350  
 gatgtgagat gatctgttac tgcaacttca gcgaattgct ctgctgcca 400  
 aaagacgttt tctttggacc aaagatctct ttcgtgattc cttgcaacaa 450  
 tcaatgagaa tcttcatgta ttctggagaa caccattcct gatttccac 500  
 aaactgcact acatcagtat aactgcattt ctagtttcta tatagtgcaa 550  
 tagagcatag attctataaa ttcttacttg tctaagacaa gtaaatctgt 600  
 gttaaacaag tagtaataaa agttaattca atctaaaaaa aaaaaa 647

<210> 616  
 <211> 98  
 <212> PRT  
 <213> Homo Sapien

<400> 616  
 Met Lys Leu Met Val Leu Val Phe Thr Ile Gly Leu Thr Leu Leu  
 1 5 10 15  
 Leu Gly Val Gln Ala Met Pro Ala Asn Arg Leu Ser Cys Tyr Arg  
 20 25 30  
 Lys Ile Leu Lys Asp His Asn Cys His Asn Leu Pro Glu Gly Val  
 35 40 45  
 Ala Asp Leu Thr Gln Ile Asp Val Asn Val Gln Asp His Phe Trp  
 50 55 60  
 Asp Gly Lys Gly Cys Glu Met Ile Cys Tyr Cys Asn Phe Ser Glu  
 65 70 75  
 Leu Leu Cys Cys Pro Lys Asp Val Phe Phe Gly Pro Lys Ile Ser  
 80 85 90  
 Phe Val Ile Pro Cys Asn Asn Gln  
 95

<210> 617  
 <211> 2558  
 <212> DNA  
 <213> Homo Sapien

<400> 617  
 cccacgcgtc cgcggacgcg tgggctggac ccaggtctg gagcgaattc 50  
 cagcctgcag ggctgataag cgaggcatta gtgagattga gagagacttt 100  
 accccgcggt ggtggttggg gggcgcgcag tagagcagca gcacaggcgc 150  
 ggggtcccggg aggcggctc tgctcgcgc gagatgtgga atctccttca 200  
 cgaaaccgac tcggctgtgg ccaccgcgcg ccgcccgcgc tggctgtgcg 250  
 ctggggcgct ggtgctggcg ggtggcttct ttctcctcgg ctctctcttc 300

ggggtggttta taaaatcctc caatgaagct actaacatta ctccaaagca 350  
 taatatgaaa gcatttttgg atgaattgaa agctgagaac atcaagaagt 400  
 tcttacataa ttttacacag ataccacatt tagcaggaac agaacaaaac 450  
 tttcagcttg caaagcaa atcaatcccag tggaaagaat ttggcctgga 500  
 ttctgttgag ctagctcatt atgatgtcct gttgtcctac ccaaataaga 550  
 ctcaccccaa ctacatctca ataattaatg aagatggaaa tgagattttc 600  
 aacacatcat tatttgaacc acctcctcca ggatatgaaa atgtttcggg 650  
 tattgtacca cttttcagtg ctttctctcc tcaaggaatg ccagagggcg 700  
 atctagtgtg tgtaactat gcacgaactg aagacttctt taaattggaa 750  
 cgggacatga aaatcaattg ctctgggaaa attgtaattg ccagatatgg 800  
 gaaagttttc agaggaaata aggttaaaaa tgcccagctg gcaggggcca 850  
 aaggagtcat tctctactcc gacctgctg actactttgc tctgggggtg 900  
 aagtcctatc cagacggttg gaatcttcct ggaggtggtg tccagcgtgg 950  
 aaatatccta aatctgaatg gtgcaggaga ccctctcaca ccaggttacc 1000  
 cagcaaatga atatgcttat aggcgtggaa ttgcagaggc tgttggtctt 1050  
 ccaagtattc ctgttcatcc aattggatac tatgatgcac agaagctcct 1100  
 agaaaaaatg ggtggctcag caccaccaga tagcagctgg agaggaagtc 1150  
 tcaaagtgcc ctacaatgtt ggacctggct ttactggaaa cttttctaca 1200  
 caaaaagtca agatgcacat ccactctacc aatgaagtga cgagaattta 1250  
 caatgtgata ggtactctca gaggagcagt ggaaccagac agatatgtca 1300  
 ttctgggagg tcaccgggac tcatgggtgt ttggtggtat tgaccctcag 1350  
 agtggagcag ctgttggtca tgaaattgtg aggagctttg gaacactgaa 1400  
 aaaggaaggg tggagacctg gaagaacaat tttgtttgca agctgggatg 1450  
 cagaagaatt tggctcttct ggttctactg agtgggcaga ggagaattca 1500  
 agactccttc aagagcgtgg cgtggcttat attaagtctg actcatctat 1550  
 agaaggaaac tacactctga gagttgattg tacaccgctg atgtacagct 1600  
 tgggtacacaa cctaacaaaa gagctgaaaa gccctgatga aggctttgaa 1650  
 ggcaaatctc tttatgaaag ttggactaaa aaaagtcctt cccagagtt 1700  
 cagtggcatg cccaggataa gcaaattggg atctggaaat gattttgagg 1750

tgttcttcca acgacttga attgcttcag gcagagcacg gtatactaaa 1800  
 aattgggaaa caaacaaatt cagcggctat ccactgtatc acagtgtcta 1850  
 tgaaacatat gagttggtgg aaaagtttta tgatccaatg tttaaatata 1900  
 acctcactgt ggcccagggt cgaggaggga tgggtgtttga gctagccaat 1950  
 tccatagtgc tcccttttga ttgtcgagat tatgctgtag ttttaagaaa 2000  
 gtatgctgac aaaatctaca gtatttctat gaaacatcca caggaaatga 2050  
 agacatacag tgtatcattt gattcacttt tttctgcagt aaagaatttt 2100  
 acagaaattg cttccaagtt cagtgcagaga ctccaggact ttgacaaaag 2150  
 caaccaata gtattaagaa tgatgaatga tcaactcatg tttctggaaa 2200  
 gagcatttat tgatccatta ggggtaccag acaggccttt ttataggcat 2250  
 gtcattctatg ctccaagcag ccacaacaag tatgcagggg agtcattccc 2300  
 aggaatttat gatgctctgt ttgatattga aagcaaagtg gacccttcca 2350  
 aggcttgggg agaagtgaag agacagattt atgttgcagc cttcacagtg 2400  
 caggcagctg cagagacttt gagtgaagta gcctaagagg attttttaga 2450  
 gaatccgtat tgaatttgtg tggatgtca ctcagaaaga atcgtaatgg 2500  
 gtatattgat aaattttaaa attggtatat ttgaaataaa gttgaatatt 2550  
 atatataa 2558

<210> 618  
 <211> 750  
 <212> PRT  
 <213> Homo Sapien

<400> 618  
 Met Trp Asn Leu Leu His Glu Thr Asp Ser Ala Val Ala Thr Ala  
 1 5 10 15  
 Arg Arg Pro Arg Trp Leu Cys Ala Gly Ala Leu Val Leu Ala Gly  
 20 25 30  
 Gly Phe Phe Leu Leu Gly Phe Leu Phe Gly Trp Phe Ile Lys Ser  
 35 40 45  
 Ser Asn Glu Ala Thr Asn Ile Thr Pro Lys His Asn Met Lys Ala  
 50 55 60  
 Phe Leu Asp Glu Leu Lys Ala Glu Asn Ile Lys Lys Phe Leu His  
 65 70 75  
 Asn Phe Thr Gln Ile Pro His Leu Ala Gly Thr Glu Gln Asn Phe  
 80 85 90

Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu	
				95					100					105	
Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro	
				110					115					120	
Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly	
				125					130					135	
Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly	
				140					145					150	
Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser	
				155					160					165	
Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala	
				170					175					180	
Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn	
				185					190					195	
Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg	
				200					205					210	
Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val	
				215					220					225	
Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys	
				230					235					240	
Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg	
				245					250					255	
Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro	
				260					265					270	
Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu	
				275					280					285	
Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr	
				290					295					300	
Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro	
				305					310					315	
Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly	
				320					325					330	
Pro	Gly	Phe	Thr	Gly	Asn	Phe	Ser	Thr	Gln	Lys	Val	Lys	Met	His	
				335					340					345	
Ile	His	Ser	Thr	Asn	Glu	Val	Thr	Arg	Ile	Tyr	Asn	Val	Ile	Gly	
				350					355					360	
Thr	Leu	Arg	Gly	Ala	Val	Glu	Pro	Asp	Arg	Tyr	Val	Ile	Leu	Gly	
				365					370					375	
Gly	His	Arg	Asp	Ser	Trp	Val	Phe	Gly	Gly	Ile	Asp	Pro	Gln	Ser	

380 385 390

Gly	Ala	Ala	Val	Val	His	Glu	Ile	Val	Arg	Ser	Phe	Gly	Thr	Leu
				395					400					405
Lys	Lys	Glu	Gly	Trp	Arg	Pro	Arg	Arg	Thr	Ile	Leu	Phe	Ala	Ser
				410					415					420
Trp	Asp	Ala	Glu	Glu	Phe	Gly	Leu	Leu	Gly	Ser	Thr	Glu	Trp	Ala
				425					430					435
Glu	Glu	Asn	Ser	Arg	Leu	Leu	Gln	Glu	Arg	Gly	Val	Ala	Tyr	Ile
				440					445					450
Asn	Ala	Asp	Ser	Ser	Ile	Glu	Gly	Asn	Tyr	Thr	Leu	Arg	Val	Asp
				455					460					465
Cys	Thr	Pro	Leu	Met	Tyr	Ser	Leu	Val	His	Asn	Leu	Thr	Lys	Glu
				470					475					480
Leu	Lys	Ser	Pro	Asp	Glu	Gly	Phe	Glu	Gly	Lys	Ser	Leu	Tyr	Glu
				485					490					495
Ser	Trp	Thr	Lys	Lys	Ser	Pro	Ser	Pro	Glu	Phe	Ser	Gly	Met	Pro
				500					505					510
Arg	Ile	Ser	Lys	Leu	Gly	Ser	Gly	Asn	Asp	Phe	Glu	Val	Phe	Phe
				515					520					525
Gln	Arg	Leu	Gly	Ile	Ala	Ser	Gly	Arg	Ala	Arg	Tyr	Thr	Lys	Asn
				530					535					540
Trp	Glu	Thr	Asn	Lys	Phe	Ser	Gly	Tyr	Pro	Leu	Tyr	His	Ser	Val
				545					550					555
Tyr	Glu	Thr	Tyr	Glu	Leu	Val	Glu	Lys	Phe	Tyr	Asp	Pro	Met	Phe
				560					565					570
Lys	Tyr	His	Leu	Thr	Val	Ala	Gln	Val	Arg	Gly	Gly	Met	Val	Phe
				575					580					585
Glu	Leu	Ala	Asn	Ser	Ile	Val	Leu	Pro	Phe	Asp	Cys	Arg	Asp	Tyr
				590					595					600
Ala	Val	Val	Leu	Arg	Lys	Tyr	Ala	Asp	Lys	Ile	Tyr	Ser	Ile	Ser
				605					610					615
Met	Lys	His	Pro	Gln	Glu	Met	Lys	Thr	Tyr	Ser	Val	Ser	Phe	Asp
				620					625					630
Ser	Leu	Phe	Ser	Ala	Val	Lys	Asn	Phe	Thr	Glu	Ile	Ala	Ser	Lys
				635					640					645
Phe	Ser	Glu	Arg	Leu	Gln	Asp	Phe	Asp	Lys	Ser	Asn	Pro	Ile	Val
				650					655					660
Leu	Arg	Met	Met	Asn	Asp	Gln	Leu	Met	Phe	Leu	Glu	Arg	Ala	Phe
				665					670					675

Ile Asp Pro Leu Gly Leu Pro Asp Arg Pro Phe Tyr Arg His Val  
680 685 690

Ile Tyr Ala Pro Ser Ser His Asn Lys Tyr Ala Gly Glu Ser Phe  
695 700 705

Pro Gly Ile Tyr Asp Ala Leu Phe Asp Ile Glu Ser Lys Val Asp  
710 715 720

Pro Ser Lys Ala Trp Gly Glu Val Lys Arg Gln Ile Tyr Val Ala  
725 730 735

Ala Phe Thr Val Gln Ala Ala Ala Glu Thr Leu Ser Glu Val Ala  
740 745 750

<210> 619  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 619  
agatgtgaag gtgcaggtgt gccg 24

<210> 620  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 620  
gaacatcagc gctcccggta attcc 25

<210> 621  
<211> 46  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 621  
ccagcctttg aatggtacaa aggagagaag aagctcttca atggcc 46

<210> 622  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 622  
ccaaactcac ccagtgagtg tgagc 25

<210> 623  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 623  
tgggaaatca ggaatggtgt tctcc 25

<210> 624  
<211> 50  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide probe

<400> 624  
cttgttttca ccattgggct aactttgctg ctaggagttc aagccatgcc 50

09978193-101501  
FOSTOT-25TB2660